

REMARKS

I. Status of the Claims and Amendment

Claims 2, 4, 5, 9, 13, 16-19, 23, 28-30 and 32-35 are all the claims pending in the application. Claims 1, 3, 6-8, 10-12, 14-15, 20-22, 24-27, 31, and 36-37 were previously canceled. Claims 16-19, 23, 28-30, and 32-35 are withdrawn as being directed to non-elected inventions. Claim 2 has been amended to further clarify that “oligonucleotides having the sequence set forth in SEQ ID Nos. 117, 127, 137, 138, 147, 169, 178, 225, 231, 272, 278, 310, 329, 335, 339, 346, 352, 361, 386, 387, 399, 420, 429, 469, 472, or 477 may only be replaced by an oligonucleotide having a sequence entirely complementary to the one of said oligonucleotides being replaced or by an oligonucleotide having at least 80% identity to the one of said 351 oligonucleotides being replaced.” Support for the amendment to claim 2 may be found throughout the specification, for example in the original claims.

In addition, the specification at Table 1a has been amended to correct an apparent typographical error with regard to SEQ ID NO.: 499. Namely, SEQ ID NO: 499 in Table 1a has been corrected to SEQ ID NO: 501. Further, the number of nucleotides has been corrected to “464” instead of “421”. Similarly, SEQ ID NO: 500 has been corrected to SEQ ID NO: 499. These amendments are consistent with the previous amendment filed March 11, 2010 to SEQ ID NOs: 500 and 501 at pages 277-278 of the Substitute Specification.

The third paragraph at page 277 of the Substitute Specification has also been amended to correct the apparent error to the number of nucleotides for SEQ ID NO: 500 so that the nucleotide number is “556” instead of “559”. Support for the correction to this apparent error is provided by the Sequence Listing as evidenced by the BLAST alignment provided herewith.

Further, a new Substitute Sequence Listing is submitted herewith to correct an apparent error with SEQ ID NO:420. Support for the correction to SEQ ID NO: 420, may be found on page 246 of the Substitute Specification filed October 3, 2008 and original Sequence ID 1205 on pages 249-250 of the as-filed specification.. Namely, an error occurred in which 59 nucleotides from the 3' end were not listed. The new Substitute Sequence Listing submitted herewith corrects this apparent error.

No new matter is added.

II. Response to the Objection to the Specification

The Examiner objects to the Amendments filed March 11, 2010, October 3, 2008, and July 6, 2009, under 35 U.S.C. § 132(a) as allegedly introducing new matter into the disclosure.

(a) The first objection concerns the amendment to SEQ ID NO: 36 to indicate that it has 527 nucleotides, rather than the 258 nucleotides previously recited.

(b) The Examiner asserts that the previous amendment to the specification concerning the sequence listing and identification of sequences by SEQ ID NOs is new matter. The Examiner asserts that the response of March 11, 2010 provided a sequence alignment in an attempt to demonstrate that no new matter was added by previous amendments. As detailed in the Office Action on pages 3-7 and 16, the Examiner noted that the alignment previously submitted showed that many of the sequences (SEQ ID NOs) are shorter than the corresponding originally submitted sequences.

With regard to (a), Applicants note that SEQ ID NO:36 contains 527 nucleotides, as determined by counting the nucleotides. In the application as filed this sequence was sequence No. 364. Whilst it was stated that the sequence had 528 nucleotides in the application as filed,

this was an error. This correction is further supported by the new Substitute Sequence Listing which is consistent with the disclosure in the Substitute Specification and as-filed specification.

With regard to (b), Applicants have identified the errors in the previous alignment submission and herewith provide a new alignment to demonstrate that the sequences in the Substitute Specification filed October 3, 2008 (which are consistent with the Substitute Sequence Listing of May 1, 2006) and the sequences in the "PCT application"¹ (which is the as-filed specification of May 19, 2005) are identical and the same.

In this respect, Applicants note that the errors presented in the BLAST alignments previously submitted were due to the propensity of the BLAST program to trim sequences (particularly after "N" bases) so that sequence identity was reported over a smaller region than the full length sequence, or the program failed to perform an appropriate alignment.

Accordingly, Applicants have revisited each comparison and provide herewith a new BLAST comparison for each of the sequences. Applicants also submit herewith a table showing the sequences that were incorrectly aligned and the cause of the error. The sequences not identified by the Examiner but showing errors are highlighted in the Table in bold. The BLAST sequence comparisons that have been corrected in the new BLAST comparison are annotated at the end of the comparison to describe the error that occurred and the remedial measures that were

¹ As the Examiner may recall, in the Amendment filed October 3, 2008, Applicants noted that a Sequence Listing was filed May 1, 2006 containing all the sequences disclosed in the original specification. The Sequence ID numbers listed in the original specification were not in consecutive order, starting at 93 and ending at 1495 (with many numbers missing in between). Additionally, Sequence IDs G6, 61, 490, 892 and 77 appeared at the end of the otherwise numerically increasing list. Subsequently a Sequence Listing was filed on May 1, 2006 in which the sequences were presented in a consecutive list of 501 sequences, but the sequences in the specification were inadvertently not amended at the same time to correspond to the list of 501 sequences. The Substitute Specification filed October 3, 2008 was merely provided to remedy this matter so that the original sequences disclosed correspond to the SEQ ID NOs in the Sequence Listing of May 1, 2006.

taken to allow the appropriate comparison to be made. As discussed above, in most cases, the trimmed sequences removed by the BLAST program were reinstated and the comparison across the full length completed. However, in some cases, where the sequences were misaligned, the sequences were compared in portions and the comparisons merged to generate the comparison of the full sequences (e.g., Sequences 313, 326, 673, 686, 1210, 1225 and 1332 as filed).

Thus, the enclosed new BLAST comparison shows 100% identity between the sequences of the application as filed and those submitted in the Substitute Specification filed October 3, 2008.

Withdrawal of the grounds of objection is respectfully requested.

III. Response to Enablement Rejection

Claims 2, 4-5, 9 and 13 remain rejected under 35 U.S.C. § 112, first paragraph, for lack of enablement.

(A) The Examiner asserts that, due to the new matter issues addressed above, it would be unpredictable for one of skill in the art to determine which nucleic acids are informative in the instant method. That is, it appears the claims are asserted to not be enabled due to the amendments to the specification that have resulted in inconsistencies in the disclosure and thus the unpredictability of the claimed invention.

In response, as discussed above, Applicants have amended the specification to correct apparent typographical errors, and submit herewith a new BLAST sequence alignment to show that the sequences in the Substitute Specification filed October 3, 2008 and the sequences in the as-filed specification of May 1, 2005 are the same. The sequence alignment supports Applicants' previous arguments to demonstrate that the specification contains no new matter,

and that the specification enables one of ordinary skill in the art to make and use the claimed invention.

(B) The Examiner asserts that the use of any fragment of a claimed SEQ ID NO that is (i) at least 30 nucleotides of the SEQ ID NO being replaced, (ii) at least 30 nucleotides and completely complementary to the sequence being replaced, or (iii) at least 80% identity to the sequence being replaced or a fragment thereof, is unpredictable.

First, the Examiner asserts that some SEQ ID NOs are shorter than 30 nucleotides, and allegedly no guidance is provided as to how they could be replaced by fragments of at least 30 nucleotides. For example, the Examiner points to: SEQ ID NO: 117, which is 28 nucleotides; SEQ ID NO: 138, which is 4 nucleotides; SEQ ID NO: 225, which is 17 nucleotides; and SEQ ID NO: 361, which is 12 nucleotides.

Second, the Examiner asserts the specification provides no indication that every or any 30 base fragment of the recited SEQ ID NOs allow detection as the full length sequences taught by the specification to be indicative of differential expression patterns. Specifically, the Examiner notes that several sequences have poly adenine regions longer than 30 nucleotides, and that replacement of the full length claimed nucleic acid sequences with a fragment of the poly adenine would allow for detection of any nucleic acid sequence with a poly T, such as every reverse transcribed RNA, but not the specific sequences of the SEQ ID NO. For example, the Examiner points to: SEQ ID NO: 346 having a stretch of 46 adenines; SEQ ID NO: 335 having a stretch of 33 adenines; and SEQ ID NO: 429 having a stretch of 33 adenines.

In response, and solely to advance prosecution of the present application, claim 2 has been amended to recite that “oligonucleotides having the sequence set forth in SEQ ID Nos. 117, 127, 137, 138, 147, 169, 178, 225, 231, 272, 278, 310, 329, 335, 339, 346, 352, 361, 386, 387,

399, 420, 429, 469, 472, or 477 may only be replaced by an oligonucleotide having a sequence entirely complementary to the one of said oligonucleotides being replaced or by an oligonucleotide having at least 80% identity to the one of said 351 oligonucleotides being replaced.”

Therefore the claimed invention is enabled and withdrawal of the rejection under 35 U.S.C. § 112, first paragraph, is respectfully requested.

IV. Conclusion

In view of the above, reconsideration and allowance of this application are now believed to be in order, and such actions are hereby solicited. If any points remain in issue which the Examiner feels may be best resolved through a personal or telephone interview, the Examiner is kindly requested to contact the undersigned at the telephone number listed below.

The USPTO is directed and authorized to charge all required fees, except for the Issue Fee and the Publication Fee, to Deposit Account No. 19-4880. Please also credit any overpayments to said Deposit Account.

SUGHRUE MION, PLLC
Telephone: (202) 293-7060
Facsimile: (202) 293-7860

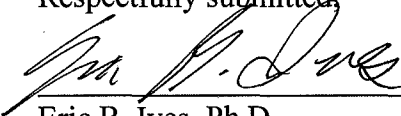
WASHINGTON OFFICE

23373

CUSTOMER NUMBER

Date: December 1, 2010

Respectfully submitted,



Eric B. Ives, Ph.D.

Registration No. 50,928

Sequence No. as filed	Sequence No. in Sequence Listing	Length	Alignment between Seqs as filed and Oct subs	Error	Missing sequence correct in compared sequences	Cause of error
308	11	373	ID over 371	Missing "NC" at 3' end	Yes	BLAST
313	15	554	ID 170/191	Misalignment of sequences	Yes	BLAST
326	24	554	ID 170/191	Misalignment of sequences	Yes	BLAST
327	25	674	ID 671/671	Missing "NAT" at 3' end	Yes	BLAST
364	36	527	ID 524/524	Missing "NCA" at 3' end	Yes	BLAST
403	66	202	ID 200/200	Missing "NG" at 3' end	Yes	BLAST
406	68	644	ID 641/641	Missing "NTC" at 3' end	Yes	BLAST
431	93	131	ID 126/126	Missing "NANCA" at 3' end	Yes	BLAST
433	95	687	ID 684/684	Missing "NTC" at 3' end	Yes	BLAST
446	102	341	ID 336/336	Missing "NANAA" at 3' end	Yes	BLAST
469	116	161	ID 159/159	Missing "NA" at 3' end	Yes	BLAST
471	117	28	ID 8/8	Missing "ATCTGCAGGATCCGTCGACT" at 3' end	Yes	BLAST
483	128	519	ID 516/516	Missing "CGN" at 5' end	Yes	BLAST
518	155	502	ID 499/499	Missing "NAT" at 3' end	Yes	BLAST
631	232	493	ID 491/491	Missing "TN" at 5' end	Yes	BLAST
661	260	256	ID 253/253	Missing "NGG" at 3' end	Yes	BLAST
673	268	683	ID 127/127	Missing 547 nucl. at 5' end, "NNNGGGGAA" at 3' end	Yes	BLAST
679	272	688	ID 682/682	Missing "GNANCN" at 5' end	Yes	BLAST
686	277	603	ID 28/ 28	Misalignment of sequences and majority of the sequence missing	Yes	BLAST
702	292	709	ID 705/705	Missing "GTNN" at 5' end	Yes	BLAST
719	306	492	ID 489/489	Missing "CGN" at 5' end	Yes	BLAST

722	309	327	ID 325/325	Missing "CN" at 5' end	Yes	BLAST
724	310	273	ID 272/272	Missing "N" at 3' end	Yes	BLAST
825	332	741	ID 735/735	Missing "NGGNTT" at 3' end	Yes	BLAST
898	360	511	ID 509/509	Missing "AN" at 5' end	Yes	BLAST
899	361	16	ID 13/13	Missing "TCN" at 5' end	Yes	BLAST
904	364	649	ID 648/648	Missing "N" at 3' end	Yes	BLAST
917	375	483	ID 481/481	Missing "NN" at 5' end	Yes	BLAST
947	379	646	ID 641/641	Missing "NGANG" at 3' end	Yes	BLAST
1071	383	571	ID 569/569	Missing "N" at 5' end and 3' end	Yes	BLAST
1109	389	601	ID 594/594	Missing "NNNNCNN" at 3' end	Yes	BLAST
1125	391	407	ID 404/404	Missing "N" at 5' end and "NT" at 3' end	Yes	BLAST
1193	409	900	ID 896/896	Missing "TNCN" at 5' end	Yes	BLAST
1204	419	365	ID 213/213	Missing from nucleotide 214 at 3' end	Yes	BLAST
1205	420	299	ID 241/241	Missing 58 nucleotides from 3' end	Yes (but missing in Seq. Listing)	BLAST
1210	424	702	ID 68/68	Misaligned and missing large portions from 5' and 3' ends	Yes	BLAST
1220	434	1354	ID1343/1343	Missing "GANNN" at 5' end and "NNNACT" at 3' end	Yes	BLAST
1255	442	928	ID 68/68	Misaligned and missing large portions from 5' and 3' ends	Yes	BLAST
1256	443	954	ID 925/925	Missing "NNNTT.....CCANT" at 3' end	Yes	BLAST
1332	445	689	ID 171/191	Misaligned and missing large portions from 5' and 3' ends	Yes	BLAST
1389	473	896	ID 895/895	Missing "N" at 3' end	Yes	BLAST

1390	474	350	ID 347/347	Missing "TCN" at 5' end	Yes	BLAST
1396	479	912	ID 909/909	Missing "NGG" at 3' end	Yes	BLAST
1450	486	854	ID 851/851	Missing "NTC" at 3' end	Yes	BLAST

Blast reference

BLASTN 2.2.22+ Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Sequence 93 matched with Sequence 1

Query= Sequence ID - 93 nt: 405
Length=405

SEQ ID NO: 1 nt: 405

ALIGNMENTS

Identities = 405/405 (100%), Gaps = 0/405 (0%)

Query	1	GGATCCTGTGGCCACAGAGCTGCCCCAGCAGACGCTCCGCCCCACCCGGTGATGGAGCC	60
Sbjct	1	GGATCCTGTGGCCACAGAGCTGCCCCAGCAGACGCTCCGCCCCACCCGGTGATGGAGCC	60
Query	61	CCGGGGGACAATCGTGCCTGGGGAGGAGCAGGGTACAGCCCATTCCCCAGCCCTGGCT	120
Sbjct	61	CCGGGGGACAATCGTGCCTGGGGAGGAGCAGGGTACAGCCCATTCCCCAGCCCTGGCT	120
Query	121	GACCTGGCCTAGCAGTTTGGCCCTGCTGGCCTTAGCAGGGAGACAGGGGAGCAAAGAACG	180
Sbjct	121	GACCTGGCCTAGCAGTTTGGCCCTGCTGGCCTTAGCAGGGAGACAGGGGAGCAAAGAACG	180
Query	181	CCAAGCCGGAGGCCCGAGGCCAGCCGGCCTCTCGAGAGCCAGAGCAGCAGTTGAATGTAA	240
Sbjct	181	CCAAGCCGGAGGCCCGAGGCCAGCCGGCCTCTCGAGAGCCAGAGCAGCAGTTGAATGTAA	240
Query	241	TGCTGGGGACAGGCATGCTGCCGCCAGTAGGGCGGGGACCCGGACAGCCAGGTGACTACC	300
Sbjct	241	TGCTGGGGACAGGCATGCTGCCGCCAGTAGGGCGGGGACCCGGACAGCCAGGTGACTACC	300
Query	301	AGTCCTGGGGACACACTCACCATAAACACATCCCCAGGCAGGACAGATCGGGGAAGGGGT	360
Sbjct	301	AGTCCTGGGGACACACTCACCATAAACACATCCCCAGGCAGGACAGATCGGGGAAGGGGT	360

PATENT SEQUENCE ALIGNMENT

Query	361	GTGTACCAGGCTATGATTTCTCTTGCATTAAAATGTATTATTATT	405
Sbjct	361	GTGTACCAGGCTATGATTTCTCTTGCATTAAAATGTATTATTATT	405

Sequence 108 matched with Sequence 2

Query= Sequence ID - 108 nt: 550
Length=550

SEQ ID NO: 2 nt: 550

ALIGNMENTS

Identities = 550/550 (100%), Gaps = 0/550 (0%)

Query	1	GGCTTTGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCATCTGGAACGCAACATAGA	60
Sbjct	1	GGCTTTGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCATCTGGAACGCAACATAGA	60
Query	61	NACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCAGCCAGACACCCTGAA	120
Sbjct	61	NACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCAGCCAGACACCCTGAA	120
Query	121	CCAGGGGGAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAA	180
Sbjct	121	CCAGGGGGAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAA	180
Query	181	TAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCA	240
Sbjct	181	TAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCA	240
Query	241	GCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCCACGAGAA	300
Sbjct	241	GCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCCACGAGAA	300
Query	301	GATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCAC	360
Sbjct	301	GATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCAC	360
Query	361	CCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGG	420
Sbjct	361	CCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGG	420
Query	421	CCACGGCCACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTNTACCCAACCAGGGCCC	480
Sbjct	421	CCACGGCCACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTNTACCCAACCAGGGCCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CGGGGCCTGTTATGTCAAACGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CGGGGCCTGTTATGTCAAACGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGT  540

Query  541  CTCTTTCTCC  550
          ||||||||
Sbjct   541  CTCTTTCTCC  550
```

Sequence 110 matched with Sequence 3

Query= Sequence ID 110
Length=423

SEQ ID NO: 3

ALIGNMENTS

Identities = 423/423 (100%), Gaps = 0/423 (0%)

```
Query 1   ACGAAGACAGACATCTGTGGAATGATTACATCCTCTCAAGTTAGGAGGATGGAGGCCTG 60
          |||
Sbjct 1   ACGAAGACAGACATCTGTGGAATGATTACATCCTCTCAAGTTAGGAGGATGGAGGCCTG 60

Query 61  CTTCATTAAGAAGCTgggggtaggggtgggggtggggAGAACACTTAACAACATGGGGACC 120
          |||
Sbjct 61  CTTCATTAAGAAGCTGGGGGTAGGGTGGGGGTGGGGAGAACACTTAACAACATGGGGACC 120

Query 121 AGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGAGCAGCCAGGTGA 180
          |||
Sbjct 121 AGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGAGCAGCCAGGTGA 180

Query 181 GGCTCTCTAGTTTAATAAAAAATCATGGAAAGACTCTTAATGCAGACTCTTCTTAAGTGTT 240
          |||
Sbjct 181 GGCTCTCTAGTTTAATAAAAAATCATGGAAAGACTCTTAATGCAGACTCTTCTTAAGTGTT 240

Query 241 AATAGGGATTTTTTCAGCTTATTTTGTTGCAGTTTCCAATTTTTTAAAAATGTTGAGGTA 300
          |||
Sbjct 241 AATAGGGATTTTTTCAGCTTATTTTGTTGCAGTTTCCAATTTTTTAAAAATGTTGAGGTA 300

Query 301 ATCTTTCCACCTTCCCAAACCTAATTCTTGTAGATGCATTAGTGTTGAACCAATGCTTT 360
          |||
Sbjct 301 ATCTTTCCACCTTCCCAAACCTAATTCTTGTAGATGCATTAGTGTTGAACCAATGCTTT 360

Query 361 CTCATGTCTCAATTCTTTGTATATGCATTCTTTTCAGATGTATTAACAAACAAAAACCC 420
          |||
Sbjct 361 CTCATGTCTCAATTCTTTGTATATGCATTCTTTTCAGATGTATTAACAAACAAAAACCC 420

Query 421 TTC 423
          |||
Sbjct 421 TTC 423
```


Sequence 192 matched with Sequence 4

Query= Sequence ID - 192 nt: 286
Length=286

SEQ ID NO: 4 nt: 286

ALIGNMENTS

Identities = 286/286 (100%), Gaps = 0/286 (0%)

Query	1	CCGGTAATAGAATAGAAAAGGGAGAGTGTCTTCATGCAATGTGGCATCCTGGATTGGGTC	60
Sbjct	1	CCGGTAATAGAATAGAAAAGGGAGAGTGTCTTCATGCAATGTGGCATCCTGGATTGGGTC	60
Query	61	TCGNNACAAAAACAGGACATTAGTGGGAAAATTGGAAATCTGAAAAAGTCTGAATTTTA	120
Sbjct	61	TCGNNACAAAAACAGGACATTAGTGGGAAAATTGGAAATCTGAAAAAGTCTGAATTTTA	120
Query	121	GTTAATATAACCAATTTTCAGTCTCTTGGTTTTGACAGATGTACCATGGTGATGTAAGATGT	180
Sbjct	121	GTTAATATAACCAATTTTCAGTCTCTTGGTTTTGACAGATGTACCATGGTGATGTAAGATGT	180
Query	181	TGACCTTGGGGTAGGCTGGGTGAAGGGTATACAGGAACCTTTGTACTATCTCTGCAACT	240
Sbjct	181	TGACCTTGGGGTAGGCTGGGTGAAGGGTATACAGGAACCTTTGTACTATCTCTGCAACT	240
Query	241	TCTCTGTAAATCTAGTATCATTCCTCAAAAATAAAAGTTTATTTAATTT	286
Sbjct	241	TCTCTGTAAATCTAGTATCATTCCTCAAAAATAAAAGTTTATTTAATTT	286

Sequence 250 matched with Sequence 5

Query= Sequence ID 250
Length=545

SEQ ID NO: 5

ALIGNMENTS

Identities = 545/545 (100%), Gaps = 0/545 (0%)

Query	1	GTGGAAGTGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC	60
Sbjct	1	GTGGAAGTGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC	60
Query	61	CAGGGAAGACAGGGCGACCTGGAAGTCCAATACTTCTTAAGATCATCCAATACTATTGGA	120
Sbjct	61	CAGGGAAGACAGGGCGACCTGGAAGTCCAATACTTCTTAAAGATCATCCAATACTATTGGA	120
Query	121	TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA	180
Sbjct	121	TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA	180
Query	181	GATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG	240
Sbjct	181	GATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG	240
Query	241	CAAGGCCATCCGAGGGCACCTGAAAAACAACCCAGCTCTGGAGAACTGCTGCCTCATAT	300
Sbjct	241	CAAGGCCATCCGAGGGCACCTGAAAAACAACCCAGCTCTGGAGAACTGCTGCCTCATAT	300
Query	301	CCGGGGGAATGTGGGCTTTGTGTTACCAAGGAGGACCTCACTGAGATCAGGGACATGTT	360
Sbjct	301	CCGGGGGAATGTGGGCTTTGTGTTACCAAGGAGGACCTCACTGAGATCAGGGACATGTT	360
Query	361	GCTGGCCAATAAGGTGCCAGCTGCTGCCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCAC	420
Sbjct	361	GCTGGCCAATAAGGTGCCAGCTGCTGCCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCAC	420
Query	421	TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGAGAAGACCTCCTTTTCCAGGCTTTAGG	480
Sbjct	421	TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGAGAAGACCTCCTTTTCCAGGCTTTAGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TATCACCCTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TATCACCCTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540

Query  541  ACTGG  545
          ||||
Sbjct  541  ACTGG  545
```

Sequence 299 matched with Sequence 6

Query= Sequence ID 299
Length=591

SEQ ID NO: 6

ALIGNMENTS

Identities = 591/591 (100%), Gaps = 0/591 (0%)

Query	1	CAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGtttt	60
Sbjct	1	CAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTT	60
Query	61	tttCTCTTTGAAAGATAGAGATTGNTACAACACTACTTAAAAAATATAGTCAATAGGTTACT	120
Sbjct	61	TTTCTCTTTGAAAGATAGAGATTGNTACAACACTACTTAAAAAATATAGTCAATAGGTTACT	120
Query	121	AAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAA	180
Sbjct	121	AAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAA	180
Query	181	AATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAAGGTTTCTAAAACATG	240
Sbjct	181	AATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAAGGTTTCTAAAACATG	240
Query	241	ACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGA	300
Sbjct	241	ACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGA	300
Query	301	GAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAAAT	360
Sbjct	301	GAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAAAT	360
Query	361	GAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAAATAATTTG	420
Sbjct	361	GAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAAATAATTTG	420
Query	421	AAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGA	480
Sbjct	421	AAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CGCANGGAGAATTGCGCATTAAAGCCTAGTTACGCATTTACTAAACGCAGACGAAAATG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CGCANGGAGAATTGCGCATTAAAGCCTAGTTACGCATTTACTAAACGCAGACGAAAATG  540

Query  541  GGAAGATTAATTGGGAGTGGTAGGATGAAACAATTTTGGAGAAGATAGAAG  591
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GGAAGATTAATTGGGAGTGGTAGGATGAAACAATTTTGGAGAAGATAGAAG  591
```

Sequence 300 matched with Sequence 7

Query= Sequence ID 300
Length=297

SEQ ID NO: 7

ALIGNMENTS

Identities = 297/297 (100%), Gaps = 0/297 (0%)

```
Query 1   CTCAAAGGAGaaaaaaaaccttgtaaaaaaagcaaaaatgacaacagaaaaaCAATCTTA  60
          |||
Sbjct 1   CTCAAAGGAGAAAAAAAAACCTTGTAaaaaaAGCAAAAATGACAACAGAAAAACAATCTTA  60

Query 61  TTCCGAGCATTCCAGTAACTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTT  120
          |||
Sbjct 61  TTCCGAGCATTCCAGTAACTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTT  120

Query 121 TGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGTTTCtttttttttcctttttgtct  180
          |||
Sbjct 121 TGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGTTTCCTTTTTTTTCCTTTTTTGTCT  180

Query 181 atgaagttgctgtttatttttttGGCCTGTTTGATGTATGTGTGAAACAATGTTGTCCA  240
          |||
Sbjct 181 ATGAAGTTGCTGTTTATTTTTTTGGCCTGTTTGATGTATGTGTGAAACAATGTTGTCCA  240

Query 241 ACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCTaaaaaaaaaaaaaaaaaaaaa  297
          |||
Sbjct 241 ACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCTAAAAAAAAAAAAAAAAAAAAA  297
```

Sequence 302 matched with Sequence 8

Query= Sequence ID 302
Length=282

SEQ ID NO: 8

ALIGNMENTS

Identities = 282/282 (100%), Gaps = 0/282 (0%)

Query	1	AGTAGAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATC	60
Sbjct	1	AGTAGAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATC	60
Query	61	CGGCCACCTCGGCCTCCCGAAAAGTGCTGGGATTACAGGCGTGAGCCACGGCGCCCAGCCC	120
Sbjct	61	CGGCCACCTCGGCCTCCCGAAAAGTGCTGGGATTACAGGCGTGAGCCACGGCGCCCAGCCC	120
Query	121	CAGCCTGTCACTTAAACTGATAAACGACAGATTAACAGTAGAAAAATTTATTTTGCATA	180
Sbjct	121	CAGCCTGTCACTTAAACTGATAAACGACAGATTAACAGTAGAAAAATTTATTTTGCATA	180
Query	181	CATAATGAGGCTTCACAAAAGAGAAGTGAAAACCCAAGTAGGAGTTTAGGGCTGGGGGCT	240
Sbjct	181	CATAATGAGGCTTCACAAAAGAGAAGTGAAAACCCAAGTAGGAGTTTAGGGCTGGGGGCT	240
Query	241	TATATACCATTTTAACAAGGGGTGATAAATTGTAAGAGAATAG	282
Sbjct	241	TATATACCATTTTAACAAGGGGTGATAAATTGTAAGAGAATAG	282

Sequence 304 matched with Sequence 9

Query= Sequence ID 304
Length=619

SEQ ID NO: 9

ALIGNMENTS

Identities = 619/619 (100%), Gaps = 0/619 (0%)

Query	1	TCCTTGGTTTCGATTTGTGGCAACAATCCAGTCtttttggttttttCAGGGATACCATAT	60
Sbjct	1	TCCTTGGTTTCGATTTGTGGCAACAATCCAGTCtttttggttttttCAGGGATACCATAT	60
Query	61	GTAACAGGTGCCATTGTTACTGTAACTTTTACACATGCCTTCAGTTTGATGTCAAAGTC	120
Sbjct	61	GTAACAGGTGCCATTGTTACTGTAACTTTTACACATGCCTTCAGTTTGATGTCAAAGTC	120
Query	121	ATCATTTAGTGTAACAGCAAGTTATCTGTTAGGCTGCACATCATGAACTTTACTTTTAG	180
Sbjct	121	ATCATTTAGTGTAACAGCAAGTTATCTGTTAGGCTGCACATCATGAACTTTACTTTTAG	180
Query	181	AAAGTCTTATCTTTTATGCCACAGAAATAGCATTTGGCTATTAGTCATGGATGGCAAAGA	240
Sbjct	181	AAAGTCTTATCTTTTATGCCACAGAAATAGCATTTGGCTATTAGTCATGGATGGCAAAGA	240
Query	241	AATTAATTTTGAGTTGTTTGGATAAAAAATGTTTCAGTTGACTGTAGTGTGTATTGAGAGA	300
Sbjct	241	AATTAATTTTGAGTTGTTTGGATAAAAAATGTTTCAGTTGACTGTAGTGTGTATTGAGAGA	300
Query	301	CACTGCCAGTAAACAAACTCTCTTGGTAGGTGGAAATCCCCTAGAAGTTACAGAAAATTG	360
Sbjct	301	CACTGCCAGTAAACAAACTCTCTTGGTAGGTGGAAATCCCCTAGAAGTTACAGAAAATTG	360
Query	361	GGAGGAGGTGAACTTAATTAAATAACTTGAATTGTTTAGACATATTCAGAGCTTCTTATG	420
Sbjct	361	GGAGGAGGTGAACTTAATTAAATAACTTGAATTGTTTAGACATATTCAGAGCTTCTTATG	420
Query	421	ACCTTGAAGAAATCACCCAACCTCAAAAGACCTCGGTTTCTTCATTTGTAAAATTAGGGA	480
Sbjct	421	ACCTTGAAGAAATCACCCAACCTCAAAAGACCTCGGTTTCTTCATTTGTAAAATTAGGGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTTGA CTAGATGTGTAAATCTAGTTGTTAGTTAACTTCTAAGATGTAAAAACCCCTCTTG  540
          |||||||
Sbjct   481  GTTTGA CTAGATGTGTAAATCTAGTTGTTAGTTAACTTCTAAGATGTAAAAACCCCTCTTG  540

Query  541  TTTAACAAAAACCTACAAGATCAAGTTGCTTATCTGAAATCTTTATGAATCAACACTAGT  600
          |||||||
Sbjct   541  TTTAACAAAAACCTACAAGATCAAGTTGCTTATCTGAAATCTTTATGAATCAACACTAGT  600

Query  601  CACTAAGTCTAGCTCGACC  619
          |||||||
Sbjct   601  CACTAAGTCTAGCTCGACC  619
```

Sequence 306 matched with Sequence 10

Query= Sequence ID 306
Length=536

SEQ ID NO: 10

ALIGNMENTS

Identities = 536/536 (100%), Gaps = 0/536 (0%)

Query	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCGCTGCATCCTTTCTGTG	60
Sbjct	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCGCTGCATCCTTTCTGTG	60
Query	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Sbjct	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Query	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Sbjct	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Query	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Sbjct	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Query	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Sbjct	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Query	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTA	360
Sbjct	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTA	360
Query	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGCTGG	420
Sbjct	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGCTGG	420
Query	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480
Sbjct	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGACCAAGAATGTGGATTTTGTGAAGGATGCNCATGAANAAATGGACNAGCTGTG	536
Sbjct	481	CTGACCAAGAATGTGGATTTTGTGAAGGATGCNCATGAANAAATGGACNAGCTGTG	536

Sequence 308 matched with Sequence 11

Query= Sequence ID - 308 nt: 373
Length=373

SEQ ID NO: 11 nt: 373

ALIGNMENTS

Identities = 373/373 (100%), Gaps = 0/373 (0%)

```
Query 1  AAGTGGGTCTTGCCATCCCTGAACTGNAATCATCCCTAACATATTCATACCTGTTTTTCAT 60
      |||
Sbjct 1  AAGTGGGTCTTGCCATCCCTGAACTGNAATCATCCCTAACATATTCATACCTGTTTTTCAT 60

Query 61 TTTAAAAGTTGGGTCAGTtttttttATTAGTACATGTATTTCTATCCTACTGATTTATTTG 120
      |||
Sbjct 61 TTTAAAAGTTGGGTCAGTTTTTTTTTATTAGTACATGTATTTCTATCCTACTGATTTATTTG 120

Query 121 CTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAGA 180
      |||
Sbjct 121 CTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAGA 180

Query 181 CCTAGCTCTTCTCAGTGTCTACTATTATAAAACAATGCTACAGTGAATATTGGTGNATAAA 240
      |||
Sbjct 181 CCTAGCTCTTCTCAGTGTCTACTATTATAAAACAATGCTACAGTGAATATTGGTGNATAAA 240

Query 241 TCCATACNCACCACGTACATATCTTAAGTTCTGGAAGAGATATTGCTAAACCAGAAGATA 300
      |||
Sbjct 241 TCCATACNCACCACGTACATATCTTAAGTTCTGGAAGAGATATTGCTAAACCAGAAGATA 300

Query 301 ACCTGCATTTAAAATTTGACTGCTAGGGNCAGGGNCACATTTAATTAAATTAGAACAANG 360
      |||
Sbjct 301 ACCTGCATTTAAAATTTGACTGCTAGGGNCAGGGNCACATTTAATTAAATTAGAACAANG 360

Query 361 AATGCATAATGNC 373
      |||
Sbjct 361 AATGCATAATGNC 373
```

Blast comparison trimmed “NC” from the 3’ end of both sequences and reported 371 identities. The report has been manually corrected for this. “NC” has been appended to both sequences and identity count has been increased to 373.

Sequence 309 matched with Sequence 12

Query= Sequence ID 309
Length=796

SEQ ID NO: 12

ALIGNMENTS

Identities = 796/796 (100%), Gaps = 0/796 (0%)

Query	1	CCGGAATCGCGCCGCGTCGACGAAAATATGTGCCCTGGCCAACTCCACAGGACTAGTTC	60
Sbjct	1	CCGGAATCGCGCCGCGTCGACGAAAATATGTGCCCTGGCCAACTCCACAGGACTAGTTC	60
Query	61	TAGGCAATCTGAAGGAAACCAGAAAATGTGAATTTCTCTCCCTCAAAAAGCTATACTGA	120
Sbjct	61	TAGGCAATCTGAAGGAAACCAGAAAATGTGAATTTCTCTCCCTCAAAAAGCTATACTGA	120
Query	121	AGTAGTATTTAATATTCAAGTACTTGTAATTTGCAGAACAGTACTTTTAAATTTGACCC	180
Sbjct	121	AGTAGTATTTAATATTCAAGTACTTGTAATTTGCAGAACAGTACTTTTAAATTTGACCC	180
Query	181	ATGAATTCTATTTAAATTTGTCACTTAATATTTAGCCAAGAAGCAAACCATCTAAAAAGA	240
Sbjct	181	ATGAATTCTATTTAAATTTGTCACTTAATATTTAGCCAAGAAGCAAACCATCTAAAAAGA	240
Query	241	TTTCTGGTTTATTTCTCCAACTCCTAATAAATAGGGTCACATAttttttaacttttttCT	300
Sbjct	241	TTTCTGGTTTATTTCTCCAACTCCTAATAAATAGGGTCACATATTTTAACTTTTTTCT	300
Query	301	AATTTGAAAAGTAATACAGGCATATGGTATTTTAAAAATGAAACAACACAAAGGGATATG	360
Sbjct	301	AATTTGAAAAGTAATACAGGCATATGGTATTTTAAAAATGAAACAACACAAAGGGATATG	360
Query	361	TTTTGAAAAGTGGTCTTGCCATCCCTGAACTGTAATCATCCCTAACATATTCATACCTGT	420
Sbjct	361	TTTTGAAAAGTGGTCTTGCCATCCCTGAACTGTAATCATCCCTAACATATTCATACCTGT	420
Query	421	TTTCATTTTAAAAGTTGGGTCAGtttttttATTAGTACATGTATTTCTATCCTACTGATT	480
Sbjct	421	TTTCATTTTAAAAGTTGGGTCAGTTTTTTTATTAGTACATGTATTTCTATCCTACTGATT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TATTTGCTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTA	540
Sbjct	481	TATTTGCTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTA	540
Query	541	TGGAGACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTG	600
Sbjct	541	TGGAGACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTG	600
Query	601	NATAAATCCTACACACCACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAAACCA	660
Sbjct	601	NATAAATCCTACACACCACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAAACCA	660
Query	661	GAAGATAACCTGCATTTAAAAATTTGACTGCTAGGGTCAGGGTCACATTTAAATTAAATTA	720
Sbjct	661	GAAGATAACCTGCATTTAAAAATTTGACTGCTAGGGTCAGGGTCACATTTAAATTAAATTA	720
Query	721	GAACAAGGAATGCATAATGTCTTCGATAGCAATCTATTCAAGGTGCACCGTGGTCACAAA	780
Sbjct	721	GAACAAGGAATGCATAATGTCTTCGATAGCAATCTATTCAAGGTGCACCGTGGTCACAAA	780
Query	781	GGAAAGCAAACTGTC	796
Sbjct	781	GGAAAGCAAACTGTC	796

Sequence 310 matched with Sequence 13

Query= Sequence ID - 310 nt:564
Length=564

SEQ ID NO: 13

nt:564

ALIGNMENTS

Identities = 564/564 (100%), Gaps = 0/564 (0%)

Query	1	CCTGGNCAGAGGCCTCTATCCTGTANTGATAATTGCCATCAAAATTGTCAAAAANGATTT	60
Sbjct	1	CCTGGNCAGAGGCCTCTATCCTGTANTGATAATTGCCATCAAAATTGTCAAAAANGATTT	60
Query	61	AATTTCTATGGGNAATAGTCCTTTTCTTAGCTTCTGCCNNTCACTTGCTTATTTTTTGTG	120
Sbjct	61	AATTTCTATGGGNAATAGTCCTTTTCTTAGCTTCTGCCNNTCACTTGCTTATTTTTTGTG	120
Query	121	TGGGAATGGGGTTGGATAAACCAATGAACCTTTATTATAAACAAATCCACCTATATCTAN	180
Sbjct	121	TGGGAATGGGGTTGGATAAACCAATGAACCTTTATTATAAACAAATCCACCTATATCTAN	180
Query	181	CAAATTTATATTTTCGGTGAAATACAGATATTTGCCTTTCTGGAGTANTATAGAAGCTGT	240
Sbjct	181	CAAATTTATATTTTCGGTGAAATACAGATATTTGCCTTTCTGGAGTANTATAGAAGCTGT	240
Query	241	CAATATGTATCTACTGTACAGTACTAAATAGTATTTCATTTATGAAATGAGTAGTGTGTTGG	300
Sbjct	241	CAATATGTATCTACTGTACAGTACTAAATAGTATTTCATTTATGAAATGAGTAGTGTGTTGG	300
Query	301	GTGGCTGGGGTTAAGGAAAAATGAGACTTGGAATTGTAGCTTTTATCCAAGTTTGTAGTA	360
Sbjct	301	GTGGCTGGGGTTAAGGAAAAATGAGACTTGGAATTGTAGCTTTTATCCAAGTTTGTAGTA	360
Query	361	TAAATAGGGttttgtttgtttttttAACCTAAAACTGAAATGCCATATAGAAAAACA	420
Sbjct	361	TAAATAGGGTTTTGTTTTGTTTTTTAACCTAAAACTGAAATGCCATATAGAAAAACA	420
Query	421	GCATTGTTTTTACAGTTTGTAGTAAGTAACTTTTTTAAAGATTTTATCAAAAAGAATTTTG	480
Sbjct	421	GCATTGTTTTTACAGTTTGTAGTAAGTAACTTTTTTAAAGATTTTATCAAAAAGAATTTTG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TCTATNGTGAGTAAAAGAAGTTCTAATAATGGCCTAATCACTGCATTTTAAAAAACAAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TCTATNGTGAGTAAAAGAAGTTCTAATAATGGCCTAATCACTGCATTTTAAAAAACAAA  540

Query  541  GTTCAACACAAATGACATTGTTT  564
          ||||||||||||||||
Sbjct   541  GTTCAACACAAATGACATTGTTT  564
```

Sequence 311 matched with Sequence 14

Query= Sequence ID 311
Length=230

SEQ ID NO: 14

ALIGNMENTS

Identities = 230/230 (100%), Gaps = 0/230 (0%)

Query	1	CCTCTCCTCCATCTAAAGGCAACATTTCCTTACCCATTAGTCTCAGAAATTGTCTTAAGCA	60
Sbjct	1	CCTCTCCTCCATCTAAAGGCAACATTTCCTTACCCATTAGTCTCAGAAATTGTCTTAAGCA	60
Query	61	ACAGCCCCAAATGCTGGCTGCCCCGGCCAAGCATTGGGGCCGCCATCCTGCCTGGCACT	120
Sbjct	61	ACAGCCCCAAATGCTGGCTGCCCCGGCCAAGCATTGGGGCCGCCATCCTGCCTGGCACT	120
Query	121	GGCTGATGGGCACCTCTGTTGGTTCCATCAGCCAGAGCTCTGCCAAAGGCCCCGCAGTCC	180
Sbjct	121	GGCTGATGGGCACCTCTGTTGGTTCCATCAGCCAGAGCTCTGCCAAAGGCCCCGCAGTCC	180
Query	181	CTCTCCCAGGAGGACCCTAGAGGCAATTAAATGATGTCCTGTTCCATTGG	230
Sbjct	181	CTCTCCCAGGAGGACCCTAGAGGCAATTAAATGATGTCCTGTTCCATTGG	230

Sequence 313 matched with Sequence 15

Query= Sequence ID - 313 nt: 554
Length=554

SEQ ID NO: 15 nt: 554

ALIGNMENTS

Identities = 554/554 (100%), Gaps = 0/554 (0%)

Query	1	CCCGGAATCGCGGCCCGCTCGACAACAAACCTGCATGTTCTGCACATGTATCCAGGAAC	60
Sbjct	1	CCCGGAATCGCGGCCCGCTCGACAACAAACCTGCATGTTCTGCACATGTATCCAGGAAC	60
Query	61	TTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTTATAGATTA	120
Sbjct	61	TTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTTATAGATTA	120
Query	121	AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATATGGATTANAAA	180
Sbjct	121	AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATATGGATTANAAA	180
Query	181	TCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATATGGATTAAAAACAT	240
Sbjct	181	TCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATATGGATTAAAAACAT	240
Query	241	CTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGG	300
Sbjct	241	CTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGG	300
Query	301	GTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGGTTAAAAATCAAAAGAAAA	360
Sbjct	301	GTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGGTTAAAAATCAAAAGAAAA	360
Query	361	TGAACTATTTGCTCCAGTGCAGGAAAATACAGGCAATACTGGATACAATTAGATGGTCAG	420
Sbjct	361	TGAACTATTTGCTCCAGTGCAGGAAAATACAGGCAATACTGGATACAATTAGATGGTCAG	420
Query	421	GAGCGATAACCCGTTGCCATTGTTTGAAGAAGAGAATAAGGNGCTAGCATTCCCTATCCG	480
Sbjct	421	GAGCGATAACCCGTTGCCATTGTTTGAAGAAGAGAATAAGGNGCTAGCATTCCCTATCCG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TAGATAATTTGACAGCTAGGAAATAGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAAT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAGATAATTTGACAGCTAGGAAATAGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAAT  540

Query  541  GAACTATTATATGC  554
          ||||||||||||
Sbjct  541  GAACTATTATATGC  554
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

Sequence 314 matched with Sequence 16

Query= Sequence ID 314
Length=610

SEQ ID NO: 16

ALIGNMENTS

Identities = 610/610 (100%), Gaps = 0/610 (0%)

Query	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCGCTGCATCCTTTCTGTG	60
Sbjct	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCGCTGCATCCTTTCTGTG	60
Query	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Sbjct	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Query	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Sbjct	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Query	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Sbjct	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Query	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Sbjct	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Query	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTA	360
Sbjct	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTA	360
Query	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGCTGG	420
Sbjct	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGCTGG	420
Query	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480
Sbjct	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA  540

Query  541  GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACAACCAC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACAACCAC  600

Query  601  AATCATGAGG   610
          ||||||||
Sbjct   601  AATCATGAGG   610
```

Sequence 315 matched with Sequence 17

Query= Sequence ID 315
Length=359

SEQ ID NO: 17

ALIGNMENTS

Identities = 359/359 (100%), Gaps = 0/359 (0%)

```
Query 1      TGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGCCCCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1      TGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGCCCCT  60

Query 61     CAGCATCCAGCAGCATGAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGCCATAATCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61     CAGCATCCAGCAGCATGAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGCCATAATCC  120

Query 121    ACCTCTTCTGCTTCAGTTGAGGTGACACGTCTCAGCCTTAGCCCTGTGCCCCCTGAAACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121    ACCTCTTCTGCTTCAGTTGAGGTGACACGTCTCAGCCTTAGCCCTGTGCCCCCTGAAACA  180

Query 181    GCTGCCACCATCACTCGCAAGAGAATCCCCTCCATCTTTGGGAGGGGTTGATGCCAGACA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181    GCTGCCACCATCACTCGCAAGAGAATCCCCTCCATCTTTGGGAGGGGTTGATGCCAGACA  240

Query 241    TCACCAGGTTGTAGAAGTTGACAGGCAGTGCCATGGGGGCAACAGCCAAAATAGGGGGGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241    TCACCAGGTTGTAGAAGTTGACAGGCAGTGCCATGGGGGCAACAGCCAAAATAGGGGGGT  300

Query 301    AATGATGTACGGGCCAAGCACTGCCCAGCTGGGGGTCAATAAAGTTACCCTTGTA CTG  359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301    AATGATGTACGGGCCAAGCACTGCCCAGCTGGGGGTCAATAAAGTTACCCTTGTA CTG  359
```

Sequence 316 matched with Sequence 18

Query= Sequence ID 316
Length=154

SEQ ID NO: 18

ALIGNMENTS

Identities = 154/154 (100%), Gaps = 0/154 (0%)

Query	1	CGCCACTTATCCAGTGAACCACTATCACGaaaaaaCTCTACCTCTCTATACTAATCTCC	60
Sbjct	1	CGCCACTTATCCAGTGAACCACTATCACGAAAAAACTCTACCTCTCTATACTAATCTCC	60
Query	61	CTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTaaaaaaaaa	120
Sbjct	61	CTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTAaaaaaaaaa	120
Query	121	aaaaaaaaaaaaaaaaaaaaaaaaaaaaa	154
Sbjct	121	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	154

Sequence 321 matched with Sequence 19

Query= Sequence ID 321
Length=661

SEQ ID NO: 19

ALIGNMENTS

Identities = 661/661 (100%), Gaps = 0/661 (0%)

Query	1	CAGAACAGTACTTTTTAATTGACCCATGAATTCTATTTAAATTTGTCACTTAATATTTA	60
Sbjct	1	CAGAACAGTACTTTTTAATTGACCCATGAATTCTATTTAAATTTGTCACTTAATATTTA	60
Query	61	GCCAAGAAGCAAACCATCTAAAAAGATTTCTGGTTTATTTCTCCAACCTCCTAATAAATAG	120
Sbjct	61	GCCAAGAAGCAAACCATCTAAAAAGATTTCTGGTTTATTTCTCCAACCTCCTAATAAATAG	120
Query	121	GGTCACATAttttttaacttttttCTAATTTGAAAAGTAATACAGGCATATGGTATTTTA	180
Sbjct	121	GGTCACATATTTTTTAACTTTTTCTAATTTGAAAAGTAATACAGGCATATGGTATTTTA	180
Query	181	AAAATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTTCTTGCCATCCCTGAACTGT	240
Sbjct	181	AAAATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTTCTTGCCATCCCTGAACTGT	240
Query	241	AATCATCCCTAACATATTCATACCTGTTTTCATTTTAAAAGTTGGGTCAGtttttttATT	300
Sbjct	241	AATCATCCCTAACATATTCATACCTGTTTTCATTTTAAAAGTTGGGTCAGTTTTTTTATT	300
Query	301	AGTACATGTATTTCTATCCTACTGATTTATTTGCTATATCATCTAATTTAGTTTGAATAT	360
Sbjct	301	AGTACATGTATTTCTATCCTACTGATTTATTTGCTATATCATCTAATTTAGTTTGAATAT	360
Query	361	TCCATAATTTACTTAATTAGTCCTGTATGGAGACCTAGCTCTTCTCAGTGTCTACTATTA	420
Sbjct	361	TCCATAATTTACTTAATTAGTCCTGTATGGAGACCTAGCTCTTCTCAGTGTCTACTATTA	420
Query	421	TAAACAATGCTACAGTGAATATTGGTGTATAAATCCATACACACCACGTAACATATCTTA	480
Sbjct	421	TAAACAATGCTACAGTGAATATTGGTGTATAAATCCATACACACCACGTAACATATCTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGTTCCTGGAAGAGATATTGCTAAACCAGAAGATAACCTGCATTAAAAATTTGACTGCT	540
Sbjct	481	AGTTCCTGGAAGAGATATTGCTAAACCAGAAGATAACCTGCATTAAAAATTTGACTGCT	540
Query	541	AGGGTCAGGGTCACATTTAAATTAAATTAGAACAAGGAATGCATAATGTCTTCGATAGCA	600
Sbjct	541	AGGGTCAGGGTCACATTTAAATTAAATTAGAACAAGGAATGCATAATGTCTTCGATAGCA	600
Query	601	ATCTATTCCAGGTGCACCGTGGTCACAAAGGAAAGCAAACTGTCAATAACTTTCTTCTC	660
Sbjct	601	ATCTATTCCAGGTGCACCGTGGTCACAAAGGAAAGCAAACTGTCAATAACTTTCTTCTC	660
Query	661	A 661	
Sbjct	661	A 661	

Sequence 322 matched with Sequence 20

Query= Sequence ID 322
Length=770

SEQ ID NO: 20

ALIGNMENTS

Identities = 770/770 (100%), Gaps = 0/770 (0%)

Query	1	TAGCATTTGGCCTTTTAAAAACATTTGTTTAttttttttCTGAGAATGGCTAACACACTTT	60
Sbjct	1	TAGCATTTGGCCTTTTAAAAACATTTGTTTATTTTTTTTCTGAGAATGGCTAACACACTTT	60
Query	61	ATTGAGGTTTCGAAATTAATAAAAGAAAATAAAAGAAATGTATCTTCATTCACTCTGTATGT	120
Sbjct	61	ATTGAGGTTTCGAAATTAATAAAAGAAAATAAAAGAAATGTATCTTCATTCACTCTGTATGT	120
Query	121	TAGTGTTTTAATTACCCTTAGAATATATGGATAAAAAATACTATTCTTTGTCTTGGAGAA	180
Sbjct	121	TAGTGTTTTAATTACCCTTAGAATATATGGATAAAAAATACTATTCTTTGTCTTGGAGAA	180
Query	181	GGTAAGAGTCTAGTTAGATGAATAAGGGTTATCTATGTAGAACAACCTAGAGAATGAGAAG	240
Sbjct	181	GGTAAGAGTCTAGTTAGATGAATAAGGGTTATCTATGTAGAACAACCTAGAGAATGAGAAG	240
Query	241	AGAGCTTATGAGATTGAGTACTACGTTATGCAGTAGAGTAGCACGTCATCTGCTACTGAG	300
Sbjct	241	AGAGCTTATGAGATTGAGTACTACGTTATGCAGTAGAGTAGCACGTCATCTGCTACTGAG	300
Query	301	TATGGTGTGATAACATTGTGTAACAGGAAAGTATGATCAATATCTACTTAAAAATTAAGGA	360
Sbjct	301	TATGGTGTGATAACATTGTGTAACAGGAAAGTATGATCAATATCTACTTAAAAATTAAGGA	360
Query	361	CAATATTAGCACTACATTGCTTTATTTTAAAGTAAAAATTAGAGAACTAAACACAAGCAT	420
Sbjct	361	CAATATTAGCACTACATTGCTTTATTTTAAAGTAAAAATTAGAGAACTAAACACAAGCAT	420
Query	421	TGTAAGTACAATAAAAGCTGATCTTTCTAGTTAAGCAGAATAATACATGTTCAAGCATCT	480
Sbjct	421	TGTAAGTACAATAAAAGCTGATCTTTCTAGTTAAGCAGAATAATACATGTTCAAGCATCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCTAAATCATTAATATAAGAATATAGGGGTTTTCTATAATCTTATTTTCTTTGGAAGAG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCTAAATCATTAATATAAGAATATAGGGGTTTTCTATAATCTTATTTTCTTTGGAAGAG  540

Query  541  TACCTCATTTTCAAGANGAGAAGTTTCTAATTGCCACTTCTTTAAAAATAAAACAGGGTT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TACCTCATTTTCAAGANGAGAAGTTTCTAATTGCCACTTCTTTAAAAATAAAACAGGGTT  600

Query  601  TTAATGTTCCCAGCACAAAAATTAATATCTCTTCAAAAAGTCTCTTGTGATTAAGTTTGA  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TTAATGTTCCCAGCACAAAAATTAATATCTCTTCAAAAAGTCTCTTGTGATTAAGTTTGA  660

Query  661  ATCCCTTGTCATACTGCTTCTAATATTGACACTGACCTCCTTAGGTATTTTTCAGGGGTT  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  ATCCCTTGTCATACTGCTTCTAATATTGACACTGACCTCCTTAGGTATTTTTCAGGGGTT  720

Query  721  ATAATCTTTTCTTAAGGTATCTTTTTTCAAGAATTGGATACCTTGGGCTT  770
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721  ATAATCTTTTCTTAAGGTATCTTTTTTCAAGAATTGGATACCTTGGGCTT  770
```

Sequence 323 matched with Sequence 21

Query= Sequence ID 323
Length=654

SEQ ID NO: 21

ALIGNMENTS

Identities = 654/654 (100%), Gaps = 0/654 (0%)

Query	1	CGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGA	60
Sbjct	1	CGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGA	60
Query	61	AAGGGTCCAAGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACC	120
Sbjct	61	AAGGGTCCAAGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACC	120
Query	121	AGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAAT	180
Sbjct	121	AGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAAT	180
Query	181	GCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAG	240
Sbjct	181	GCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAG	240
Query	241	TGCAACCCTTGCCTCGCTTGTCACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGG	300
Sbjct	241	TGCAACCCTTGCCTCGCTTGTCACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGG	300
Query	301	AAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTaaaaaaaGATTAACCAGTGTGAA	360
Sbjct	301	AAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAGATTAACCAGTGTGAA	360
Query	361	CATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAGAA	420
Sbjct	361	CATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAGAA	420
Query	421	TAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGA	480
Sbjct	421	TAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATGGACTGGCGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATGGACTGGCGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAA  540

Query  541  CTGACCTGCTATCCCACCCCAAATTCAACCTGAGGTATATTTTCAGTGAAGCAGGTAGCTG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CTGACCTGCTATCCCACCCCAAATTCAACCTGAGGTATATTTTCAGTGAAGCAGGTAGCTG  600

Query  601  TGCTTCTCAAAGCAGAGAAGCAGTTTTTAAGAACCAAAAAGGTAGAGGAAATCTA  654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TGCTTCTCAAAGCAGAGAAGCAGTTTTTAAGAACCAAAAAGGTAGAGGAAATCTA  654
```

Sequence 324 matched with Sequence 22

Query= Sequence ID 324
Length=676

SEQ ID NO: 22

ALIGNMENTS

Identities = 676/676 (100%), Gaps = 0/676 (0%)

Query	1	GTTTGTTACAGGCAGAATTGGATAGATACAGCCCTACAAATGTATATGCCCTCCCCTGaa	60
Sbjct	1	GTTTGTTACAGGCAGAATTGGATAGATACAGCCCTACAAATGTATATGCCCTCCCCTGAA	60
Query	61	aaaaaTTGGATGAAAATCTGCACAGCAAAGTGAAACACACAGATAATAGGAACAAAATGT	120
Sbjct	61	AAAAATTGGATGAAAATCTGCACAGCAAAGTGAAACACACAGATAATAGGAACAAAATGT	120
Query	121	AGTTCCCATGTGCCAAACAAAATAAATGAAATCTCTGCATGTTTGCAGCATATCTGCCTT	180
Sbjct	121	AGTTCCCATGTGCCAAACAAAATAAATGAAATCTCTGCATGTTTGCAGCATATCTGCCTT	180
Query	181	TTGGGAATGTAATCAAGGNATAATCTTTGGCTAGTGTTATGTGCCTGTAttttttAAAA	240
Sbjct	181	TTGGGAATGTAATCAAGGNATAATCTTTGGCTAGTGTTATGTGCCTGTATTTTTTTAAAA	240
Query	241	TGGTACACCAGAAAAGGACTGGCAGTCTACTTCTACCATAGTTAAACTTCACCCTCTTTA	300
Sbjct	241	TGGTACACCAGAAAAGGACTGGCAGTCTACTTCTACCATAGTTAAACTTCACCCTCTTTA	300
Query	301	ATTTCACACATATTCTTTGGAAGCAGGAAGAAATGCTCATAAAGAGGATCAGACCTTCT	360
Sbjct	301	ATTTCACACATATTCTTTGGAAGCAGGAAGAAATGCTCATAAAGAGGATCAGACCTTCT	360
Query	361	TTCCCGTGAAACCAGTATTTGGCGCCATATATAAGCCTGGTTAAATTGGTCATCTAAAGC	420
Sbjct	361	TTCCCGTGAAACCAGTATTTGGCGCCATATATAAGCCTGGTTAAATTGGTCATCTAAAGC	420
Query	421	TGTCAAATAAGACATTCTGTGAAAGGTAAACATCGAAACTGGTTATAAGTAAAACCATCA	480
Sbjct	421	TGTCAAATAAGACATTCTGTGAAAGGTAAACATCGAAACTGGTTATAAGTAAAACCATCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGCCAACAACAGGGTCTTGAGATAACCTTTGAAGCTTATTGTCTGGCCTGCACCAGAAGA	540
Sbjct	481	AGCCAACAACAGGGTCTTGAGATAACCTTTGAAGCTTATTGTCTGGCCTGCACCAGAAGA	540
Query	541	TGTCTGCATTACTCATTGCTAAAAATGTGTACACAGAACTGCACTAGGATTAATTGGTTC	600
Sbjct	541	TGTCTGCATTACTCATTGCTAAAAATGTGTACACAGAACTGCACTAGGATTAATTGGTTC	600
Query	601	AAGAAGAAATTTAACTTACGTTTGGGTTTCCATACAGCACTCTATTGAATACATGCATC	660
Sbjct	601	AAGAAGAAATTTAACTTACGTTTGGGTTTCCATACAGCACTCTATTGAATACATGCATC	660
Query	661	TGAATTTAAGTTGCAA	676
Sbjct	661	TGAATTTAAGTTGCAA	676

Sequence 325 matched with Sequence 23

Query= Sequence ID 325
Length=609

SEQ ID NO: 23

ALIGNMENTS

Identities = 609/609 (100%), Gaps = 0/609 (0%)

Query	1	GACCAGTAATGGCTTTTAAGAGTCCATTTTGTCAATTGTCTCCCTAGTTAATTACAGGTGG	60
Sbjct	1	GACCAGTAATGGCTTTTAAGAGTCCATTTTGTCAATTGTCTCCCTAGTTAATTACAGGTGG	60
Query	61	GGGATCTTTTGCCTCTATTCTCTTCATATTGAAATGAATCATACTCATGTTTTGTGGAAC	120
Sbjct	61	GGGATCTTTTGCCTCTATTCTCTTCATATTGAAATGAATCATACTCATGTTTTGTGGAAC	120
Query	121	TCCTTAAAGTTGTAGCTGTCATGATCAGAtttttttATATTCCTCAGCTTAACTCTGC	180
Sbjct	121	TCCTTAAAGTTGTAGCTGTCATGATCAGATTTTTTTATATTCCTCAGCTTAACTCTGC	180
Query	181	TACTTGATTTACAGTGACCCATAACCTACTCATCCTTGGTTTATAGTGACACATAATCTT	240
Sbjct	181	TACTTGATTTACAGTGACCCATAACCTACTCATCCTTGGTTTATAGTGACACATAATCTT	240
Query	241	ATCTCTTTATAGAACCTTAAATTTTATCATTATTTTCGCTTAGAATACAGCATTTCTTTG	300
Sbjct	241	ATCTCTTTATAGAACCTTAAATTTTATCATTATTTTCGCTTAGAATACAGCATTTCTTTG	300
Query	301	CTTCTGTTGCTGGTTTGACTTAAGAAATAAGGCAGTAACTCTGATCAATCAATTATCCAT	360
Sbjct	301	CTTCTGTTGCTGGTTTGACTTAAGAAATAAGGCAGTAACTCTGATCAATCAATTATCCAT	360
Query	361	AAGGAAGGGCTTTTCATGGGTCTATTAATTTGTTAGTACCCTAAGTATATCTGAAAAAT	420
Sbjct	361	AAGGAAGGGCTTTTCATGGGTCTATTAATTTGTTAGTACCCTAAGTATATCTGAAAAAT	420
Query	421	ATGTCTATTGAGAGAAGATTTTGGCATTCCAGATGGTATAGTCTATATATATTTAAAGTT	480
Sbjct	421	ATGTCTATTGAGAGAAGATTTTGGCATTCCAGATGGTATAGTCTATATATATTTAAAGTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTGAATTTGCTTATATATACTCAGCTTTCTTTTCTAGCATTTTGCATTTACCTGTTAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTGAATTTGCTTATATATACTCAGCTTTCTTTTCTAGCATTTTGCATTTACCTGTTAA  540

Query  541  TTGAAGTATACCCCCACATATAAAAGTTCCTCTTAAAGACACTGGACTCTTTCTGGGGG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TTGAAGTATACCCCCACATATAAAAGTTCCTCTTAAAGACACTGGACTCTTTCTGGGGG  600

Query  601  GCTAAAATA  609
          |||||||
Sbjct   601  GCTAAAATA  609
```

Sequence 326 matched with Sequence 24

Query= Sequence ID - 326 nt: 554
Length=554

SEQ ID NO: 24 nt: 554

ALIGNMENTS

Identities = 554/554 (100%), Gaps = 0/554 (6%)

Query	1	CCCGGAATCGCGGCCCGCTCGACAACAAACCTGCATGTTCTGCACATGTATCCAGGAAC	60
Sbjct	1	CCCGGAATCGCGGCCCGCTCGACAACAAACCTGCATGTTCTGCACATGTATCCAGGAAC	60
Query	61	TTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTTATAGATTA	120
Sbjct	61	TTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTTATAGATTA	120
Query	121	AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATATGGATTANAAA	180
Sbjct	121	AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATATGGATTANAAA	180
Query	181	TCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATATGGATTAAAAAACAT	240
Sbjct	181	TCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATATGGATTAAAAAACAT	240
Query	241	CTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGG	300
Sbjct	241	CTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGG	300
Query	301	GTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGGTTAAAAATCAAAAGAAAA	360
Sbjct	301	GTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGGTTAAAAATCAAAAGAAAA	360
Query	361	TGAACTATTTGCTCCAGTGCAGGAAAATACAGGCAATACTGGATACAATTAGATGGTCAG	420
Sbjct	361	TGAACTATTTGCTCCAGTGCAGGAAAATACAGGCAATACTGGATACAATTAGATGGTCAG	420
Query	421	GAGCGATAACCCGTTGCCATTGTTTGAAGAAGAGAATAAGGNGCTAGCATTCCTATCCG	480
Sbjct	421	GAGCGATAACCCGTTGCCATTGTTTGAAGAAGAGAATAAGGNGCTAGCATTCCTATCCG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TAGATAATTTGACAGCTAGGAAATAGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAAT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAGATAATTTGACAGCTAGGAAATAGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAAT  540

Query  541  GAACTATTATATGC  554
          ||||||||||||
Sbjct  541  GAACTATTATATGC  554
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

Sequence 327 matched with Sequence 25

Query= Sequence ID 327
Length=674

SEQ ID NO: 25

ALIGNMENTS

Identities = 674/674 (100%), Gaps = 0/674 (0%)

Query	1	CGGCTACCGACAGAAGGACTATTTTCATCGCCACCCAGGGGCCACTGGCACACACGGTTGA	60
Sbjct	1	CGGCTACCGACAGAAGGACTATTTTCATCGCCACCCAGGGGCCACTGGCACACACGGTTGA	60
Query	61	GGACTTCTGGAGGATGATCTGGGAGGGGAAGTCCCACACTATCGTGATGCTGACGGAGGT	120
Sbjct	61	GGACTTCTGGAGGATGATCTGGGAGGGGAAGTCCCACACTATCGTGATGCTGACGGAGGT	120
Query	121	GCAGGAGAGAGAGCAGGATAAATGCTACCAGTATTGGCCAACCGAGGGCTCAGTTACTCA	180
Sbjct	121	GCAGGAGAGAGAGCAGGATAAATGCTACCAGTATTGGCCAACCGAGGGCTCAGTTACTCA	180
Query	181	TGGAGAAATAACGATTGAGATAAAGAATGATACCCTTTCAGAAGCCATCAGTATACGAGA	240
Sbjct	181	TGGAGAAATAACGATTGAGATAAAGAATGATACCCTTTCAGAAGCCATCAGTATACGAGA	240
Query	241	CTTTCTGGTCACTCTCAATCAGCCCCAGGCCCGCCAGGAGGAGCAGGTCCGAGTAGTGCG	300
Sbjct	241	CTTTCTGGTCACTCTCAATCAGCCCCAGGCCCGCCAGGAGGAGCAGGTCCGAGTAGTGCG	300
Query	301	CCAGTTTCACTTCCACGGCTGGCCTGAGATCGGGATTCCCGCCGAGGGCAAAGGCATGAT	360
Sbjct	301	CCAGTTTCACTTCCACGGCTGGCCTGAGATCGGGATTCCCGCCGAGGGCAAAGGCATGAT	360
Query	361	TGACCTCATCGCAGCCGTGCAGAAGCANCAGCAGCAGACAGGCAACCACCCCATCACCGT	420
Sbjct	361	TGACCTCATCGCAGCCGTGCAGAAGCANCAGCAGCAGACAGGCAACCACCCCATCACCGT	420
Query	421	GCACTGCAGTGCCGGAGCTGGGCGAACAGGTACATTCATAGCCCTCAGCAACATTTTGGA	480
Sbjct	421	GCACTGCAGTGCCGGAGCTGGGCGAACAGGTACATTCATAGCCCTCAGCAACATTTTGGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCGAGTAAAAGCCGAGGGACTTTTANATGTATTTCAAGCTGTGAAGAGTTTACGACTTCA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCGAGTAAAAGCCGAGGGACTTTTANATGTATTTCAAGCTGTGAAGAGTTTACGACTTCA  540

Query  541  GAGACCACATATGGTGCAACCCTGGAACAGTATGAAATGTGCTACAAAGTGGTACAAGAT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GAGACCACATATGGTGCAACCCTGGAACAGTATGAAATGTGCTACAAAGTGGTACAAGAT  600

Query  601  TTATTGATATATTTCTGATTATGCTAATTTCAATGAAGATCCTGCCTTAAATATTTTTTA  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TTATTGATATATTTCTGATTATGCTAATTTCAATGAAGATCCTGCCTTAAATATTTTTTA  660

Query  661  ATTTAATGGCANAT  674
          |||||||||||||
Sbjct   661  ATTTAATGGCANAT  674
```

Blast comparison trimmed “NAT” from the 3’ end of both sequences and reported 671 identities. The report has been manually corrected for this. “NAT” has been appended to both sequences and identity count has been increased to 674.

Sequence 328 matched with Sequence 26

Query= Sequence ID 328
Length=609

SEQ ID NO: 26

ALIGNMENTS

Identities = 609/609 (100%), Gaps = 0/609 (0%)

Query	1	CAAGACTCCATCTCaaaaaaaaaaaaaTCTACAGTGCTGAGTATATAAAATTATTAAC	60
Sbjct	1	CAAGACTCCATCTCAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTATTAAC	60
Query	61	ACATTTTACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Sbjct	61	ACATTTTACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Query	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Sbjct	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Query	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Sbjct	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Query	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTAACT	300
Sbjct	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTAACT	300
Query	301	GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT	360
Sbjct	301	GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT	360
Query	361	GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Sbjct	361	GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Query	421	GAGGAAAGATGGATTTTCACTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480
Sbjct	421	GAGGAAAGATGGATTTTCACTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAAATAAGaaaaaaaTTAAACTGCATTCTGCTGTTCTTCTTTANAAGCATTCTGCGTAA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AAAATAAGAAAAAAATTAAACTGCATTCTGCTGTTCTTCTTTANAAGCATTCTGCGTAA  540

Query  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600

Query  601  GTGGTTTTT  609
          |||||||
Sbjct   601  GTGGTTTTT  609
```

Sequence 330 matched with Sequence 27

Query= Sequence ID 330
Length=383

SEQ ID NO: 27

ALIGNMENTS

Identities = 383/383 (100%), Gaps = 0/383 (0%)

Query	1	GCGGGAATCGCGGCCCGCTCGACCTCAAAGGAGaaaaaaaccttgtaaaaaagcaaa	60
Sbjct	1	GCGGGAATCGCGGCCCGCTCGACCTCAAAGGAGAAAAAACCTTGTAaaaaaAGCAAA	60
Query	61	aatgacaacagaaaaCAATCTTATTCCGAGCATTCCAGTAACTTTTTGTGTATGTACT	120
Sbjct	61	AATGACAACAGAAAAACAATCTTATTCCGAGCATTCCAGTAACTTTTTGTGTATGTACT	120
Query	121	TAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGT	180
Sbjct	121	TAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGT	180
Query	181	TTCTtttttttttcttttttgtctatgaagttgctgtttatttttttGGCCTGTTTGAT	240
Sbjct	181	TTCTTTTTTTTTCCTTTTTTGTCTATGAAGTTGCTGTTTATTTTTTTTGGCCTGTTTGAT	240
Query	241	GTATGTGTGAAACAATGTTGTCCAACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCT	300
Sbjct	241	GTATGTGTGAAACAATGTTGTCCAACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCT	300
Query	301	aaattttaaaatt	360
Sbjct	301	AAATTTTAAAT	360
Query	361	tttaaaataaaaCCCTTGTTAT	383
Sbjct	361	TTTAAATAAAACCCTTGTTAT	383

Sequence 331 matched with Sequence 28

Query= Sequence ID 331
Length=729

SEQ ID NO: 28

ALIGNMENTS

Identities = 729/729 (100%), Gaps = 0/729 (0%)

Query	1	GCCGCGTCGACCTGCATGAGCCACAGTTTCTTGACTGGAGGCCATCAACCCTCTTGGTTG	60
Sbjct	1	GCCGCGTCGACCTGCATGAGCCACAGTTTCTTGACTGGAGGCCATCAACCCTCTTGGTTG	60
Query	61	AGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCACTGGTGGGCCTGGGCTTCTGAGGTG	120
Sbjct	61	AGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCACTGGTGGGCCTGGGCTTCTGAGGTG	120
Query	121	GCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTCCTGGGCCTCTCAGTTGAACAAAGCA	180
Sbjct	121	GCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTCCTGGGCCTCTCAGTTGAACAAAGCA	180
Query	181	GCAAAACAAAGGCAGTTTTATATGAAAGATTANAAGCCTGGAATAATCAGGCTTTTTAAA	240
Sbjct	181	GCAAAACAAAGGCAGTTTTATATGAAAGATTANAAGCCTGGAATAATCAGGCTTTTTAAA	240
Query	241	TGATGTAATTCCTACTGTAATAGCATAGGGATTTTGAAGCAGCTGCTGGTGGCTTGGGA	300
Sbjct	241	TGATGTAATTCCTACTGTAATAGCATAGGGATTTTGAAGCAGCTGCTGGTGGCTTGGGA	300
Query	301	CATCANTGGGGCCAAGGGTTCTCTGTCCCTGGTTCAACTGTGATTTGGCTTTCCCGTGTC	360
Sbjct	301	CATCANTGGGGCCAAGGGTTCTCTGTCCCTGGTTCAACTGTGATTTGGCTTTCCCGTGTC	360
Query	361	TTTCCTGGTGATGCCTTGTTTGGGGTTCTGTGGGTTTGGGTGGGAAGAGGGCCATCTGCC	420
Sbjct	361	TTTCCTGGTGATGCCTTGTTTGGGGTTCTGTGGGTTTGGGTGGGAAGAGGGCCATCTGCC	420
Query	421	TGAATGTAACCTGCTAGCTCTCCGAAGCCCTGCGGGCCTGGCTTGTGTGAGCGTGTGGAC	480
Sbjct	421	TGAATGTAACCTGCTAGCTCTCCGAAGCCCTGCGGGCCTGGCTTGTGTGAGCGTGTGGAC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTCCCTGGCTTGTGAGGCGCT	540
Sbjct	481	AGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTCCCTGGCTTGTGAGGCGCT	540
Query	541	GCTTCAACCTGCACCCCTCCTTGTCTCATAGATGCTCCTTTTGACCTTTTCAAAATTAAT	600
Sbjct	541	GCTTCAACCTGCACCCCTCCTTGTCTCATAGATGCTCCTTTTGACCTTTTCAAAATTAAT	600
Query	601	ATGGATGGGAAAGCTCCTATGCCTTTTGGCTTCCTGGTAGAAGGCGGGATGCCCAAGGGT	660
Sbjct	601	ATGGATGGGAAAGCTCCTATGCCTTTTGGCTTCCTGGTAGAAGGCGGGATGCCCAAGGGT	660
Query	661	CTGCCTGGGTGTGGATTGGATGCTTGGGGTGTGGGGTTGGAAACTGTCTTGTGGCCCAC	720
Sbjct	661	CTGCCTGGGTGTGGATTGGATGCTTGGGGTGTGGGGTTGGAAACTGTCTTGTGGCCCAC	720
Query	721	TTGGGCCCC	729
Sbjct	721	TTGGGCCCC	729

Sequence 335 matched with Sequence 29

Query= Sequence ID 335
Length=552

SEQ ID NO: 29

ALIGNMENTS

Identities = 552/552 (100%), Gaps = 0/552 (0%)

Query	1	CCCGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAA	60
Sbjct	1	CCCGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAA	60
Query	61	GAAAGGGTCCAAGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTA	120
Sbjct	61	GAAAGGGTCCAAGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTA	120
Query	121	CCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGA	180
Sbjct	121	CCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGA	180
Query	181	ATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCC	240
Sbjct	181	ATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCC	240
Query	241	AGTGCAACCCTTGCCTCGCTTGTC AACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCT	300
Sbjct	241	AGTGCAACCCTTGCCTCGCTTGTC AACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCT	300
Query	301	GGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTaaaaaaaGATTAACCAGTGTG	360
Sbjct	301	GGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAGATTAACCAGTGTG	360
Query	361	AACATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAG	420
Sbjct	361	AACATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAG	420
Query	421	AATAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAA	480
Sbjct	421	AATAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAATGGACTGGCGGCGTGGGTGAGCTGATTTGGAAAAGTCCCCTTCTGCAAAAAACACTG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GAATGGACTGGCGGCGTGGGTGAGCTGATTTGGAAAAGTCCCCTTCTGCAAAAAACACTG  540

Query  541  GCCTGCTTTCCA  552
          |||||||||
Sbjct   541  GCCTGCTTTCCA  552
```


Sequence 337 matched with Sequence 30

Query= Sequence ID 337
Length=606

SEQ ID NO: 30

ALIGNMENTS

Identities = 606/606 (100%), Gaps = 0/606 (0%)

Query	1	CAAGACTCCATCTCaaaaaaaaaaaaaTCTACAGTGCTGAGTATATAAAATTATTAAC	60
Sbjct	1	CAAGACTCCATCTCAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTATTAAC	60
Query	61	ACATTTTACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Sbjct	61	ACATTTTACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Query	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Sbjct	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Query	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Sbjct	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Query	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Sbjct	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Query	301	GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT	360
Sbjct	301	GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT	360
Query	361	GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Sbjct	361	GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Query	421	GAGGAAAGATGGATTTTCAGTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480
Sbjct	421	GAGGAAAGATGGATTTTCAGTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAAATAAGaaaaaaaTTAAACTGCATTCTGCTGTTCTTCTTTAGAACGATTCCTGCGTAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AAAATAAGAAAAAAATTAAACTGCATTCTGCTGTTCTTCTTTAGAACGATTCCTGCGTAA  540

Query  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600

Query  601  GTGGTT  606
          |||||
Sbjct   601  GTGGTT  606
```

Sequence 338 matched with Sequence 31

Query= Sequence ID 338
Length=734

SEQ ID NO: 31

ALIGNMENTS

Identities = 734/734 (100%), Gaps = 0/734 (0%)

Query	1	CTGGACTGCATGACCAGATCTGATGGGTGAGACTCAGGTGGCATGGAAGAGCCGAAAGAG	60
Sbjct	1	CTGGACTGCATGACCAGATCTGATGGGTGAGACTCAGGTGGCATGGAAGAGCCGAAAGAG	60
Query	61	GATACCATATGTGGGTGCCgggggggATAGGTGAGAAGTACTAGAAGGCGGAATGGAAGG	120
Sbjct	61	GATACCATATGTGGGTGCCGGGGGGGATAGGTGAGAAGTACTAGAAGGCGGAATGGAAGG	120
Query	121	ACACTTCTGCTCAGCTCTGTGACACGGGCAGGGACCCTGCAGGGCTCAGGTCCTTTAACA	180
Sbjct	121	ACACTTCTGCTCAGCTCTGTGACACGGGCAGGGACCCTGCAGGGCTCAGGTCCTTTAACA	180
Query	181	CAGCAGCTTCATTCTAACACCAGCAGCGTTGGAACACACGTACAAGTATGCAGACTAAGC	240
Sbjct	181	CAGCAGCTTCATTCTAACACCAGCAGCGTTGGAACACACGTACAAGTATGCAGACTAAGC	240
Query	241	TCTTGCTTGGCTGATACGGCTTTTGGGTTTTAGAGAACATGCATATATGTTCTCATTC	300
Sbjct	241	TCTTGCTTGGCTGATACGGCTTTTGGGTTTTAGAGAACATGCATATATGTTCTCATTC	300
Query	301	ATGGTACATGAACTCAGAAGCCTTACTGCCTATTTTTGTTAATACTTCTGGGCAAACATT	360
Sbjct	301	ATGGTACATGAACTCAGAAGCCTTACTGCCTATTTTTGTTAATACTTCTGGGCAAACATT	360
Query	361	ACCACTTACAACCTCACACCAGTTAGAAATCATTTGTAAATGTTATTTAATAAAGCCAAA	420
Sbjct	361	ACCACTTACAACCTCACACCAGTTAGAAATCATTTGTAAATGTTATTTAATAAAGCCAAA	420
Query	421	GAACTAAATCATATTTATTTTCCAAGNNTTCTAAGATCTCTGAACTAATGAGGTTTTT	480
Sbjct	421	GAACTAAATCATATTTATTTTCCAAGNNTTCTAAGATCTCTGAACTAATGAGGTTTTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAAATCCCCATTAAGTACTCATCACTGCTAGTAAAAGCAGTTGTCTTTACCTTTAATTCC	540
Sbjct	481	TAAATCCCCATTAAGTACTCATCACTGCTAGTAAAAGCAGTTGTCTTTACCTTTAATTCC	540
Query	541	AGTGAGTCCCCTTAAATTTATTTTTTATTATCTTTGGCTACATTGCCTTAGACAAAATGT	600
Sbjct	541	AGTGAGTCCCCTTAAATTTATTTTTTATTATCTTTGGCTACATTGCCTTAGACAAAATGT	600
Query	601	GGTCACCCTAATTTAANGGATAAAATTCACATCCTCACAGATTTCTTATTAAGAGGGTCT	660
Sbjct	601	GGTCACCCTAATTTAANGGATAAAATTCACATCCTCACAGATTTCTTATTAAGAGGGTCT	660
Query	661	AANCCTTGAATAATCANCAGTGGAAATGGAAGTCTTCTTTACTGGNTTTCCTTTCCC	720
Sbjct	661	AANCCTTGAATAATCANCAGTGGAAATGGAAGTCTTCTTTACTGGNTTTCCTTTCCC	720
Query	721	TTTTTTATCCCATG	734
Sbjct	721	TTTTTTATCCCATG	734

Sequence 339 matched with Sequence 32

Query= Sequence ID 339
Length=517

SEQ ID NO: 32

ALIGNMENTS

Identities = 517/517 (100%), Gaps = 0/517 (0%)

Query	1	tttttttttAAATAAGCTGTCGGCACTCAAGGGTAATTCATATCAGTGTGNTCTACAA	60
Sbjct	1	TTTTTTTTTAAATAAGCTGTCGGCACTCAAGGGTAATTCATATCAGTGTGNTCTACAA	60
Query	61	GCTGGGGGAAAATGAGTTCTAATTGTCANAGCTACCAAATCCTTCACCTTTAGCATAAAG	120
Sbjct	61	GCTGGGGGAAAATGAGTTCTAATTGTCANAGCTACCAAATCCTTCACCTTTAGCATAAAG	120
Query	121	GTTTAAAGATATCACAAAGATGCCAAGTGATTAATAATGTTTTAAACCAACCCCTTTTCT	180
Sbjct	121	GTTTAAAGATATCACAAAGATGCCAAGTGATTAATAATGTTTTAAACCAACCCCTTTTCT	180
Query	181	GTCTGAAAAACAACATAAACAATATTACAACAGTATAGTTACAGAAGGGTTCTATTTTC	240
Sbjct	181	GTCTGAAAAACAACATAAACAATATTACAACAGTATAGTTACAGAAGGGTTCTATTTTC	240
Query	241	ATATGTTTTATGCACACTGTGCCTCAAAGGTACTATTTAAATATATATACTTTTGAGGGG	300
Sbjct	241	ATATGTTTTATGCACACTGTGCCTCAAAGGTACTATTTAAATATATATACTTTTGAGGGG	300
Query	301	GTGGCTAATGCAGAAACACCCAAGACCTAAGGAAGATACAACCCATTCTAGGTGTGAG	360
Sbjct	301	GTGGCTAATGCAGAAACACCCAAGACCTAAGGAAGATACAACCCATTCTAGGTGTGAG	360
Query	361	GTCTAAATGCTTCACACACCCACTTGTGACCTTTTTTCATGAAGAATCATAACACTGTGC	420
Sbjct	361	GTCTAAATGCTTCACACACCCACTTGTGACCTTTTTTCATGAAGAATCATAACACTGTGC	420
Query	421	AGTGAGAAACAGTGGCAAAGCAATACTGAAAGCATTTTAAATTATTTACTAGGTAAAAAG	480
Sbjct	421	AGTGAGAAACAGTGGCAAAGCAATACTGAAAGCATTTTAAATTATTTACTAGGTAAAAAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGTGAACTGATACTTTAAATACATCAAATTTTCATCAT  517
          |||
Sbjct  481  GGTGAACTGATACTTTAAATACATCAAATTTTCATCAT  517
```

Sequence 360 matched with Sequence 33

Query= Sequence ID 360
Length=536

SEQ ID NO: 33

ALIGNMENTS

Identities = 536/536 (100%), Gaps = 0/536 (0%)

Query	1	GCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTCGCTGAGGAAAAATAACTAA	60
Sbjct	1	GCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTCGCTGAGGAAAAATAACTAA	60
Query	61	ACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCATTTTTTG	120
Sbjct	61	ACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCATTTTTTG	120
Query	121	TGCAAACCTTGTCGGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAGTCAACTTCTCAG	180
Sbjct	121	TGCAAACCTTGTCGGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAGTCAACTTCTCAG	180
Query	181	AGTTTTCTAAGAAGTGCTCAGAGAGGTGGAAGACCATGTCTGCTAAAGAGAAAGGAAAAAT	240
Sbjct	181	AGTTTTCTAAGAAGTGCTCAGAGAGGTGGAAGACCATGTCTGCTAAAGAGAAAGGAAAAAT	240
Query	241	TTGAAGATATGGCAAAAGCGGACAAGGCCCGTTATGAAAGAGAAATGAAAACCTATATCC	300
Sbjct	241	TTGAAGATATGGCAAAAGCGGACAAGGCCCGTTATGAAAGAGAAATGAAAACCTATATCC	300
Query	301	CTCCCAAAGGGGAGACAAAAAAGAAGTTCAAGGATCCCAATGCACCCAAGAGGCCTCCTT	360
Sbjct	301	CTCCCAAAGGGGAGACAAAAAAGAAGTTCAAGGATCCCAATGCACCCAAGAGGCCTCCTT	360
Query	361	CGGCCTTCTTCCTCTTCTGCTCTGAGTATCGCCCAAAAATCAAAGGAGAACATCCTGGCC	420
Sbjct	361	CGGCCTTCTTCCTCTTCTGCTCTGAGTATCGCCCAAAAATCAAAGGAGAACATCCTGGCC	420
Query	421	TGTCCATTGGTGATGTTGCGAAGAAACTGGGAGAGATGTGGAATAACACTGCTGCAGATG	480
Sbjct	421	TGTCCATTGGTGATGTTGCGAAGAAACTGGGAGAGATGTGGAATAACACTGCTGCAGATG	480

PATENT SEQUENCE ALIGNMENT

Query	481	ACAAGCAGCCTTATGAAAAGAAGGCTGCGAAGCTGAAGGAAAAATACGAAAAGGTA	536
Sbjct	481	ACAAGCAGCCTTATGAAAAGAAGGCTGCGAAGCTGAAGGAAAAATACGAAAAGGTA	536

Sequence 361 matched with Sequence 34

Query= Sequence ID - 361 nt: 622
Length=622

SEQ ID NO: 34 nt: 622

ALIGNMENTS

Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query	1	CTGTNATNGAATCTGCTTGTNACTNAAATGCTAAACTCAATTCTGTAATTCAATAGGTGC	60
Sbjct	1	CTGTNATNGAATCTGCTTGTNACTNAAATGCTAAACTCAATTCTGTAATTCAATAGGTGC	60
Query	61	ACCTNTCTGAGAAACATANNAGACAATGAGGAAAAGGATTCANCATTCCGTGGAATTTGT	120
Sbjct	61	ACCTNTCTGAGAAACATANNAGACAATGAGGAAAAGGATTCANCATTCCGTGGAATTTGT	120
Query	121	ACCATGATCAGTGTGAATCCCAANTGGCGTAATCCAAGTAAGATGTTACAAAAGATTTGTT	180
Sbjct	121	ACCATGATCAGTGTGAATCCCAANTGGCGTAATCCAAGTAAGATGTTACAAAAGATTTGTT	180
Query	181	TTTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAA	240
Sbjct	181	TTTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAA	240
Query	241	AGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAATGTATATTTCTTAA	300
Sbjct	241	AGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAATGTATATTTCTTAA	300
Query	301	TATCTTGAAATTGTAATGCCtttttttttcctaaatttttttGTCATGAAATGAGATA	360
Sbjct	301	TATCTTGAAATTGTAATGCCTTTTTTTTTCTAAATTTTTTTTGTGTCATGAAATGAGATA	360
Query	361	GTAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTT	420
Sbjct	361	GTAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTT	420
Query	421	TCATCCAAATTTAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCA	480
Sbjct	421	TCATCCAAATTTAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	NGTTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATT	540
Sbjct	481	NGTTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATT	540
Query	541	CTGAATAAAATACTTTGAATCAGATTTAGAAATAATGAATAAAATACAAATCACCATTGA	600
Sbjct	541	CTGAATAAAATACTTTGAATCAGATTTAGAAATAATGAATAAAATACAAATCACCATTGA	600
Query	601	AATTGCTCTAATTTTGAGAGCT	622
Sbjct	601	AATTGCTCTAATTTTGAGAGCT	622

Sequence 363 matched with Sequence 35

Query= Sequence ID - 363 nt: 628
Length=628

SEQ ID NO: 35 nt: 628

ALIGNMENTS

Identities = 628/628 (100%), Gaps = 0/628 (0%)

Query	1	ATCACNTGAGGCAAGAGTTTGAGCCAGCCTAGCTAACATGGTGAAACCCCATCTCTACAA	60
Sbjct	1	ATCACNTGAGGCAAGAGTTTGAGCCAGCCTAGCTAACATGGTGAAACCCCATCTCTACAA	60
Query	61	AAATATAAAAATTAGCCTGGGTGGTGATGGGCACCTGTAACCCAGCTACTCGGGAGGCT	120
Sbjct	61	AAATATAAAAATTAGCCTGGGTGGTGATGGGCACCTGTAACCCAGCTACTCGGGAGGCT	120
Query	121	GAGGTAGGAGAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCA	180
Sbjct	121	GAGGTAGGAGAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCA	180
Query	181	CTGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCaaaaaaaaataataataaa	240
Sbjct	181	CTGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAAAAAAATAATAATAAA	240
Query	241	taataataaaaaggaataacatagctaggaataaatTTAATCAAAGAGGTGAAAGACTTA	300
Sbjct	241	TAATAATAAAAAGGAATAACATAGCTAGGAATAAATTTAATCAAAGAGGTGAAAGACTTA	300
Query	301	TAACTTAAACTACaaaaaaaaTCACTGAAGGAATTATAGACCCaaataaaaaataaa	360
Sbjct	301	TAACTTAAACTACAAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAAATAAA	360
Query	361	taaaaaGACATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTA	420
Sbjct	361	TAAAAAGACATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTA	420
Query	421	CCCAAAGTGATCTACAGATTCAACATAATCCCTATCAAAATCCAACAGCCTACTTTGTA	480
Sbjct	421	CCCAAAGTGATCTACAGATTCAACATAATCCCTATCAAAATCCAACAGCCTACTTTGTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAAATGGAAAAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GAAATGGAAAAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAA  540

Query  541  ACAATCTTGGGGGaaaaaaaaacaaaaacaaaGTCAAAGAACTCACACTTCTCTATTTATA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ACAATCTTGGGGGAAAAAAAAACAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATA  600

Query  601  AATTTACTACAAAGTTATAGTAATCAAA  628
          ||||||||||||||||||||||||
Sbjct   601  AATTTACTACAAAGTTATAGTAATCAAA  628
```

Sequence 364 matched with Sequence 36

Query= Sequence ID - 364 nt: 528
Length=527

SEQ ID NO: 36 nt: 528

ALIGNMENTS

Identities = 527/527 (100%), Gaps = 0/527 (0%)

Query	1	TGAACATCCAGCCATGTCATTTCTTCCATTCTGCCCTGGAGTAAAGTAGATTTACTGAG	60
Sbjct	1	TGAACATCCAGCCATGTCATTTCTTCCATTCTGCCCTGGAGTAAAGTAGATTTACTGAG	60
Query	61	CTGATGACTTGTGTGCATTTGTACATTGCAACCTTAGCTTACCTCTTGAAGCATGTAGAG	120
Sbjct	61	CTGATGACTTGTGTGCATTTGTACATTGCAACCTTAGCTTACCTCTTGAAGCATGTAGAG	120
Query	121	CATTCATCACCCACCATTCACTGCCTACTCCCACCACAGCTGTTTCGTGGTCTGTC	180
Sbjct	121	CATTCATCACCCACCATTCACTGCCTACTCCCACCACAGCTGTTTCGTGGTCTGTC	180
Query	181	TGCTCCCTGTGCCACCCCCACCCCATCAGGTGGGCCTTTTGCAAGTGATGAAGTCACCTG	240
Sbjct	181	TGCTCCCTGTGCCACCCCCACCCCATCAGGTGGGCCTTTTGCAAGTGATGAAGTCACCTG	240
Query	241	TGGGGGAAGAGCTTTCCTTTCCTCTCCTCAACTCAGAAGGCCTCTTCCTCTTGCTCAAGA	300
Sbjct	241	TGGGGGAAGAGCTTTCCTTTCCTCTCCTCAACTCAGAAGGCCTCTTCCTCTTGCTCAAGA	300
Query	301	GGGTGCTGCTGCTTTCTGCCTCCTTCCCCGGCCGGCCTCCATCCCAGTTCACCTTTTCAG	360
Sbjct	301	GGGTGCTGCTGCTTTCTGCCTCCTTCCCCGGCCGGCCTCCATCCCAGTTCACCTTTTCAG	360
Query	361	AAATGGCCCCTCAGTCAACTCTTCCCTTTTCTCCTGGCTTTTTATTTCTCCCAGTCTCTT	420
Sbjct	361	AAATGGCCCCTCAGTCAACTCTTCCCTTTTCTCCTGGCTTTTTATTTCTCCCAGTCTCTT	420
Query	421	AAGAGTATCCTTAGCTTTAAAAACAATAACACAGAGGATGGGTGCAGTGGCTCATGCCTG	480
Sbjct	421	AAGAGTATCCTTAGCTTTAAAAACAATAACACAGAGGATGGGTGCAGTGGCTCATGCCTG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TAATCCCAGCACTTTGGAGCCTGGGGCGGGCGGATCACTTGAGGNCA  527
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAATCCCAGCACTTTGGAGCCTGGGGCGGGCGGATCACTTGAGGNCA  527
```

Blast comparison trimmed “NCA” from the 3’ end of both sequences and reported 524 identities. The report has been manually corrected for this. “NCA” has been appended to both sequences and identity count has been increased to 527.

Sequence 365 matched with Sequence 37

Query= Sequence ID 365
Length=403

SEQ ID NO: 37

ALIGNMENTS

Identities = 403/403 (100%), Gaps = 0/403 (0%)

Query	1	GTCCCGGAATCGCGGCCGCTCGACCTTTTCTATGCCTGCTATATAAACAGTACCTTGCA	60
Sbjct	1	GTCCCGGAATCGCGGCCGCTCGACCTTTTCTATGCCTGCTATATAAACAGTACCTTGCA	60
Query	61	AGATGTCCTGTCTGATATCCACAAAGGGGTATTGTCAACCCCAAGTTCAGACAGCTTTGT	120
Sbjct	61	AGATGTCCTGTCTGATATCCACAAAGGGGTATTGTCAACCCCAAGTTCAGACAGCTTTGT	120
Query	121	ATTCTTCTGTCCCTGGATACATGAATTACTGCCATCTTTACACAGCGCCCTAAAATACCA	180
Sbjct	121	ATTCTTCTGTCCCTGGATACATGAATTACTGCCATCTTTACACAGCGCCCTAAAATACCA	180
Query	181	ACGCGAAGTTACCTGCTCAGCTTGAAGCTGCGCTGTACCCTGGAACCAGCACTTCTGCTG	240
Sbjct	181	ACGCGAAGTTACCTGCTCAGCTTGAAGCTGCGCTGTACCCTGGAACCAGCACTTCTGCTG	240
Query	241	AATGACTCAGGATGAAGCCTCGACTTCTCCTTCCCATCCCATGCCAGACCCAGTGGCT	300
Sbjct	241	AATGACTCAGGATGAAGCCTCGACTTCTCCTTCCCATCCCATGCCAGACCCAGTGGCT	300
Query	301	CCTTTCCCAATCTGATCCAGTGACTTTAAGTCCAGCTGTTGCAACCTGGGCATGAGGAGG	360
Sbjct	301	CCTTTCCCAATCTGATCCAGTGACTTTAAGTCCAGCTGTTGCAACCTGGGCATGAGGAGG	360
Query	361	AGTGCAAGATGGCTTTGTCCTACCTGGAAAGAGGCTTTCTGGA	403
Sbjct	361	AGTGCAAGATGGCTTTGTCCTACCTGGAAAGAGGCTTTCTGGA	403

Sequence 366 matched with Sequence 38

Query= Sequence ID 366
Length=111

SEQ ID NO: 38

ALIGNMENTS

Identities = 111/111 (100%), Gaps = 0/111 (0%)

Query	1	CACCATTTACACACAGTGGGTCCTTGAATAGCATCGTTTTATTCAATGTCATTTTGTTAT	60
Sbjct	1	CACCATTTACACACAGTGGGTCCTTGAATAGCATCGTTTTATTCAATGTCATTTTGTTAT	60
Query	61	AACATTGAGaaaaaaaTTGATTCCCGGCTGGGGCCACTGTCTGTGCACCGT	111
Sbjct	61	AACATTGAGAAAAAATTGATTCCCGGCTGGGGCCACTGTCTGTGCACCGT	111

Sequence 368 matched with Sequence 39

Query= Sequence ID - 368 nt: 329
Length=329

SEQ ID NO: 39 nt: 329

ALIGNMENTS

Identities = 329/329 (100%), Gaps = 0/329 (0%)

```
Query 1  GAAAGATCTAAATCGACACCCTAACATCACAATTAAGAAGCAAGAGCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  GAAAGATCTAAATCGACACCCTAACATCACAATTAAGAAGCAAGAGCAA 60

Query 61 ATTCAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG 120
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 ATTCAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG 120

Query 121 AGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTAAAAAGAT 180
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTAAAAAGAT 180

Query 181 CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT 240
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT 240

Query 241 CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAACTACCATCA 300
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAACTACCATCA 300

Query 301 GAGAACACTATAAACACCTCTATGCAAAT 329
          ||||||||||||||||||||||||
Sbjct 301 GAGAACACTATAAACACCTCTATGCAAAT 329
```

Sequence 369 matched with Sequence 40

Query= Sequence ID 369
Length=341

SEQ ID NO: 40

ALIGNMENTS

Identities = 341/341 (100%), Gaps = 0/341 (0%)

```
Query 1   GAAAGATCTAAATCGACACCCTAACATCACAATTAAGAAGCAAGAGCAA 60
          |||
Sbjct 1   GAAAGATCTAAATCGACACCCTAACATCACAATTAAGAAGCAAGAGCAA 60

Query 61  ATTCAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG 120
          |||
Sbjct 61  ATTCAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG 120

Query 121 AGACACAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTAAAAAGAT 180
          |||
Sbjct 121 AGACACAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTAAAAAGAT 180

Query 181 CAACAGAATTGACAGACTGCTAGCAAGACTAATAAGAAGAGAGAAGCATCAAATAGACT 240
          |||
Sbjct 181 CAACAGAATTGACAGACTGCTAGCAAGACTAATAAGAAGAGAGAAGCATCAAATAGACT 240

Query 241 CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAACTACCATCA 300
          |||
Sbjct 241 CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAACTACCATCA 300

Query 301 GAGAACACTATAAACACCTCTATGCAAATAAACTAGAAAAT 341
          |||
Sbjct 301 GAGAACACTATAAACACCTCTATGCAAATAAACTAGAAAAT 341
```

Sequence 370 matched with Sequence 41

Query= Sequence ID 370
Length=185

SEQ ID NO: 41

ALIGNMENTS

Identities = 185/185 (100%), Gaps = 0/185 (0%)

```
Query 1      GAAAGATCTAAATCGACACCCTAACATCACAATTTAAAAGAACTAGAGAAGCAAGAGCAA 60
            |||
Sbjct 1      GAAAGATCTAAATCGACACCCTAACATCACAATTTAAAAGAACTAGAGAAGCAAGAGCAA 60

Query 61     ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG 120
            |||
Sbjct 61     ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG 120

Query 121    AGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTTAAAAAGAT 180
            |||
Sbjct 121    AGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTTAAAAAGAT 180

Query 181    CAACA 185
            ||||
Sbjct 181    CAACA 185
```

Sequence 371 matched with Sequence 42

Query= Sequence ID 371
Length=553

SEQ ID NO: 42

ALIGNMENTS

Identities = 553/553 (100%), Gaps = 0/553 (0%)

Query	1	GCCCGGAATCGCGCCGCGTCGACGTAAGCTCGGCTGAATCCACGGTTCAAGAACAGGAA	60
Sbjct	1	GCCCGGAATCGCGCCGCGTCGACGTAAGCTCGGCTGAATCCACGGTTCAAGAACAGGAA	60
Query	61	AGAAGGCCAAGGCATAGGGAGTGGGGCAGTTGGGTGAATATTAGTACCTTTCCTCAGNT	120
Sbjct	61	AGAAGGCCAAGGCATAGGGAGTGGGGCAGTTGGGTGAATATTAGTACCTTTCCTCAGNT	120
Query	121	NCATTAATTACCCCTGCCTACTCTGCACAAAAGGATNTAACAACAGTTTCCTTTTAAATG	180
Sbjct	121	NCATTAATTACCCCTGCCTACTCTGCACAAAAGGATNTAACAACAGTTTCCTTTTAAATG	180
Query	181	GCCAGGTACAGCTGCTTATATGGANGGGCATTNTNAATGATATCCTTNATCACTGTCTT	240
Sbjct	181	GCCAGGTACAGCTGCTTATATGGANGGGCATTNTNAATGATATCCTTNATCACTGTCTT	240
Query	241	AATCATCACATNCTTAAACAATCACTTTATTGTGTTAAGGAAGATAAAAAATGGCTGGGT	300
Sbjct	241	AATCATCACATNCTTAAACAATCACTTTATTGTGTTAAGGAAGATAAAAAATGGCTGGGT	300
Query	301	TCAATTTCCGTTCTGGAAGAAATCGANTNAAAAGGTAACCATTTAATAATGCANAGGGCA	360
Sbjct	301	TCAATTTCCGTTCTGGAAGAAATCGANTNAAAAGGTAACCATTTAATAATGCANAGGGCA	360
Query	361	NTTTCAGTGCAGACCCTAATACTGGAAATTTTTAAAAACAAATGAAAACTTCTACTTTT	420
Sbjct	361	NTTTCAGTGCAGACCCTAATACTGGAAATTTTTAAAAACAAATGAAAACTTCTACTTTT	420
Query	421	TCTTCTAAGCTTACTTAACCACCCAAATTTTCCAGCCACATATCTTCCTAGTCTACAAC	480
Sbjct	421	TCTTCTAAGCTTACTTAACCACCCAAATTTTCCAGCCACATATCTTCCTAGTCTACAAC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCCTTTAACTTTAAGAGATGCTCaaaaaaTGTAATTCTCAAATACATTCTTATTACAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCCTTTAACTTTAAGAGATGCTCAAAAAAATGTAAATTCTCAAATACATTCTTATTACAA  540

Query  541  TTACTGCTAACCT  553
          |||||||||
Sbjct   541  TTACTGCTAACCT  553
```

Sequence 373 matched with Sequence 43

Query= Sequence ID 373
Length=510

SEQ ID NO: 43

ALIGNMENTS

Identities = 510/510 (100%), Gaps = 0/510 (0%)

Query	1	CCAGTGTGCTGGGATTACAGGCATGAGCCCTGCACCCAGCCTCTTAAACTGATCATATGA	60
Sbjct	1	CCAGTGTGCTGGGATTACAGGCATGAGCCCTGCACCCAGCCTCTTAAACTGATCATATGA	60
Query	61	TATTGGTTCTCAACCAAGGGTGACTTTGCCCCAGAGGATACTTGGCAATGTCTGGAGAT	120
Sbjct	61	TATTGGTTCTCAACCAAGGGTGACTTTGCCCCAGAGGATACTTGGCAATGTCTGGAGAT	120
Query	121	ACTCAGTTGTCATGACTTGGACAGGTGCTACTGTCACCCAGTGGGTAGAGGTCAGGGATG	180
Sbjct	121	ACTCAGTTGTCATGACTTGGACAGGTGCTACTGTCACCCAGTGGGTAGAGGTCAGGGATG	180
Query	181	GTGCTAAACATAGGACAGCTGTCAAGAGAAAAGAATGTACCCAGCCCCAAATGTCAGTAG	240
Sbjct	181	GTGCTAAACATAGGACAGCTGTCAAGAGAAAAGAATGTACCCAGCCCCAAATGTCAGTAG	240
Query	241	GGCTGAGGTTGAGAAACCCAGCTGTAGCTGACGTGTGAAGGACAGACTGGCCTGGAAGTG	300
Sbjct	241	GGCTGAGGTTGAGAAACCCAGCTGTAGCTGACGTGTGAAGGACAGACTGGCCTGGAAGTG	300
Query	301	TGTTTTCTGCCCCTTTCCACCCCTGCATATTAGTTAAGGCCAAAGGAAAAAAGGAATGCA	360
Sbjct	301	TGTTTTCTGCCCCTTTCCACCCCTGCATATTAGTTAAGGCCAAAGGAAAAAAGGAATGCA	360
Query	361	GGAAATGCCCGTTAAAAATCTTCAAAACAATATAAAATGATCAATTCCACTAAAAACCTT	420
Sbjct	361	GGAAATGCCCGTTAAAAATCTTCAAAACAATATAAAATGATCAATTCCACTAAAAACCTT	420
Query	421	TACACATTTAAGTATAAAGGTATTGGTAGGAAAATTTGTTATTCACTGCTTTTCTCAGTG	480
Sbjct	421	TACACATTTAAGTATAAAGGTATTGGTAGGAAAATTTGTTATTCACTGCTTTTCTCAGTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCATGAAATAATTATTTCTGCTGTCAGTTT	510
Sbjct	481	TCATGAAATAATTATTTCTGCTGTCAGTTT	510

Sequence 374 matched with Sequence 44

Query= Sequence ID 374
Length=335

SEQ ID NO: 44

ALIGNMENTS

Identities = 335/335 (100%), Gaps = 0/335 (0%)

```
Query 1      aaaaaaaaaTCACTGAAGGAATTATAGACCCaaataaaaaataaataaaaaGACATTCTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1      AAAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAAATAAATAAAAGACATTCTG  60

Query 61     TGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTGATCTAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61     TGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTGATCTAC  120

Query 121    AGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAAAAGCCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121    AGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAAAAGCCA  180

Query 181    ATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAAACAATCTTGGGGaaa  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181    ATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAAACAATCTTGGGGAAA  240

Query 241    aaaaacaaaaaacaaaGTCAAAGAACTCACACTTCTCTATTTATAATTTACTACAAAGTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241    AAAAACAAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATAATTTACTACAAAGTT  300

Query 301    ATAGTAATCAAAGTCGACGCGGCCGCGATTCCGGG  335
            ||||||||||||||||||||||||||||||||
Sbjct 301    ATAGTAATCAAAGTCGACGCGGCCGCGATTCCGGG  335
```


Sequence 378 matched with Sequence 45

Query= Sequence ID 378
Length=314

SEQ ID NO: 45

ALIGNMENTS

Identities = 314/314 (100%), Gaps = 0/314 (0%)

Query	1	CGACTGCGGCTCTTCCTCGGGCAGCGGAAGCGGCGGGCGGTTCGAGAAAGTGGCCTAAAA	60
Sbjct	1	CGACTGCGGCTCTTCCTCGGGCAGCGGAAGCGGCGGGCGGTTCGAGAAAGTGGCCTAAAA	60
Query	61	CTTCGGCGTTGGGTGAAAGAAAATGGCCCGAACCAAGCAGACTGCTCGTAAGTCCACCGG	120
Sbjct	61	CTTCGGCGTTGGGTGAAAGAAAATGGCCCGAACCAAGCAGACTGCTCGTAAGTCCACCGG	120
Query	121	TGGGAAAGCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTAC	180
Sbjct	121	TGGGAAAGCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTAC	180
Query	181	CGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCTG	240
Sbjct	181	CGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCTG	240
Query	241	TCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAG	300
Sbjct	241	TCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAG	300
Query	301	GGANATCGCCCAGG	314
Sbjct	301	GGANATCGCCCAGG	314

Sequence 380 matched with Sequence 46

Query= Sequence ID 380
Length=537

SEQ ID NO: 46

ALIGNMENTS

Identities = 537/537 (100%), Gaps = 0/537 (0%)

Query	1	GCAATTTAATTTTAAATAACAAAGATACTGTATTTTAACATGGTGAAATATACTTGGCTA	60
Sbjct	1	GCAATTTAATTTTAAATAACAAAGATACTGTATTTTAACATGGTGAAATATACTTGGCTA	60
Query	61	AGTCCAGATTaaaaaaaaGTATCTAGCCCAACAGTACAATTATACAGCTTTGTACAG	120
Sbjct	61	AGTCCAGATTAAAAAAAAAGTATCTAGCCCAACAGTACAATTATACAGCTTTGTACAG	120
Query	121	AACATTCCATAGATCAACAGAAAATACATTTGAGCGCaaaaataaaaaTATTTAAGGAG	180
Sbjct	121	AACATTCCATAGATCAACAGAAAATACATTTGAGCGCAAAAATAAAAAATATTTAAGGAG	180
Query	181	AATCTCTAAGCAGCATTTTATTTCTGCAAAAGACATATCTTGTCTGATTAAATATCTACA	240
Sbjct	181	AATCTCTAAGCAGCATTTTATTTCTGCAAAAGACATATCTTGTCTGATTAAATATCTACA	240
Query	241	AGTGCTTTTCCTTTCAAAAATACATATATTCTTAATAGACTAAGTCATTAACAATGACCT	300
Sbjct	241	AGTGCTTTTCCTTTCAAAAATACATATATTCTTAATAGACTAAGTCATTAACAATGACCT	300
Query	301	GGTAATTCTTTCACTTCAATTTGAATGATTTATAAGCTAAATCTTCAACCACAAAAAGGT	360
Sbjct	301	GGTAATTCTTTCACTTCAATTTGAATGATTTATAAGCTAAATCTTCAACCACAAAAAGGT	360
Query	361	TTTTATTTGTATTAAGATGTTACCACTTTTGACAAAAAGCTTAAATATTTTATATTTCA	420
Sbjct	361	TTTTATTTGTATTAAGATGTTACCACTTTTGACAAAAAGCTTAAATATTTTATATTTCA	420
Query	421	AAGGAAAATTAGCAACATAACTTTACAATATATTCTATGATATTTTGATTGTGAGGGCTA	480
Sbjct	421	AAGGAAAATTAGCAACATAACTTTACAATATATTCTATGATATTTTGATTGTGAGGGCTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTCTATTTAAAACTGATGATCTCTGTTGTGTTGCTCAGATGCAGGAAAGCAGCAAAA  537
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTCTATTTAAAACTGATGATCTCTGTTGTGTTGCTCAGATGCAGGAAAGCAGCAAAA  537
```

Sequence 381 matched with Sequence 47

Query= Sequence ID - 381 nt: 534
Length=534

SEQ ID NO: 47 nt: 534

ALIGNMENTS

Identities = 534/534 (100%), Gaps = 0/534 (0%)

Query	1	GACTTANATCTAAATGGACCACATTCTCTACTTaaaaaaaTGCTATTAACCATGTGATCT	60
Sbjct	1	GACTTANATCTAAATGGACCACATTCTCTACTTAAAAAATGCTATTAACCATGTGATCT	60
Query	61	TCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATATTCTTTG	120
Sbjct	61	TCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATATTCTTTG	120
Query	121	AATAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTG	180
Sbjct	121	AATAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTG	180
Query	181	CTAGAAAATAGGAAGTTTAAAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCACCC	240
Sbjct	181	CTAGAAAATAGGAAGTTTAAAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCACCC	240
Query	241	TCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCT	300
Sbjct	241	TCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCT	300
Query	301	TGAAGATTCTAGTCATCTGAAGAAAGTCTCTTTATTAAAGATTTTCATAAAAGAGACCAA	360
Sbjct	301	TGAAGATTCTAGTCATCTGAAGAAAGTCTCTTTATTAAAGATTTTCATAAAAGAGACCAA	360
Query	361	AGCAGACAAACAGAAAAAGACATCTTGGGGaaaaaaaCAAGGATAATGGGAAGAGAAGGA	420
Sbjct	361	AGCAGACAAACAGAAAAAGACATCTTGGGGAAAAAACAAGGATAATGGGAAGAGAAGGA	420
Query	421	AAGTTTTTAAAAATTATCAATATCCTCAGGGGGACAAATATTATATCCTATAAAGACAGA	480
Sbjct	421	AAGTTTTTAAAAATTATCAATATCCTCAGGGGGACAAATATTATATCCTATAAAGACAGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	tttttatttttttaaaaaaTAGAAAGCAAAACAAGCTCCTAAAAATAAAGTTTG	534
Sbjct	481	TTTTTATTTTTTAAAAAAATAGAAAGCAAAACAAGCTCCTAAAAATAAAGTTTG	534

Sequence 382 matched with Sequence 48

Query= Sequence ID - 382 nt: 444
Length=444

SEQ ID NO: 48 nt: 444

ALIGNMENTS

Identities = 444/444 (100%), Gaps = 0/444 (0%)

```
Query 1  GTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGCATTT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  GTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGCATTT 60

Query 61 GTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGG 120

Query 121 TTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGCTTGAG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGCTTGAG 180

Query 181 GCTCTGGACTGCATCCTACCACCAACTCGTCCAAGTACAAGCCCTTGCGCCTGCCTCTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 GCTCTGGACTGCATCCTACCACCAACTCGTCCAAGTACAAGCCCTTGCGCCTGCCTCTC 240

Query 241 CAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 CAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCTGTTGGCCGAGTGGAGACTGGT 300

Query 301 GTTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACGGAAGTAAAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 GTTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACGGAAGTAAAA 360

Query 361 TCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTTTTCCTGGGGACAATGTGGGCTTC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 TCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTTTTCCTGGGGACAATGTGGGCTTC 420

Query 421 AATGTCAAGAATGTGTCTGTCAAG 444
          ||||||||||||||||||
Sbjct 421 AATGTCAAGAATGTGTCTGTCAAG 444
```


Sequence 383 matched with Sequence 49

Query= Sequence ID - 383 nt: 566
Length=566

SEQ ID NO: 49 nt: 566

ALIGNMENTS

Identities = 566/566 (100%), Gaps = 0/566 (0%)

Query	1	CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA	60
Sbjct	1	CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA	60
Query	61	GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA	120
Sbjct	61	GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA	120
Query	121	ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGA	180
Sbjct	121	ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGA	180
Query	181	aaaaaaTGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAAAATGACCC	240
Sbjct	181	AAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAAAATGACCC	240
Query	241	CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA	300
Sbjct	241	CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA	300
Query	301	ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA	360
Sbjct	301	ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA	360
Query	361	ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA	420
Sbjct	361	ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA	420
Query	421	ATTTCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG	480
Sbjct	421	ATTTCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTCCTTTACCTTTTCTATAAGTTGTACCAAACATCCACTTAAGTTCTTTGATTTGTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTCCTTTACCTTTTCTATAAGTTGTACCAAACATCCACTTAAGTTCTTTGATTTGTCC  540

Query  541  ATTCCTTCAAATAAAGAAATTTGGTA  566
          ||||||||||||||||||||
Sbjct   541  ATTCCTTCAAATAAAGAAATTTGGTA  566
```

Sequence 384 matched with Sequence 50

Query= Sequence ID 384
Length=400

SEQ ID NO: 50

ALIGNMENTS

Identities = 400/400 (100%), Gaps = 0/400 (0%)

Query	1	TTTTGGGGTTTATATATAAGCCTGGTTCTTGCTGAAACTGCTTATGTTGATAACCAGTTA	60
Sbjct	1	TTTTGGGGTTTATATATAAGCCTGGTTCTTGCTGAAACTGCTTATGTTGATAACCAGTTA	60
Query	61	GTGAGTTCCTCTCTATTGACTTGCTGGGAAGTTTATAGAGACATTTTTTATGCATTTCAGA	120
Sbjct	61	GTGAGTTCCTCTCTATTGACTTGCTGGGAAGTTTATAGAGACATTTTTTATGCATTTCAGA	120
Query	121	GATTTTCAGTACAAATCTTGAAAAAGGGACATTTAGGCCGGGCGCGGTGGCTCACATCTGT	180
Sbjct	121	GATTTTCAGTACAAATCTTGAAAAAGGGACATTTAGGCCGGGCGCGGTGGCTCACATCTGT	180
Query	181	AACCCTAGCACTCTGGGAGGCTGAGGTGGGTGGATCATGAAGTCAAGAGATAGAGACCAT	240
Sbjct	181	AACCCTAGCACTCTGGGAGGCTGAGGTGGGTGGATCATGAAGTCAAGAGATAGAGACCAT	240
Query	241	CCTGGCAAAAATTAGCTGGGCGTGGTGGGGTGCGCCCGTAGTCCCAGCTACTCGGGAGGC	300
Sbjct	241	CCTGGCAAAAATTAGCTGGGCGTGGTGGGGTGCGCCCGTAGTCCCAGCTACTCGGGAGGC	300
Query	301	TGAGGCAGGAGAATTGCTTGAGCCCGGGAGGCGGAGGTTTCATTGAGCCGAGATAGTGCC	360
Sbjct	301	TGAGGCAGGAGAATTGCTTGAGCCCGGGAGGCGGAGGTTTCATTGAGCCGAGATAGTGCC	360
Query	361	ACTGCACTCCAGCCTGGACAACAGAGCGAGACTGTGTCTT	400
Sbjct	361	ACTGCACTCCAGCCTGGACAACAGAGCGAGACTGTGTCTT	400

Sequence 386 matched with Sequence 51

Query= Sequence ID 386
Length=562

SEQ ID NO: 51

ALIGNMENTS

Identities = 562/562 (100%), Gaps = 0/562 (0%)

Query	1	CTAAGGGTTTAAAGATGGAAAGAGGCATTGATGAACAGCTGGGGAAGGAGTAGTTTGAGG	60
Sbjct	1	CTAAGGGTTTAAAGATGGAAAGAGGCATTGATGAACAGCTGGGGAAGGAGTAGTTTGAGG	60
Query	61	TAGATGTGCAGATGGAATGAAGAGAAGGTCTCAAGAAGAGGGTGGAGCCAAAGAGGGCTG	120
Sbjct	61	TAGATGTGCAGATGGAATGAAGAGAAGGTCTCAAGAAGAGGGTGGAGCCAAAGAGGGCTG	120
Query	121	CAGATTTAGAAGGCTAAAGTCTTTAGATGGCTTTGGATAGCCTGTTGTATCTTGGACCAT	180
Sbjct	121	CAGATTTAGAAGGCTAAAGTCTTTAGATGGCTTTGGATAGCCTGTTGTATCTTGGACCAT	180
Query	181	GCAGGTTACAGTGGAGCATGGAGTGGGGACAGAAGTGGAGGAAGGAACCAGGGAACATGG	240
Sbjct	181	GCAGGTTACAGTGGAGCATGGAGTGGGGACAGAAGTGGAGGAAGGAACCAGGGAACATGG	240
Query	241	AGTGAGAAGCTAAAGGAAAGTGATGCAGTAGATACATGGCTCTAAAGTACTCAGGACTTT	300
Sbjct	241	AGTGAGAAGCTAAAGGAAAGTGATGCAGTAGATACATGGCTCTAAAGTACTCAGGACTTT	300
Query	301	CAGAGGCTTAAACATAGGGTGACCAACTATCCCACTATGCCTGATACTAAGGGCATTCCC	360
Sbjct	301	CAGAGGCTTAAACATAGGGTGACCAACTATCCCACTATGCCTGATACTAAGGGCATTCCC	360
Query	361	TGGATGTGGACCTTTCATTCCCCAAATTAGGAAAGTCTTGGGCATACCAAGACAAGTTGG	420
Sbjct	361	TGGATGTGGACCTTTCATTCCCCAAATTAGGAAAGTCTTGGGCATACCAAGACAAGTTGG	420
Query	421	CCACCCTACTCAAAAGTATGTAAGCTAACATATCTGTTCTCTAAGAGGTTAAAGCTGGAT	480
Sbjct	421	CCACCCTACTCAAAAGTATGTAAGCTAACATATCTGTTCTCTAAGAGGTTAAAGCTGGAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGGATACCAGATGTATGTACGTGATGCAGTTAAACAGCAATACAAGGGGGCAAGTCTAC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGGGATACCAGATGTATGTACGTGATGCAGTTAAACAGCAATACAAGGGGGCAAGTCTAC  540

Query  541  CTGATCGGCCAATTCAATGGGA  562
          ||||||||||||||||
Sbjct   541  CTGATCGGCCAATTCAATGGGA  562
```

Sequence 387 matched with Sequence 52

Query= Sequence ID 387
Length=614

SEQ ID NO: 52

ALIGNMENTS

Identities = 614/614 (100%), Gaps = 0/614 (0%)

Query	1	GAAGCCAAACCAAAGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAGA	60
Sbjct	1	GAAGCCAAACCAAAGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAGA	60
Query	61	AAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAGA	120
Sbjct	61	AAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAGA	120
Query	121	AGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGACT	180
Sbjct	121	AGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGACT	180
Query	181	ACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTGTCTTATT	240
Sbjct	181	ACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTGTCTTATT	240
Query	241	AGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCAGT	300
Sbjct	241	AGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCAGT	300
Query	301	CACTAGGTGAACAACCTTACTGCTCCAATCAGCCTTAGAGCAGGAATCAAACCTCATGTCTC	360
Sbjct	301	CACTAGGTGAACAACCTTACTGCTCCAATCAGCCTTAGAGCAGGAATCAAACCTCATGTCTC	360
Query	361	AGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGCTG	420
Sbjct	361	AGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGCTG	420
Query	421	AAATAGTAAATGTTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTCTA	480
Sbjct	421	AAATAGTAAATGTTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTCTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGG  540

Query  541  TCTACTATTTCTTCTGTAATACTGATTTTTACCCCATCAGGGTCAGTCCCCAGAGGTTGT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TCTACTATTTCTTCTGTAATACTGATTTTTACCCCATCAGGGTCAGTCCCCAGAGGTTGT  600

Query  601  AAATGTGAAGCTTG  614
          ||||||||||||
Sbjct   601  AAATGTGAAGCTTG  614
```

Sequence 388 matched with Sequence 53

Query= Sequence ID 388
Length=685

SEQ ID NO: 53

ALIGNMENTS

Identities = 685/685 (100%), Gaps = 0/685 (0%)

Query	1	CTTTGGACACTAGGAAAAACCTTGTAGAGAGAGTAAAAATTTAACACCCATAGTAGGC	60
Sbjct	1	CTTTGGACACTAGGAAAAACCTTGTAGAGAGAGTAAAAATTTAACACCCATAGTAGGC	60
Query	61	CTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAATCC	120
Sbjct	61	CTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAATCC	120
Query	121	CAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGAAC	180
Sbjct	121	CAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGAAC	180
Query	181	TAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAA	240
Sbjct	181	TAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAA	240
Query	241	ACACTGAACTGACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCC	300
Sbjct	241	ACACTGAACTGACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCC	300
Query	301	TCACTGTCAACCCAACACAGGCATGCTCATAAGGAAAGGTTaaaaaaaGTAAAAGGAACT	360
Sbjct	301	TCACTGTCAACCCAACACAGGCATGCTCATAAGGAAAGGTTAAAAAAGTAAAAGGAACT	360
Query	361	CGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCACCTCTAGCATCACCAGTATTAGA	420
Sbjct	361	CGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCACCTCTAGCATCACCAGTATTAGA	420
Query	421	GGCACCGCCTGCCAGTGACACATGTTTAAACGGCCGCGGTACCCTAACCGTGCAAAGGTA	480
Sbjct	421	GGCACCGCCTGCCAGTGACACATGTTTAAACGGCCGCGGTACCCTAACCGTGCAAAGGTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCATAATCACTTGTTCCCTTAATTAGGGACCTGTATGAATGGCTCCACGAGGGTTCAGCTG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCATAATCACTTGTTCCCTTAATTAGGGACCTGTATGAATGGCTCCACGAGGGTTCAGCTG  540

Query  541  TCTCTTACTTTTAAACCAGTGAAATTGACCTGCCCCGTGAAGAGGCGGGCATAACACAGCAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TCTCTTACTTTTAAACCAGTGAAATTGACCTGCCCCGTGAAGAGGCGGGCATAACACAGCAA  600

Query  601  GACGAGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACAGTCCTAACAAACCCCAGG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GACGAGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACAGTCCTAACAAACCCCAGG  660

Query  661  TCCTAAACTCCAAACCTGCATTAAA  685
          ||||||||||||||||||||
Sbjct   661  TCCTAAACTCCAAACCTGCATTAAA  685
```


Sequence 389 matched with Sequence 54

Query= Sequence ID 389
Length=533

SEQ ID NO: 54

ALIGNMENTS

Identities = 533/533 (100%), Gaps = 0/533 (0%)

Query	1	CGACCCGGAATTCGCGGCCGCGTCGACTGAGTTCTTGACAAGAGTGTTTTCCCTTCCCG	60
Sbjct	1	CGACCCGGAATTCGCGGCCGCGTCGACTGAGTTCTTGACAAGAGTGTTTTCCCTTCCCG	60
Query	61	TCACAGAGTGGGCCCAACGACCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTC	120
Sbjct	61	TCACAGAGTGGGCCCAACGACCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTC	120
Query	121	CCCAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGCGTCAAGGAAGCT	180
Sbjct	121	CCCAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGCGTCAAGGAAGCT	180
Query	181	GCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCACGGACTCTTTCCTCTGAACCTG	240
Sbjct	181	GCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCACGGACTCTTTCCTCTGAACCTG	240
Query	241	TTAGGGCTTGGTTTTAAAGGATTTTATGTGTGTTTCCGAATGTTTGTAGTTCCTTTTG	300
Sbjct	241	TTAGGGCTTGGTTTTAAAGGATTTTATGTGTGTTTCCGAATGTTTGTAGTTCCTTTTG	300
Query	301	TGGAGCCGCCAGCTGACAGGACATCTTACAAGAGAATTTGCACATCTCTGGAAGCTTAGC	360
Sbjct	301	TGGAGCCGCCAGCTGACAGGACATCTTACAAGAGAATTTGCACATCTCTGGAAGCTTAGC	360
Query	361	AATCTTATTGCACACTGTTTCGCTGGAAGCTTTTTGAAGAGCACATTCTCCTCAGTGAGCT	420
Sbjct	361	AATCTTATTGCACACTGTTTCGCTGGAAGCTTTTTGAAGAGCACATTCTCCTCAGTGAGCT	420
Query	421	CATGAGGTTTTCATTTTTATTCTTCCTTCCAACGTGGTGCTATCTCTGAAACGAGCGTTA	480
Sbjct	421	CATGAGGTTTTCATTTTTATTCTTCCTTCCAACGTGGTGCTATCTCTGAAACGAGCGTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GAGTGCCGCCTTAGACGGAGGCAGGAGTTTCGTTAGAAAGCGGACGCTGTTCT	533
Sbjct	481	GAGTGCCGCCTTAGACGGAGGCAGGAGTTTCGTTAGAAAGCGGACGCTGTTCT	533

Sequence 390 matched with Sequence 55

Query= Sequence ID - 390 nt: 523
Length=523

SEQ ID NO: 55 nt: 523

ALIGNMENTS

Identities = 523/523 (100%), Gaps = 0/523 (0%)

```
Query 1 GAATCCCTAGAAAAAGAGAATTCCCAACTTGATGAGGAAACTTAGAACTGCGAAGGAAT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GAATCCCTAGAAAAAGAGAATTCCCAACTTGATGAGGAAACTTAGAACTGCGAAGGAAT 60

Query 61 GTAGAATCTTTGAAGTGTGCAAGCATGAAAATGGCTCAGCTACAGCTAGAAAACAAAGAA 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GTAGAATCTTTGAAGTGTGCAAGCATGAAAATGGCTCAGCTACAGCTAGAAAACAAAGAA 120

Query 121 CTGGAAAGTGAAAAAGAGCAACTTAAGAAGGGTTTGGAGCTCCTGAAAGCATCTTTCAAG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 CTGGAAAGTGAAAAAGAGCAACTTAAGAAGGGTTTGGAGCTCCTGAAAGCATCTTTCAAG 180

Query 181 AAAACAGAACGCTTAGAAGTTAGCTACCAGGGTTTAGATATAGAAAATCAAAGACTGCAA 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AAAACAGAACGCTTAGAAGTTAGCTACCAGGGTTTAGATATAGAAAATCAAAGACTGCAA 240

Query 241 AAAACTTTAGAGAACAGCAATAaaaaaaTCCAGCAATTAGAGAGTGAAGTACAAGACTTA 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AAAACTTTAGAGAACAGCAATAAAAAAATCCAGCAATTAGAGAGTGAAGTACAAGACTTA 300

Query 301 GAGATGGAAAATCAAACATTGCagaaaaacctagaagaactaaaaatatctagcaaaaga 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 GAGATGGAAAATCAAACATTGCAGAAAAACCTAGAAGAACTAAAAATATCTAGCAAAAGA 360

Query 361 ctagaacagctggaaaaagaaaataaaTCATTAGAGCAAGAGACTTCTCAACTGGAAAAG 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 CTAGAACAGCTGGAAAAAGAAAATAAATCATTAGAGCAAGAGACTTCTCAACTGGAAAAG 420

Query 421 GATAAGAAACAATTGGAGAAGGAAAAATAAGAGACTCCGACANCAAGCAGAAATTAAGAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 GATAAGAAACAATTGGAGAAGGAAAAATAAGAGACTCCGACANCAAGCAGAAATTAAGAT 480
```

PATENT SEQUENCE ALIGNMENT

Query	481	CCACATTTGAAGAAAATAATGTGAAGATTGGAAATTTGGAAAA	523
Sbjct	481	CCACATTTGAAGAAAATAATGTGAAGATTGGAAATTTGGAAAA	523

Sequence 391 matched with Sequence 56

Query= Sequence ID - 391 nt: 566
Length=566

SEQ ID NO: 56 nt: 566

ALIGNMENTS

Identities = 566/566 (100%), Gaps = 0/566 (0%)

Query	1	CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA	60
Sbjct	1	CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA	60
Query	61	GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA	120
Sbjct	61	GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA	120
Query	121	ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGa	180
Sbjct	121	ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGA	180
Query	181	aaaaaaTGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAAAATGACCC	240
Sbjct	181	AAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAAAATGACCC	240
Query	241	CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA	300
Sbjct	241	CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA	300
Query	301	ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA	360
Sbjct	301	ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA	360
Query	361	ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA	420
Sbjct	361	ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA	420
Query	421	ATTTCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG	480
Sbjct	421	ATTTCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTCCTTTACCTTTTCTATAAGTTGTACCAAACATCCACTTAAGTTCTTTGATTTGTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTCCTTTACCTTTTCTATAAGTTGTACCAAACATCCACTTAAGTTCTTTGATTTGTCC  540

Query  541  ATTCCTTCAAATAAAGAAATTTGGTA  566
          ||||||||||||||||||||
Sbjct   541  ATTCCTTCAAATAAAGAAATTTGGTA  566
```

Sequence 394 matched with Sequence 57

Query= Sequence ID 394
Length=616

SEQ ID NO: 57

ALIGNMENTS

Identities = 616/616 (100%), Gaps = 0/616 (0%)

Query	1	GACCCGGAATCGCGGCCGCGTCGACCATTTTAGCCAAGGTGCCTCTATAGGGGTCAAGAC	60
Sbjct	1	GACCCGGAATCGCGGCCGCGTCGACCATTTTAGCCAAGGTGCCTCTATAGGGGTCAAGAC	60
Query	61	ATCATGTGCCCAGACCTAAGGTCAGGAATGTCATATTTTCTGTTAAAAATCATTTTATTT	120
Sbjct	61	ATCATGTGCCCAGACCTAAGGTCAGGAATGTCATATTTTCTGTTAAAAATCATTTTATTT	120
Query	121	CTGTGTATCTTACCTTTAAATCATTGTGGTTTACTCTGAGATTCTGTAGTCCTAATATTG	180
Sbjct	121	CTGTGTATCTTACCTTTAAATCATTGTGGTTTACTCTGAGATTCTGTAGTCCTAATATTG	180
Query	181	TATCATTGTGCTGTCTGCAAAACAACCTGAATCTATTTTGTGTTGCATCTTTGTTACATG	240
Sbjct	181	TATCATTGTGCTGTCTGCAAAACAACCTGAATCTATTTTGTGTTGCATCTTTGTTACATG	240
Query	241	TAACGCAGCTGTACTTTATGTTCTTTGCAACTGTTTCCATTATGAGAACGCTGTGCTATT	300
Sbjct	241	TAACGCAGCTGTACTTTATGTTCTTTGCAACTGTTTCCATTATGAGAACGCTGTGCTATT	300
Query	301	TACAAGGTTACATTTTCTTGCCAGGCGAGGTGGTCATGCCTGTGATCCCAGCACTTTG	360
Sbjct	301	TACAAGGTTACATTTTCTTGCCAGGCGAGGTGGTCATGCCTGTGATCCCAGCACTTTG	360
Query	361	GGAGGCCAAGGTGGGCGGATCACTTGAGGTAAAGAGTTGAGACCAGCCTGGCTAGCATGG	420
Sbjct	361	GGAGGCCAAGGTGGGCGGATCACTTGAGGTAAAGAGTTGAGACCAGCCTGGCTAGCATGG	420
Query	421	CGAAGCCCAGTCTCTACTAAAAATACAAAAATTGGCCGGGTGAAATTAGCCGGGCGTGGT	480
Sbjct	421	CGAAGCCCAGTCTCTACTAAAAATACAAAAATTGGCCGGGTGAAATTAGCCGGGCGTGGT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGTGTGTGCTTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCCG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGTGTGTGCTTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCCG  540

Query  541  GGAGGCAGAGGTTGCAGTGAGCCAAGATCANGCCACTGCACTCCACCTCGGGGTCAAGAG  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GGAGGCAGAGGTTGCAGTGAGCCAAGATCANGCCACTGCACTCCACCTCGGGGTCAAGAG  600

Query  601  CGAAACTCTGTCTCAA  616
          |||||||||||||||
Sbjct   601  CGAAACTCTGTCTCAA  616
```


Sequence 395 matched with Sequence 58

Query= Sequence ID 395
Length=598

SEQ ID NO: 58

ALIGNMENTS

Identities = 598/598 (100%), Gaps = 0/598 (0%)

Query	1	CCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCCTCCC	60
Sbjct	1	CCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCCTCCC	60
Query	61	AAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTAAATG	120
Sbjct	61	AAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTAAATG	120
Query	121	TTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGGGAAT	180
Sbjct	121	TTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGGGAAT	180
Query	181	ATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTAGAAT	240
Sbjct	181	ATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTAGAAT	240
Query	241	CAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTCATATGC	300
Sbjct	241	CAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTCATATGC	300
Query	301	AAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTTAAAAAACTGACCCTATT	360
Sbjct	301	AAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTTAAAAAACTGACCCTATT	360
Query	361	CTCAGGATGAAAATAATACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTAAGGA	420
Sbjct	361	CTCAGGATGAAAATAATACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTAAGGA	420
Query	421	GGTCAATTAATAATGCTGTAGTGTGCAAGGGAAGGAGAGGAAGAATCATATTCCTTCACT	480
Sbjct	421	GGTCAATTAATAATGCTGTAGTGTGCAAGGGAAGGAGAGGAAGAATCATATTCCTTCACT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGATTGGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGATTGGT  540

Query  541  AAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTGCAT  598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTGCAT  598
```

Sequence 396 matched with Sequence 59

Query= Sequence ID 396
Length=524

SEQ ID NO: 59

ALIGNMENTS

Identities = 524/524 (100%), Gaps = 0/524 (0%)

Query	1	CTTAAATCTAAATGGACCACATTCTCTACTTaaaaaaaTGCTATTAACCATGTGATCTTC	60
Sbjct	1	CTTAAATCTAAATGGACCACATTCTCTACTTAAAAAATGCTATTAACCATGTGATCTTC	60
Query	61	TCAGTCATGAGGTAATCTGGTGACTACCCCTTCCTCAAAGCCAGTTGGGATATTCTTTGAA	120
Sbjct	61	TCAGTCATGAGGTAATCTGGTGACTACCCCTTCCTCAAAGCCAGTTGGGATATTCTTTGAA	120
Query	121	TAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTGCT	180
Sbjct	121	TAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTGCT	180
Query	181	AGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCACCCCTC	240
Sbjct	181	AGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCACCCCTC	240
Query	241	ATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCTTG	300
Sbjct	241	ATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCTTG	300
Query	301	AAGATTACTAGTCATCTGAAGAAAGTCTCTTTATTAAGATTTTCATAAAAGAGACCAAA	360
Sbjct	301	AAGATTACTAGTCATCTGAAGAAAGTCTCTTTATTAAGATTTTCATAAAAGAGACCAAA	360
Query	361	GCAGACAAACAGAAAAAGACATCTTGGGGaaaaaaaCAAGGATAATGGGAAGAGAAGGAA	420
Sbjct	361	GCAGACAAACAGAAAAAGACATCTTGGGGAAAAAACAAGGATAATGGGAAGAGAAGGAA	420
Query	421	AGTTTTAAAAATTATCAATATCCTCAGGGGGACAAAATATTATATCCTATAAAGACAGAt	480
Sbjct	421	AGTTTTAAAAATTATCAATATCCTCAGGGGGACAAAATATTATATCCTATAAAGACAGAT	480

PATENT SEQUENCE ALIGNMENT

Query	481	ttttattttttaaaaaaTAGAAAGCAAAACAAGCTCCTAAAAA	524
Sbjct	481	TTTTATTTTATAAAAAATAGAAAGCAAAACAAGCTCCTAAAAA	524

Sequence 397 matched with Sequence 60

Query= Sequence ID - 397 nt: 534
Length=534

SEQ ID NO: 60 nt: 534

ALIGNMENTS

Identities = 534/534 (100%), Gaps = 0/534 (0%)

Query	1	GACCCGGAATCGCGGCCGCTCGACGGAAGCTCCTGCCCCTCCTAAAGCTGAAGCCAAAG	60
Sbjct	1	GACCCGGAATCGCGGCCGCTCGACGGAAGCTCCTGCCCCTCCTAAAGCTGAAGCCAAAG	60
Query	61	CGAAGGCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCACAGCCACAAAAAGAAGG	120
Sbjct	61	CGAAGGCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCACAGCCACAAAAAGAAGG	120
Query	121	AGATCCGCACGTCACCCACCTTCCGGCGGCCGAAGACACTGCGACTCCGGAGACAGCCCA	180
Sbjct	121	AGATCCGCACGTCACCCACCTTCCGGCGGCCGAAGACACTGCGACTCCGGAGACAGCCCA	180
Query	181	AATATCCTCGGAAGAGCGCTCCAGGAGAAAACAAGCTTGACCACTATGCTATCATCAAGT	240
Sbjct	181	AATATCCTCGGAAGAGCGCTCCAGGAGAAAACAAGCTTGACCACTATGCTATCATCAAGT	240
Query	241	TTCCGCTGACCACTGAGTCTGCCATGAAGAAGATAGAAGACAACAACACACTTGTGTTCA	300
Sbjct	241	TTCCGCTGACCACTGAGTCTGCCATGAAGAAGATAGAAGACAACAACACACTTGTGTTCA	300
Query	301	TTGTGGATGTTAAAGCCAACAAGCACCAGATTAAACAGGCTGTGAAGAAGCTGTATGACA	360
Sbjct	301	TTGTGGATGTTAAAGCCAACAAGCACCAGATTAAACAGGCTGTGAAGAAGCTGTATGACA	360
Query	361	TTGATGTGGCCAAGGTCAACACCCTGATTCCGGCCTGATGGAGAGAAGAAGGCATATGTTC	420
Sbjct	361	TTGATGTGGCCAAGGTCAACACCCTGATTCCGGCCTGATGGAGAGAAGAAGGCATATGTTC	420
Query	421	GACTGGCTCCTGATTACGATGCTTTGGATGTTGCCAACAAAATTGGGATCATTTAAACTG	480
Sbjct	421	GACTGGCTCCTGATTACGATGCTTTGGATGTTGCCAACAAAATTGGGATCATTTAAACTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGTCCAGCTGCCTAATTCTGAatatatatatatatatatatCTTTTCACCATAA	534
Sbjct	481	AGTCCAGCTGCCTAATTCTGAATATATATATATATATATATCTTTTCACCATAA	534

Sequence 398 matched with Sequence 61

Query= Sequence ID - 398 nt: 512
Length=512

SEQ ID NO: 61 nt: 512

ALIGNMENTS

Identities = 512/512 (100%), Gaps = 0/512 (0%)

Query	1	GGGGAGCCCCCTCTCCCTCAGTTGTTCTACTCAGACTGTTGCACTCTAAACCTAGGGA	60
Sbjct	1	GGGGAGCCCCCTCTCCCTCAGTTGTTCTACTCAGACTGTTGCACTCTAAACCTAGGGA	60
Query	61	GGTTGAAGAATGAGACCCTTAGGTTTTAACACGAATCCTGACACCACCATCTATAGGGTC	120
Sbjct	61	GGTTGAAGAATGAGACCCTTAGGTTTTAACACGAATCCTGACACCACCATCTATAGGGTC	120
Query	121	CCAACTTGTTATTGTAGGCAACCTTCCCTCTCTCCTTGGTGAAGAACATCCCAAGCCAG	180
Sbjct	121	CCAACTTGTTATTGTAGGCAACCTTCCCTCTCTCCTTGGTGAAGAACATCCCAAGCCAG	180
Query	181	AAAGAAGTTAACTACAGTGTTTTCTTTGCACCGATCCCCACCCCAATTCAATCCCGGAA	240
Sbjct	181	AAAGAAGTTAACTACAGTGTTTTCTTTGCACCGATCCCCACCCCAATTCAATCCCGGAA	240
Query	241	GGGACTTACTTAGGAAACCTTCTTTACTAGATATCCTGGCCCCCTGGGCTTGTGAACAC	300
Sbjct	241	GGGACTTACTTAGGAAACCTTCTTTACTAGATATCCTGGCCCCCTGGGCTTGTGAACAC	300
Query	301	CTCCTAGCCACATCACTACAGTACAGTGAGTGACCCAGCCTCCTGCCTACCCCAAGATG	360
Sbjct	301	CTCCTAGCCACATCACTACAGTACAGTGAGTGACCCAGCCTCCTGCCTACCCCAAGATG	360
Query	361	CCCCTCCCCACCCTGACCGTGCTAACTGTGTGTACATATATATTCTACATATATGTATAT	420
Sbjct	361	CCCCTCCCCACCCTGACCGTGCTAACTGTGTGTACATATATATTCTACATATATGTATAT	420
Query	421	TAAAACTGCACTGCCATGTCTGCCCTTTTTTGTGGTGTCTAGCATTAACTTATTGTCTAG	480
Sbjct	421	TAAAACTGCACTGCCATGTCTGCCCTTTTTTGTGGTGTCTAGCATTAACTTATTGTCTAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCCAAAGCGGGGTGGGAGGGGAATGCCACAG  512
          |||||||||||||||||||||||||||
Sbjct  481  GCCAAAGCGGGGTGGGAGGGGAATGCCACAG  512
```


Sequence 399 matched with Sequence 62

Query= Sequence ID 399
Length=642

SEQ ID NO: 62

ALIGNMENTS

Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query	1	TTTTGGCATTACTTAATCCAATTATAAAAACTGAATTTTAAAAACAGCACTTGTTTTT	60
Sbjct	1	TTTTGGCATTACTTAATCCAATTATAAAAACTGAATTTTAAAAACAGCACTTGTTTTT	60
Query	61	TCTTCCAAGATTAATTTGAAttttttATGGACATTAGAAAACATTGCAGTTTAGTCATA	120
Sbjct	61	TCTTCCAAGATTAATTTGAATTTTTTATGGACATTAGAAAACATTGCAGTTTAGTCATA	120
Query	121	ATCAAAAATAAATCTTGAGGCTGGTAGAGCAGCTTTGTTGCTGTTTATATTTTATTGCT	180
Sbjct	121	ATCAAAAATAAATCTTGAGGCTGGTAGAGCAGCTTTGTTGCTGTTTATATTTTATTGCT	180
Query	181	TACTGGATTTTCAGTGTTACCTAGTGCCATCAGTTTGGTATTTTGCCACCTTGCACATTCA	240
Sbjct	181	TACTGGATTTTCAGTGTTACCTAGTGCCATCAGTTTGGTATTTTGCCACCTTGCACATTCA	240
Query	241	GTGATGTTTGATtttttcttttcttttttCATATTACTTTTAAATCCTGAATAGTTTG	300
Sbjct	241	GTGATGTTTGATTTTTCTTTTCCTTTTTTTCATATTACTTTTAAATCCTGAATAGTTTG	300
Query	301	TGGCAGCTGGAGATCACCTAGTCCACCACTGTCCAACATGGCAATGGTAAGTAATATTGA	360
Sbjct	301	TGGCAGCTGGAGATCACCTAGTCCACCACTGTCCAACATGGCAATGGTAAGTAATATTGA	360
Query	361	GTAAAGAATAGAAAATTAGTAAAAATGCATGGCTTCAGAATTATAGCAATTTGCAAAATAG	420
Sbjct	361	GTAAAGAATAGAAAATTAGTAAAAATGCATGGCTTCAGAATTATAGCAATTTGCAAAATAG	420
Query	421	GTTAATGGATGAAAATTAGAATGACCAGTTTAACTTTCCCCCAGCAGATTCTTCTGTTA	480
Sbjct	421	GTTAATGGATGAAAATTAGAATGACCAGTTTAACTTTCCCCCAGCAGATTCTTCTGTTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AACAAATGCCCCTTCAAAATAAAGGAAGAACAAGTGGGTGTTATACCTATGTTATTTGGCT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AACAAATGCCCCTTCAAAATAAAGGAAGAACAAGTGGGTGTTATACCTATGTTATTTGGCT  540

Query  541  ATGTTAGCACAATATGATGGACTAATTTGAGAAAAAGCATTCTCCTTTACTATTACT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATGTTAGCACAATATGATGGACTAATTTGAGAAAAAGCATTCTCCTTTACTATTACT  600

Query  601  TCTTTTCTTTATAGGGCTAAGTCTGCCTTCTGGGTCTTTGAA  642
          ||||||||||||||||||||||||||||||||||||
Sbjct   601  TCTTTTCTTTATAGGGCTAAGTCTGCCTTCTGGGTCTTTGAA  642
```

Sequence 400 matched with Sequence 63

Query= Sequence ID 400
Length=446

SEQ ID NO: 63

ALIGNMENTS

Identities = 446/446 (100%), Gaps = 0/446 (0%)

```
Query 1   GAAGAAGCGCGAAGAGCCGTTAGTCATGCCGGTGTGGTGGCGGCGGCGGAGACTGCGGGC 60
          |||
Sbjct 1   GAAGAAGCGCGAAGAGCCGTTAGTCATGCCGGTGTGGTGGCGGCGGCGGAGACTGCGGGC 60

Query 61  CCGTAGCTGGGCTCTGCGAGGTGCAAGAAAGCCTTTGAGGTGAAGGTGTATGAAAGTCAT 120
          |||
Sbjct 61  CCGTAGCTGGGCTCTGCGAGGTGCAAGAAAGCCTTTGAGGTGAAGGTGTATGAAAGTCAT 120

Query 121 CATAACAGATGTTTTCCAAAAAAGTTGTAGAAGGTTGTGAAAAAACTACTAGGATCACGCG 180
          |||
Sbjct 121 CATAACAGATGTTTTCCAAAAAAGTTGTAGAAGGTTGTGAAAAAACTACTAGGATCACGCG 180

Query 181 GCATGTATTGAGCATATAGGTTGCTGTAGATGAATGTTCTTAGCTGTCATGTTTAAAAAT 240
          |||
Sbjct 181 GCATGTATTGAGCATATAGGTTGCTGTAGATGAATGTTCTTAGCTGTCATGTTTAAAAAT 240

Query 241 ACTTCTGCTTCGTTACCTCAAGTGTGGCATGCAGCATTTTGAAGGAAAAATTGAAGACGT 300
          |||
Sbjct 241 ACTTCTGCTTCGTTACCTCAAGTGTGGCATGCAGCATTTTGAAGGAAAAATTGAAGACGT 300

Query 301 GTTCAAGAAAACATGAACAGAAGCAAATGATGAAAATGAGCATTTTACTTGATGTTGATA 360
          |||
Sbjct 301 GTTCAAGAAAACATGAACAGAAGCAAATGATGAAAATGAGCATTTTACTTGATGTTGATA 360

Query 361 ACATCACAATAAATTATGGAGAAAAATACATATTTGGCTAACTTTTAATTGCTGAACAAT 420
          |||
Sbjct 361 ACATCACAATAAATTATGGAGAAAAATACATATTTGGCTAACTTTTAATTGCTGAACAAT 420

Query 421 AAAGTGTTTTCTTTTAAATCNAAAAAA 446
          |||
Sbjct 421 AAAGTGTTTTCTTTTAAATCNAAAAAA 446
```


Sequence 401 matched with Sequence 64

Query= Sequence ID 401
Length=629

SEQ ID NO: 64

ALIGNMENTS

Identities = 629/629 (100%), Gaps = 0/629 (0%)

Query	1	GAAGCCAAACCAAAGGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAG	60
Sbjct	1	GAAGCCAAACCAAAGGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAG	60
Query	61	AAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAG	120
Sbjct	61	AAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAG	120
Query	121	AAGTCATGATTGGGATTTCTGGGTCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGAC	180
Sbjct	121	AAGTCATGATTGGGATTTCTGGGTCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGAC	180
Query	181	TACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTGTCTTAT	240
Sbjct	181	TACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTGTCTTAT	240
Query	241	TAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACCTGAGTAATCAGCTAGGCCAG	300
Sbjct	241	TAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACCTGAGTAATCAGCTAGGCCAG	300
Query	301	TCACTAGGTGAACAACCTTACTGCTACCAATCAGCCTTAGAGCAGGAATCAAACCTCATGTC	360
Sbjct	301	TCACTAGGTGAACAACCTTACTGCTACCAATCAGCCTTAGAGCAGGAATCAAACCTCATGTC	360
Query	361	TCAGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGC	420
Sbjct	361	TCAGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGC	420
Query	421	TGAAATAGTAAATGTTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTC	480
Sbjct	421	TGAAATAGTAAATGTTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TAATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TAATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGA  540

Query  541  GGTCTACTATTTCTTCTGTAATACTGATTTTTACCCCATCAGGGTCAGTCCCCAAAGGTT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GGTCTACTATTTCTTCTGTAATACTGATTTTTACCCCATCAGGGTCAGTCCCCAAAGGTT  600

Query  601  GTAAATGTGAAGCTTGGTCTTTTCTTTA  629
          ||||||||||||||||||||
Sbjct   601  GTAAATGTGAAGCTTGGTCTTTTCTTTA  629
```

Sequence 402 matched with Sequence 65

Query= Sequence ID 402
Length=366

SEQ ID NO: 65

ALIGNMENTS

Identities = 366/366 (100%), Gaps = 0/366 (0%)

Query	1	GACCCTATTCTCAGGATGAAAAATAACTAGTAATAGTCTGCTCTGTTGGTTAACTCC	60
Sbjct	1	GACCCTATTCTCAGGATGAAAAATAACTAGTAATAGTCTGCTCTGTTGGTTAACTCC	60
Query	61	TCGTAAGGAGGTACAATTAATAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATA	120
Sbjct	61	TCGTAAGGAGGTACAATTAATAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATA	120
Query	121	TTCCTTCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTG	180
Sbjct	121	TTCCTTCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTG	180
Query	181	AAGGATTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATT	240
Sbjct	181	AAGGATTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATT	240
Query	241	TATTGCATGCTTATCTTGTATCAACATTGNGATGAAAGCNCAAGAATGAAAGAGGAGGGA	300
Sbjct	241	TATTGCATGCTTATCTTGTATCAACATTGNGATGAAAGCNCAAGAATGAAAGAGGAGGGA	300
Query	301	GAATGTTTANAGAATAAGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANA	360
Sbjct	301	GAATGTTTANAGAATAAGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANA	360
Query	361	AAACAG 366	
Sbjct	361	AAACAG 366	

Sequence 403 matched with Sequence 66

Query= Sequence ID 403
Length=202

SEQ ID NO: 66

ALIGNMENTS

Identities = 202/202 (100%), Gaps = 0/202 (0%)

```
Query 1  AAGACACCTGATAGATTGTCTTGTATTATTTTTCCTTGCCTTCTTACAATCTCAGTGAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  AAGACACCTGATAGATTGTCTTGTATTATTTTTCCTTGCCTTCTTACAATCTCAGTGAT 60

Query 61 TAGAATTGGGCTGAAAACAATACATCAAATTCTCAGCAAAATCCTTATGGGTTGCTGGAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 TAGAATTGGGCTGAAAACAATACATCAAATTCTCAGCAAAATCCTTATGGGTTGCTGGAT 120

Query 121 ACCGAGGGTTTTTAAGATCTTTAGACTTCACTATATAGAACAAATGTTGAATGGGAATTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 ACCGAGGGTTTTTAAGATCTTTAGACTTCACTATATAGAACAAATGTTGAATGGGAATTT 180

Query 181 TCTTTATTTCTATANCGTTTNG 202
          ||||||||||||||||
Sbjct 181 TCTTTATTTCTATANCGTTTNG 202
```

Blast comparison trimmed “NG” from the 3’ end of both sequences and reported 200 identities. The report has been manually corrected for this. “NG” has been appended to both sequences and identity count has been increased to 202.

Sequence 405 matched with Sequence 67

Query= Sequence ID 405
Length=634

SEQ ID NO: 67

ALIGNMENTS

Identities = 634/634 (100%), Gaps = 0/634 (0%)

Query	1	CCCGGAATCGCGCCGCGTCGACGATGAGCATTTTTTCATGTGTCTTTGGCTGCATAAA	60
Sbjct	1	CCCGGAATCGCGCCGCGTCGACGATGAGCATTTTTTCATGTGTCTTTGGCTGCATAAA	60
Query	61	TGTCTTCTTTTGAGAAGTGTCGGTTCATATCCTTTGCCCACTTTTGGATGGGGTTGtttt	120
Sbjct	61	TGTCTTCTTTTGAGAAGTGTCGGTTCATATCCTTTGCCCACTTTTGGATGGGGTTGTTTT	120
Query	121	tttCTTGTAATTTGTTTGAGTTCATTGTAGATTCTGGATATTAGCCCTTTGTCAGATGA	180
Sbjct	121	TTTCTTGTAATTTGTTTGAGTTCATTGTAGATTCTGGATATTAGCCCTTTGTCAGATGA	180
Query	181	GTAGGTTGCGAAAATTTCTCCCATTTTGTAGGTTGCCTGTTCACTCTGATGGTAGTTTC	240
Sbjct	181	GTAGGTTGCGAAAATTTCTCCCATTTTGTAGGTTGCCTGTTCACTCTGATGGTAGTTTC	240
Query	241	ATTTGCTGTGCAGAAGCTCTTAGTTTAATTAGATCCCATTTGTCAATTTGGCTTTTGT	300
Sbjct	241	ATTTGCTGTGCAGAAGCTCTTAGTTTAATTAGATCCCATTTGTCAATTTGGCTTTTGT	300
Query	301	TGCCATTGCTTTTGGTGTTTTAGACTTGAAGTCCTTGCCCATGCCTATGTCCTGAATGGT	360
Sbjct	301	TGCCATTGCTTTTGGTGTTTTAGACTTGAAGTCCTTGCCCATGCCTATGTCCTGAATGGT	360
Query	361	AATGCCTAGGTTTTCTTCTAGGGTTTTGATGGTTTTAGGTCTAACGTTTCAGTCTTTAAT	420
Sbjct	361	AATGCCTAGGTTTTCTTCTAGGGTTTTGATGGTTTTAGGTCTAACGTTTCAGTCTTTAAT	420
Query	421	CCATCTTTTAAAAGTCTCTTCACAGTACATGAGTAGTAGTGACACCAATAATGTCAGAGC	480
Sbjct	421	CCATCTTTTAAAAGTCTCTTCACAGTACATGAGTAGTAGTGACACCAATAATGTCAGAGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGGGAAC TCCAGGTTCTGCCCATCCACAAAAACAACAAATAAGCTGGCAAAAAC TTTAA 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGGGAAC TCCAGGTTCTGCCCATCCACAAAAACAACAAATAAGCTGGCAAAAAC TTTAA 540

Query  541  GAATCAACTTTTGCAGATCTCTGAAATCTAGTCAAAACTTAAACAGAGGAAAGATTAATA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GAATCAACTTTTGCAGATCTCTGAAATCTAGTCAAAACTTAAACAGAGGAAAGATTAATA 600

Query  601  AAGACNGGCTGCCTGAGATAACACTAACACACAC 634
          |||||||||||||||||||||||||||||||
Sbjct   601  AAGACNGGCTGCCTGAGATAACACTAACACACAC 634
```

Sequence 406 matched with Sequence 68

Query= Sequence ID 406
Length=644

SEQ ID NO: 68

ALIGNMENTS

Identities = 644/644 (100%), Gaps = 0/644 (0%)

Query	1	CATCAAATAAATAAATAAATAAATTTTAAAAGTCACAGCATTGAATTTTAAATGTTTGG	60
Sbjct	1	CATCAAATAAATAAATAAATAAATTTTAAAAGTCACAGCATTGAATTTTAAATGTTTGG	60
Query	61	GATGATAAAGCACCTGCTTATCATGAAGCTANAGAAATTCAATGACACGTTTGCCAGGGT	120
Sbjct	61	GATGATAAAGCACCTGCTTATCATGAAGCTANAGAAATTCAATGACACGTTTGCCAGGGT	120
Query	121	CTTTGCTAGTGATGTTGGAACAAGTCTGTAATGCTGATGAAACATCACTGTTCCGGGCATT	180
Sbjct	121	CTTTGCTAGTGATGTTGGAACAAGTCTGTAATGCTGATGAAACATCACTGTTCCGGGCATT	180
Query	181	ATTGCCCCAGAAAGACACTGACTGCAGCTGATGAAACAGCCCTTCCAAGAATTAAGGATG	240
Sbjct	181	ATTGCCCCAGAAAGACACTGACTGCAGCTGATGAAACAGCCCTTCCAAGAATTAAGGATG	240
Query	241	CCAAAGACCAAATAACTGTGCTGAGATATACTTACGCAGCAGGCATGCATAAGTGTA AAC	300
Sbjct	241	CCAAAGACCAAATAACTGTGCTGAGATATACTTACGCAGCAGGCATGCATAAGTGTA AAC	300
Query	301	TTGCTGTTATAAGCAAAAGCTTGCGTTCTCACTGTTTTCAAGGAGTGAATTTCATACCAA	360
Sbjct	301	TTGCTGTTATAAGCAAAAGCTTGCGTTCTCACTGTTTTCAAGGAGTGAATTTCATACCAA	360
Query	361	TCCATTATTATGCTAATAAAAAAGGCATGGATCACCAGGGACATCTTTTCAGATTGGTTTC	420
Sbjct	361	TCCATTATTATGCTAATAAAAAAGGCATGGATCACCAGGGACATCTTTTCAGATTGGTTTC	420
Query	421	ACAAACATTTTGTACCAGCAGCTTGTGCTTACTGCAGGGAAGCTGACTGGATGATGACTG	480
Sbjct	421	ACAAACATTTTGTACCAGCAGCTTGTGCTTACTGCAGGGAAGCTGACTGGATGATGACTG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CAAGATTTTGTATATCTTAACAACTGTTGTGCTCATCCTCCAGCTGAAATTCTCATCAA  540
          |||
Sbjct  481  CAAGATTTTGTATATCTTAACAACTGTTGTGCTCATCCTCCAGCTGAAATTCTCATCAA  540

Query  541  AAATAATGTTTATGGCTCACACCTGTAATCTCAACACTTTGGGAGGATTGCCTGACCCAG  600
          |||
Sbjct  541  AAATAATGTTTATGGCTCACACCTGTAATCTCAACACTTTGGGAGGATTGCCTGACCCAG  600

Query  601  GAGTTCAAGCCCACCCTGGGCAACACAGCAAGACCCAACCTNTC  644
          |||
Sbjct  601  GAGTTCAAGCCCACCCTGGGCAACACAGCAAGACCCAACCTNTC  644
```

Blast comparison trimmed “NTC” from the 3’ end of both sequences and reported 641 identities. The report has been manually corrected for this. “NTC” has been appended to both sequences and identity count has been increased to 644.

Sequence 407 matched with Sequence 69

Query= Sequence ID 407
Length=639

SEQ ID NO: 69

ALIGNMENTS

Identities = 639/639 (100%), Gaps = 0/639 (0%)

Query	1	TTTTAAAAATCATAAAACGTTTCTTACAAAAGAGCATTACATTNTGCACACTGCTCTGAA	60
Sbjct	1	TTTTAAAAATCATAAAACGTTTCTTACAAAAGAGCATTACATTNTGCACACTGCTCTGAA	60
Query	61	CAGATGCCAGGGACATGTGGACTATTGTTACTTTTCCTCCCTGTCCCACCCCCCAAATGT	120
Sbjct	61	CAGATGCCAGGGACATGTGGACTATTGTTACTTTTCCTCCCTGTCCCACCCCCCAAATGT	120
Query	121	TACAGTGACCACAAAGCAAGGTGTTTACAATAATTACATGGGGGGAATTTTTTAAACCAC	180
Sbjct	121	TACAGTGACCACAAAGCAAGGTGTTTACAATAATTACATGGGGGGAATTTTTTAAACCAC	180
Query	181	CAACAATAACGAAAAATAAAATCCACTCACTCTGCTGCTGTTTCAAAATTTCAATGTTAG	240
Sbjct	181	CAACAATAACGAAAAATAAAATCCACTCACTCTGCTGCTGTTTCAAAATTTCAATGTTAG	240
Query	241	TTTTTGCACGCCCTTcccccccccAACCCCTGTTTGTAAAGGAACATAAACATTACATCTGG	300
Sbjct	241	TTTTTGCACGCCCTTCCCCCCCCAACCCCTGTTTGTAAAGGAACATAAACATTACATCTGG	300
Query	301	TGAACAGCAAAGATTTCACTACACCTCAAATGCAGAACACCTATGAAGCAGAGGAATGTT	360
Sbjct	301	TGAACAGCAAAGATTTCACTACACCTCAAATGCAGAACACCTATGAAGCAGAGGAATGTT	360
Query	361	GGCTTTTTTAAACAGAAGCAGATaaaaaaaaaGATGCAGGACTCCTTCAGTTCTTCACTA	420
Sbjct	361	GGCTTTTTTAAACAGAAGCAGATAAAAAAAAAAAGATGCAGGACTCCTTCAGTTCTTCACTA	420
Query	421	GTCTTAGAAAAACTTTCCAGAATACTGCTTCACACTATAaaaaagaaaaaTATCTTGCA	480
Sbjct	421	GTCTTAGAAAAACTTTCCAGAATACTGCTTCACACTATAAAAAAGAAAAAATATCTTGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTAGAATCCTTCAACATCTGCATACTGCTTCACACTGTTTCGTTTCTAGGAGCACTTTGTC	540
Sbjct	481	TTAGAATCCTTCAACATCTGCATACTGCTTCACACTGTTTCGTTTCTAGGAGCACTTTGTC	540
Query	541	ACAGGACACTTCTGCTTATATTTCTTTAATCAGAACTTAGTTGGATGGGCCGGGCATGGT	600
Sbjct	541	ACAGGACACTTCTGCTTATATTTCTTTAATCAGAACTTAGTTGGATGGGCCGGGCATGGT	600
Query	601	GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG	639
Sbjct	601	GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG	639

Sequence 408 matched with Sequence 70

Query= Sequence ID 408
Length=752

SEQ ID NO: 70

ALIGNMENTS

Identities = 752/752 (100%), Gaps = 0/752 (0%)

Query	1	CCATCTCCAAATTTAGTATTCACTTCTGTTTAGCATATTATCAGTTGCCATCTATTTGTTT	60
Sbjct	1	CCATCTCCAAATTTAGTATTCACTTCTGTTTAGCATATTATCAGTTGCCATCTATTTGTTT	60
Query	61	TAACTGATTACTTGAATCTGATTAAACATCACAGAAATGGGCTTTGATAAGAACAATATT	120
Sbjct	61	TAACTGATTACTTGAATCTGATTAAACATCACAGAAATGGGCTTTGATAAGAACAATATT	120
Query	121	GAATAAGAAATTTTAAATAACAAAACAGCTTATAGAAAATTCAGCATAACTTTTCCATC	180
Sbjct	121	GAATAAGAAATTTTAAATAACAAAACAGCTTATAGAAAATTCAGCATAACTTTTCCATC	180
Query	181	ACCTTCACCACCCTTGCCTTTTATTATCCTGTCCTGTATCACTGCTTTCTGTTAGCAGTG	240
Sbjct	181	ACCTTCACCACCCTTGCCTTTTATTATCCTGTCCTGTATCACTGCTTTCTGTTAGCAGTG	240
Query	241	TTGTGTGAGTTAGGATTTGGGCAGGAAAGCAAAAGCAACCACCCGTCATTTTCCCAGAAT	300
Sbjct	241	TTGTGTGAGTTAGGATTTGGGCAGGAAAGCAAAAGCAACCACCCGTCATTTTCCCAGAAT	300
Query	301	GAAGGGTTTGACGTAGGATGTAGACTTTGTATAGTAGTTGGGAGAGCTGTGGGAGTGAAG	360
Sbjct	301	GAAGGGTTTGACGTAGGATGTAGACTTTGTATAGTAGTTGGGAGAGCTGTGGGAGTGAAG	360
Query	361	GTCAGGGATGTCACCTACAGAAGTCAGGGAATCTGCCACCAGAGATCCTGCATCAGAAAC	420
Sbjct	361	GTCAGGGATGTCACCTACAGAAGTCAGGGAATCTGCCACCAGAGATCCTGCATCAGAAAC	420
Query	421	AGCCAACAGCGTGCTTCTGAAGAACTAGTGGGGAAGTGGCTATAATTCTTAGGAATCCCA	480
Sbjct	421	AGCCAACAGCGTGCTTCTGAAGAACTAGTGGGGAAGTGGCTATAATTCTTAGGAATCCCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCAAGTCCGCACCACTGTCTCAGTCTACAGCAGTGGAGAAAGGGGTTTCCAGGAGCTCTC	540
Sbjct	481	GCAAGTCCGCACCACTGTCTCAGTCTACAGCAGTGGAGAAAGGGGTTTCCAGGAGCTCTC	540
Query	541	TGGAAAGTTCCTGCCCACACTTTGCAACAATCTTCAGAGGATAATGGGCTTCTCTTCCAG	600
Sbjct	541	TGGAAAGTTCCTGCCCACACTTTGCAACAATCTTCAGAGGATAATGGGCTTCTCTTCCAG	600
Query	601	CTTCCACACCCAACAAGAGTGCCTTTCATCGGCCAACTCTAACCTGGAACCCTATGGCAG	660
Sbjct	601	CTTCCACACCCAACAAGAGTGCCTTTCATCGGCCAACTCTAACCTGGAACCCTATGGCAG	660
Query	661	AGGGGATTTAGGAGACAGTTTGTNATGTCTGTGGAATGCAAATGAANANGTANCAATGCT	720
Sbjct	661	AGGGGATTTAGGAGACAGTTTGTNATGTCTGTGGAATGCAAATGAANANGTANCAATGCT	720
Query	721	TANTTGACAGCGGNCATACACAAATNTNGAAA	752
Sbjct	721	TANTTGACAGCGGNCATACACAAATNTNGAAA	752

Sequence 409 matched with Sequence 71

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 409
Length=12

SEQ ID NO: 71	18.3	2e-04
---------------	------	-------

ALIGNMENTS

Identities = 12/12 (100%), Gaps = 0/12 (0%)

Query	1	GATCCGTNGACT	12
Sbjct	1	GATCCGTNGACT	12

Sequence 410 matched with Sequence 72

Query= Sequence ID 410
Length=505

SEQ ID NO: 72

ALIGNMENTS

Identities = 505/505 (100%), Gaps = 0/505 (0%)

Query	1	CTCTTCCCAGCCCCTGAGCCCAGCCCCTTCCCAAGTGGTGCCAGACAAAAAACTACATGG	60
Sbjct	1	CTCTTCCCAGCCCCTGAGCCCAGCCCCTTCCCAAGTGGTGCCAGACAAAAAACTACATGG	60
Query	61	CCCTTTCGTGTCTTGGGGGTGAAAGGGAGGGATGAATTGGGGTGATAGAACCCTGGTGA	120
Sbjct	61	CCCTTTCGTGTCTTGGGGGTGAAAGGGAGGGATGAATTGGGGTGATAGAACCCTGGTGA	120
Query	121	ATTCAGAGTAATCTTTCTTTAGAAAACTGGTGTTTTCTAAAGAAACAGGATAGGAGTTTA	180
Sbjct	121	ATTCAGAGTAATCTTTCTTTAGAAAACTGGTGTTTTCTAAAGAAACAGGATAGGAGTTTA	180
Query	181	GAGAAGGCACCAAAGCTTTCACTTTGGTTTGGCACCAGTTTCTAACCATCTGTTTTTTCT	240
Sbjct	181	GAGAAGGCACCAAAGCTTTCACTTTGGTTTGGCACCAGTTTCTAACCATCTGTTTTTTCT	240
Query	241	ACCCTAGCTATCTTTTATTGGTAAATATAAATGTATAATTATGTTTGTAGAGCTTTACC	300
Sbjct	241	ACCCTAGCTATCTTTTATTGGTAAATATAAATGTATAATTATGTTTGTAGAGCTTTACC	300
Query	301	AAGGAGTTTCCCTCCTTTTTTGTGTTGATTAGCAAATTTTGTATTCTCCATTTTCCAA	360
Sbjct	301	AAGGAGTTTCCCTCCTTTTTTGTGTTGATTAGCAAATTTTGTATTCTCCATTTTCCAA	360
Query	361	AAGTAAGAGACTCCAGCATGGCCTTCTGTTTGCCCCGCAGTAAAGTAACTTCCATATAAA	420
Sbjct	361	AAGTAAGAGACTCCAGCATGGCCTTCTGTTTGCCCCGCAGTAAAGTAACTTCCATATAAA	420
Query	421	ATGGTATTTGAAAGTGAGAGTTCATGACAACAGACCGTTTTCCATTTTCATCTGTATTTTA	480
Sbjct	421	ATGGTATTTGAAAGTGAGAGTTCATGACAACAGACCGTTTTCCATTTTCATCTGTATTTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCTCCGTGACTCCACTTGTGGGTTT	505
Sbjct	481	TCTCCGTGACTCCACTTGTGGGTTT	505

Sequence 411 matched with Sequence 73

Query= Sequence ID - 411 nt: 505
Length=505

SEQ ID NO: 73 nt: 505

ALIGNMENTS

Identities = 505/505 (100%), Gaps = 0/505 (0%)

Query	1	TGGAGCTGAAAAATTCCTATTACCTAGGGGCATCACAACGCATTGCATTTCGCCCCGTGTT	60
Sbjct	1	TGGAGCTGAAAAATTCCTATTACCTAGGGGCATCACAACGCATTGCATTTCGCCCCGTGTT	60
Query	61	TGGGATGATGCTGGTGTAAACCTACTATGCTGCCAGTCATGTAAAAGTATAGCACACACA	120
Sbjct	61	TGGGATGATGCTGGTGTAAACCTACTATGCTGCCAGTCATGTAAAAGTATAGCACACACA	120
Query	121	ATTAGTAGGTAATGCTTGCAAATAATAATGAAAGACTCTGCTACTGGTTTATGTATTTAC	180
Sbjct	121	ATTAGTAGGTAATGCTTGCAAATAATAATGAAAGACTCTGCTACTGGTTTATGTATTTAC	180
Query	181	TATGCTATACTTTTTGTCACTACTTTAGAGTGTACTCCTACTttttttttttttttttttt	240
Sbjct	181	TATGCTATACTTTTTGTCACTACTTTAGAGTGTACTCCTACTTTTTTTTTTTTTTTTTTTT	240
Query	241	GAGATGGAGTTTCACTCTTGTCTGTAGGCTGGAGCGAANTGGCGCGATCTCGGCTTACT	300
Sbjct	241	GAGATGGAGTTTCACTCTTGTCTGTAGGCTGGAGCGAANTGGCGCGATCTCGGCTTACT	300
Query	301	GCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCANCTTCCCAGAGTAGCTGAG	360
Sbjct	301	GCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCANCTTCCCAGAGTAGCTGAG	360
Query	361	ATTACAGGCATGCACCGCCACGCACGGGTAATTTTGTATTTTGGTAGAGACAGGGTTTC	420
Sbjct	361	ATTACAGGCATGCACCGCCACGCACGGGTAATTTTGTATTTTGGTAGAGACAGGGTTTC	420
Query	421	ACCATGTTGGCCAGGCTGGTCACCAACTCCTGACCTCAGGTGACCCGCCTCCTCACCTCC	480
Sbjct	421	ACCATGTTGGCCAGGCTGGTCACCAACTCCTGACCTCAGGTGACCCGCCTCCTCACCTCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGAGTGTTGGGATTACAGGNGTGAG	505
Sbjct	481	AGAGTGTTGGGATTACAGGNGTGAG	505

Sequence 412 matched with Sequence 74

Query= Sequence ID 412
Length=580

SEQ ID NO: 74

ALIGNMENTS

Identities = 580/580 (100%), Gaps = 0/580 (0%)

Query	1	ATAAAAATTAGCTGGGGGTGATGGGCCCTGTACCCCAGCTACTCGGGAGGTGAGGTAGGA	60
Sbjct	1	ATAAAAATTAGCTGGGGGTGATGGGCCCTGTACCCCAGCTACTCGGGAGGTGAGGTAGGA	60
Query	61	GAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCC	120
Sbjct	61	GAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCC	120
Query	121	AGCCTGTGTGACAGAACAAGACTCTGTCTCaaaaaaaaataataataataataataa	180
Sbjct	121	AGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAAAAAAATAATAATAATAATAATAA	180
Query	181	aaaggaataacatagctaggaataaatTTAATCAAAGAGGTGAAAGACTTATACACTTAA	240
Sbjct	181	AAAGGAATAACATAGCTAGGAATAAATTTAATCAAAGAGGTGAAAGACTTATACACTTAA	240
Query	241	AACTACaaaaaaaaTCACTGAAGGAATTATAGACCCaaataaaaaataaaaaaGAC	300
Sbjct	241	AACTACAAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAAATAATAAAAGAC	300
Query	301	ATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTG	360
Sbjct	301	ATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTG	360
Query	361	ATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAA	420
Sbjct	361	ATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAA	420
Query	421	AAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAACACAATCTT	480
Sbjct	421	AAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAACACAATCTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGGaaaaaaaaacaaaaacaaaGTCAAAGAACTCACACTTCTCTATTTATAATTTACTA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGGGAAAAAAAAACAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATAATTTACTA  540

Query  541  CAAAGTTATAGNATCAAAGTCGACGCGCCGCGATCCGGGC  580
          ||||||||||||||||||||||||||||||||||||
Sbjct   541  CAAAGTTATAGNATCAAAGTCGACGCGCCGCGATCCGGGC  580
```

Sequence 413 matched with Sequence 75

Query= Sequence ID 413
Length=535

SEQ ID NO: 75

ALIGNMENTS

Identities = 535/535 (100%), Gaps = 0/535 (0%)

Query	1	CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAATAATAAAATGCTTACACGAA	60
Sbjct	1	CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAATAATAAAATGCTTACACGAA	60
Query	61	AATTATTTATTGAGAATATTCATATAAAAAATTACCTAAAGCAAAGTaaaaaaaGTAAAT	120
Sbjct	61	AATTATTTATTGAGAATATTCATATAAAAAATTACCTAAAGCAAAGTAAAAAAGTAAAT	120
Query	121	CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTGTAGCTGTAACAAAAAGAAAG	180
Sbjct	121	CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTGTAGCTGTAACAAAAAGAAAG	180
Query	181	AAAACAACtttttttAAAGCCTCATTCTCTTTTCTTTCAAATGTACCTTATTCCCACAC	240
Sbjct	181	AAAACAACTTTTTTTAAAGCCTCATTCTCTTTTCTTTCAAATGTACCTTATTCCCACAC	240
Query	241	ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAAATAAGAT	300
Sbjct	241	ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAAATAAGAT	300
Query	301	GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAACTCCTCTTCACGATTG	360
Sbjct	301	GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAACTCCTCTTCACGATTG	360
Query	361	ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA	420
Sbjct	361	ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA	420
Query	421	AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA	480
Sbjct	421	AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTGTTCTAT	535
Sbjct	481	ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTGTTCTAT	535

Sequence 414 matched with Sequence 76

Query= Sequence ID 414
Length=505

SEQ ID NO: 76

ALIGNMENTS

Identities = 505/505 (100%), Gaps = 0/505 (0%)

Query	1	CTCAGACTCTTTCTGCCCTAATGGCCATTACTATCCAGTCTGTATTGCTACAAGGGACCC	60
Sbjct	1	CTCAGACTCTTTCTGCCCTAATGGCCATTACTATCCAGTCTGTATTGCTACAAGGGACCC	60
Query	61	ACTGGTACCCCTTTTAGATTCTATCAAAAGGAACAGGGTTTTCCTAGAGGCAGGCAGCCT	120
Sbjct	61	ACTGGTACCCCTTTTAGATTCTATCAAAAGGAACAGGGTTTTCCTAGAGGCAGGCAGCCT	120
Query	121	GGTGGTATGGCACAGCAGAAGCTTACTGCTAATGAAATGGGAACCTCCCCCTCCCTTG	180
Sbjct	121	GGTGGTATGGCACAGCAGAAGCTTACTGCTAATGAAATGGGAACCTCCCCCTCCCTTG	180
Query	181	GTTTCAGCACAGAACCTGAATGCCAGGAAAAATTCTGGGCCAAGAAGCTAAAGCTAAAG	240
Sbjct	181	GTTTCAGCACAGAACCTGAATGCCAGGAAAAATTCTGGGCCAAGAAGCTAAAGCTAAAG	240
Query	241	AAACCTTCCTTTTTTCAACGtTTTTTTTCTTTCAAAGTGTAGGGTCACTTTTGATTGAG	300
Sbjct	241	AAACCTTCCTTTTTTCAACGTTTTTTTTCTTTCAAAGTGTAGGGTCACTTTTGATTGAG	300
Query	301	GCAAAGGGGTCCTACTGTAAGTGGAAGAAAGACTCACTCCCCTAACATAAGTTTTCACTGTG	360
Sbjct	301	GCAAAGGGGTCCTACTGTAAGTGGAAGAAAGACTCACTCCCCTAACATAAGTTTTCACTGTG	360
Query	361	GTGGGATGGTGCCGCCCGATATGCTTGATATGCTTTTCCTTCCACATGTAAAGCTAGGAA	420
Sbjct	361	GTGGGATGGTGCCGCCCGATATGCTTGATATGCTTTTCCTTCCACATGTAAAGCTAGGAA	420
Query	421	ACCTAACAGGATGTCAGCAGGGCAGTTAACTCTGGACTCANAGCCCTCAAGGGCATGTGG	480
Sbjct	421	ACCTAACAGGATGTCAGCAGGGCAGTTAACTCTGGACTCANAGCCCTCAAGGGCATGTGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CANAACCTCATGGCATNCAAGACCA	505
Sbjct	481	CANAACCTCATGGCATNCAAGACCA	505

Sequence 415 matched with Sequence 77

Query= Sequence ID - 415 nt: 596
Length=596

SEQ ID NO: 77 nt: 596

ALIGNMENTS

Identities = 596/596 (100%), Gaps = 0/596 (0%)

Query	1	GTATAATTGATTCTTTTGAACCTAAAGTATAAGACTTCACGATTAGaaaaaaTTATCCA	60
Sbjct	1	GTATAATTGATTCTTTTGAACCTAAAGTATAAGACTTCACGATTAGAAAAAAATTATCCA	60
Query	61	AAGACTAATGTAATTAAGTGAGGAAAAGGTGCTGGAGGAAGTGGATAACCCACATGGAAAT	120
Sbjct	61	AAGACTAATGTAATTAAGTGAGGAAAAGGTGCTGGAGGAAGTGGATAACCCACATGGAAAT	120
Query	121	GTATGAACCATGACCTCTATGTCACATACTATATATAAACTTAATTTGAGGTGTATCAC	180
Sbjct	121	GTATGAACCATGACCTCTATGTCACATACTATATATAAACTTAATTTGAGGTGTATCAC	180
Query	181	AGAGCTAACTGTGGGGGCTAAAAACGTTGAAGCCTTTGGATGGCCGCACAAGAGATGTCTG	240
Sbjct	181	AGAGCTAACTGTGGGGGCTAAAAACGTTGAAGCCTTTGGATGGCCGCACAAGAGATGTCTG	240
Query	241	CATTCATAACCTTGGGGAGGTATGAACATTTCTTGTAACATGCAAAAAGCACTAACTG	300
Sbjct	241	CATTCATAACCTTGGGGAGGTATGAACATTTCTTGTAACATGCAAAAAGCACTAACTG	300
Query	301	TAAAAGAGAACAGTTGGTCAGTTGAATTTTCATGAAACATTGTAACTTCTGCTAAACAAC	360
Sbjct	301	TAAAAGAGAACAGTTGGTCAGTTGAATTTTCATGAAACATTGTAACTTCTGCTAAACAAC	360
Query	361	TGACACCATTAAGAATGTGGAAAAAGGCTGGGCACAGTGGCTCATGCCTATAATCCCAGC	420
Sbjct	361	TGACACCATTAAGAATGTGGAAAAAGGCTGGGCACAGTGGCTCATGCCTATAATCCCAGC	420
Query	421	ATTTTGGGAGGCCGGGGCGGAGAATCACTTGAGGCCAGGAGTTTGAAACCAGCCTGGGC	480
Sbjct	421	ATTTTGGGAGGCCGGGGCGGAGAATCACTTGAGGCCAGGAGTTTGAAACCAGCCTGGGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AACATGGCAAGACCCCGACTCTACAAAAATATTTTTAAAAATTAGTTGGGTGTGGTGATG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AACATGGCAAGACCCCGACTCTACAAAAATATTTTTAAAAATTAGTTGGGTGTGGTGATG  540

Query  541  CACTCCTGTAGTCCTAGCTGCCAGGANGCTAAGGNNGAAGGATCACTTAACCCTGG  596
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CACTCCTGTAGTCCTAGCTGCCAGGANGCTAAGGNNGAAGGATCACTTAACCCTGG  596
```

Sequence 416 matched with Sequence 78

Query= Sequence ID 416
Length=504

SEQ ID NO: 78

ALIGNMENTS

Identities = 504/504 (100%), Gaps = 0/504 (0%)

Query	1	CTGGTGGCGGCGGTCTGCGGACGCAAACATGCAGATCTTTGTGAAGACCCTCACTGGCA	60
Sbjct	1	CTGGTGGCGGCGGTCTGCGGACGCAAACATGCAGATCTTTGTGAAGACCCTCACTGGCA	60
Query	61	AAACCATCACCTTGAGGTCGAGCCCAGTGACACCATTGAGAATGTCAAAGCCAAAATTC	120
Sbjct	61	AAACCATCACCTTGAGGTCGAGCCCAGTGACACCATTGAGAATGTCAAAGCCAAAATTC	120
Query	121	AAGACAAGGAGGGTATCCACCTGACCAGCAGCGTCTGATATTTGCCGGCAAACAGCTGG	180
Sbjct	121	AAGACAAGGAGGGTATCCACCTGACCAGCAGCGTCTGATATTTGCCGGCAAACAGCTGG	180
Query	181	AGGATGGCCGCACTCTCTCAGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGT	240
Sbjct	181	AGGATGGCCGCACTCTCTCAGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGT	240
Query	241	TGCGCCTGCGAGGTGGCATTATTGAGCCTTCTCTCCGCCAGCTTGCCAGAAATACAAC	300
Sbjct	241	TGCGCCTGCGAGGTGGCATTATTGAGCCTTCTCTCCGCCAGCTTGCCAGAAATACAAC	300
Query	301	GCGACAAGATGATCTGCCGCAAGTGCTATGCTCGCCTTCACCCTCGTGCTGTCAACTGCC	360
Sbjct	301	GCGACAAGATGATCTGCCGCAAGTGCTATGCTCGCCTTCACCCTCGTGCTGTCAACTGCC	360
Query	361	GCAAGAAGAAGTGTGGTCACACCAACAACCTGCGTCCCAAGAAGAAGGTCAAATAAGGTT	420
Sbjct	361	GCAAGAAGAAGTGTGGTCACACCAACAACCTGCGTCCCAAGAAGAAGGTCAAATAAGGTT	420
Query	421	GTTCTTTTCCTTGAAGGGCAGCCTCCTGCCCAGGCCCCGTGGCCCTGGAGCCTCAATAAAG	480
Sbjct	421	GTTCTTTTCCTTGAAGGGCAGCCTCCTGCCCAGGCCCCGTGGCCCTGGAGCCTCAATAAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGTCCCTTTCATTGACTGGAGCAG	504
Sbjct	481	TGTCCCTTTCATTGACTGGAGCAG	504

Sequence 417 matched with Sequence 79

Query= Sequence ID 417
Length=564

SEQ ID NO: 79

ALIGNMENTS

Identities = 564/564 (100%), Gaps = 0/564 (0%)

Query	1	GCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCCGAGATAAGttttttt	60
Sbjct	1	GCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCCGAGATAAGTTTTTTT	60
Query	61	CTCTTTGAAAGATAGAGATTAATACAACACTTTAAAAAATATAGTCAATAGGTTACTAAG	120
Sbjct	61	CTCTTTGAAAGATAGAGATTAATACAACACTTTAAAAAATATAGTCAATAGGTTACTAAG	120
Query	121	ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT	180
Sbjct	121	ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT	180
Query	181	ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAAACATGACG	240
Sbjct	181	ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAAACATGACG	240
Query	241	GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAAATTGAGAGAA	300
Sbjct	241	GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAAATTGAGAGAA	300
Query	301	AGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAA	360
Sbjct	301	AGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAA	360
Query	361	GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAAATAATTTGAAG	420
Sbjct	361	GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAAATAATTTGAAG	420
Query	421	GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAGACCTTGAAATCCATGACGC	480
Sbjct	421	GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAGACCTTGAAATCCATGACGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACCAAAATGG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACCAAAATGG  540

Query  541  AAAGATTAATTGGGAGTGGTAGGA  564
          |||||||||||||||||||
Sbjct   541  AAAGATTAATTGGGAGTGGTAGGA  564
```

Sequence 418 matched with Sequence 80

Query= Sequence ID 418
Length=270

SEQ ID NO: 80

ALIGNMENTS

Identities = 270/270 (100%), Gaps = 0/270 (0%)

Query	1	CCC	GGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA	60
Sbjct	1	CCC	GGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA	60
Query	61	TGCAAAA	tttttttaatcttcgccttaataacttttttattttgttttattttGAATGATG	120
Sbjct	61	TGCAAA	ATTTTTTAATCTTCGCCTTAATACTTTTTTATTTTGTTTTATTTGAATGATG	120
Query	121	AGCCTTCGTG	cccccccttcccccttttttgtcccccAACTTGAGATGTATGAAGGCTTT	180
Sbjct	121	AGCCTTCGTG	CCCCCCCCTTCCCCTTTTTTGTCCCCAACTTGAGATGTATGAAGGCTTT	180
Query	181	TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA	240	
Sbjct	181	TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA	240	
Query	241	GTTGAATAAAAGTGCACACCTTATAAAAAA	270	
Sbjct	241	GTTGAATAAAAGTGCACACCTTATAAAAAA	270	

Sequence 419 matched with Sequence 81

Query= Sequence ID 419
Length=268

SEQ ID NO: 81

ALIGNMENTS

Identities = 268/268 (100%), Gaps = 0/268 (0%)

Query	1	CCC	GGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA	60
Sbjct	1	CCC	GGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA	60
Query	61	TGCAAAA	tttttttaatcttcgccttaataacttttttattttgttttattttGAATGATG	120
Sbjct	61	TGCAAA	ATTTTTTTAATCTTCGCCTTAATACTTTTTTATTTTGTTTTATTTTGAATGATG	120
Query	121	AGCCTTCGTG	cccccccttcccccttttttgtccccAACTTGAGATGTATGAAGGCTTT	180
Sbjct	121	AGCCTTCGTG	CCCCCCCCTTCCCCCTTTTTTGTCCCCAACTTGAGATGTATGAAGGCTTT	180
Query	181	TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA	240	
Sbjct	181	TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA	240	
Query	241	GTTGAATAAAAAGTGCACACCTTATAAAA	268	
Sbjct	241	GTTGAATAAAAAGTGCACACCTTATAAAA	268	

Sequence 420 matched with Sequence 82

Query= Sequence ID 420
Length=334

SEQ ID NO: 82

ALIGNMENTS

Identities = 334/334 (100%), Gaps = 0/334 (0%)

Query	1	CTTCATTTGAAATGGTTGAATCTGCTGTGTAATAAAGTGGTTCAACCATGATTAGGAACT	60
Sbjct	1	CTTCATTTGAAATGGTTGAATCTGCTGTGTAATAAAGTGGTTCAACCATGATTAGGAACT	60
Query	61	GAAATTTAGTAGAAGAGGGAAAAGGAGTTAATGTAACAAATTATTTTAGCTACAAACCCC	120
Sbjct	61	GAAATTTAGTAGAAGAGGGAAAAGGAGTTAATGTAACAAATTATTTTAGCTACAAACCCC	120
Query	121	GGTAATAGAGCACTTGGGGGATGGGATGGGGTGGGTTGGTGAGACAATCAGAATGGTAAA	180
Sbjct	121	GGTAATAGAGCACTTGGGGGATGGGATGGGGTGGGTTGGTGAGACAATCAGAATGGTAAA	180
Query	181	TTGATTAAATGCTCCTAACCCCTGTAATTTTGTGCATAGAGCACCCCTATGCTGTGGAAATA	240
Sbjct	181	TTGATTAAATGCTCCTAACCCCTGTAATTTTGTGCATAGAGCACCCCTATGCTGTGGAAATA	240
Query	241	ACTGTTCTTAGATTTTCATTGTAAGTGGACTGTTTCAGGTTGCCAGAGGGAAAGAACATTC	300
Sbjct	241	ACTGTTCTTAGATTTTCATTGTAAGTGGACTGTTTCAGGTTGCCAGAGGGAAAGAACATTC	300
Query	301	CTAATTCTAATAAAATAAACTTTTATTTTGTTTA	334
Sbjct	301	CTAATTCTAATAAAATAAACTTTTATTTTGTTTA	334

Sequence 421 matched with Sequence 83

Query= Sequence ID 421
Length=675

SEQ ID NO: 83

ALIGNMENTS

Identities = 675/675 (100%), Gaps = 0/675 (0%)

Query	1	TGTCATTGAATCTGCTTGTTACTTAAATGCTAAACTCAATTCTGTAATTCAATAGGTGCA	60
Sbjct	1	TGTCATTGAATCTGCTTGTTACTTAAATGCTAAACTCAATTCTGTAATTCAATAGGTGCA	60
Query	61	CCTCTCTGAGAAACATAAGAGACAATGAGGAAAAGGATTTCAGCATTCCGTGGAATTTGTA	120
Sbjct	61	CCTCTCTGAGAAACATAAGAGACAATGAGGAAAAGGATTTCAGCATTCCGTGGAATTTGTA	120
Query	121	CCATGATCAGTGTGAATCCCAGTGGCGTAATCCAAGTAAGATGTTACAAAAGATTTGTTT	180
Sbjct	121	CCATGATCAGTGTGAATCCCAGTGGCGTAATCCAAGTAAGATGTTACAAAAGATTTGTTT	180
Query	181	TTAATGTCTAATTAATAAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAAA	240
Sbjct	181	TTAATGTCTAATTAATAAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAAA	240
Query	241	GTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAAATGTATATTTCTTAAT	300
Sbjct	241	GTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAAATGTATATTTCTTAAT	300
Query	301	ATCTTGAAATTGTAATGCCtttttttttcttaaatttttttGTCATGAAATGAGATAG	360
Sbjct	301	ATCTTGAAATTGTAATGCCTTTTTTTTTCTAAATTTTTTTTGTGTCATGAAATGAGATAG	360
Query	361	TAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTTT	420
Sbjct	361	TAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTTT	420
Query	421	CATCCAAATTTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCAG	480
Sbjct	421	CATCCAAATTTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATTCT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATTCT  540

Query  541  GAATAAAATCTTTGAATCAGATTTAGAAAATAATGAATAAAATACAAATCAGCCATTGAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GAATAAAATCTTTGAATCAGATTTAGAAAATAATGAATAAAATACAAATCAGCCATTGAAA  600

Query  601  TTGCTCTAATTTTGAGAGCTTATGATTTATTCATCTTTGGTTTCCAAGTTCAAGTTATAT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TTGCTCTAATTTTGAGAGCTTATGATTTATTCATCTTTGGTTTCCAAGTTCAAGTTATAT  660

Query  661  GTAGACATTTTAATT  675
          |||||||||||||
Sbjct   661  GTAGACATTTTAATT  675
```

Sequence 422 matched with Sequence 84

Query= Sequence ID 422
Length=485

SEQ ID NO: 84

ALIGNMENTS

Identities = 485/485 (100%), Gaps = 0/485 (0%)

Query	1	GCTTCCTAGGTGAGGTCACGAGGAAACCTGCTGGCCAAGTGACCTGGCAGGGTGTGGCCA	60
Sbjct	1	GCTTCCTAGGTGAGGTCACGAGGAAACCTGCTGGCCAAGTGACCTGGCAGGGTGTGGCCA	60
Query	61	GTGTGGCCAGGGCCGCCGAGCCTGCTTTCCTTCCCTGCAGCAGGAACCCCTTCTGGGGCTG	120
Sbjct	61	GTGTGGCCAGGGCCGCCGAGCCTGCTTTCCTTCCCTGCAGCAGGAACCCCTTCTGGGGCTG	120
Query	121	TGATCCTGCGATGGTGCCTGGGTGGGAGTgggggtgggggCGGGATGGTCTCCCTACCT	180
Sbjct	121	TGATCCTGCGATGGTGCCTGGGTGGGAGTGGGGGTGGGGGGCGGGATGGTCTCCCTACCT	180
Query	181	GCCAGCTTCTTGTTTTGAGGTGAGGACAGCCCCGGAAGCTCANACTTGGCTCCTGTCCAT	240
Sbjct	181	GCCAGCTTCTTGTTTTGAGGTGAGGACAGCCCCGGAAGCTCANACTTGGCTCCTGTCCAT	240
Query	241	GTACTTGGGGCCATGAGCTCTGCAGGGACCTTGGAAGANAGAGACGGGTGGTGTANGGC	300
Sbjct	241	GTACTTGGGGCCATGAGCTCTGCAGGGACCTTGGAAGANAGAGACGGGTGGTGTANGGC	300
Query	301	ANGGGAAGGCATTGTCTTCAAACAGGAAAAAGCTGANAATGGAAACAGGCGAAACTTACC	360
Sbjct	301	ANGGGAAGGCATTGTCTTCAAACAGGAAAAAGCTGANAATGGAAACAGGCGAAACTTACC	360
Query	361	AAGTGTAACATCACCTGGAAGTGAAGGAGGGTGGGAAGGTTTTAATTATTTTAAAAATAG	420
Sbjct	361	AAGTGTAACATCACCTGGAAGTGAAGGAGGGTGGGAAGGTTTTAATTATTTTAAAAATAG	420
Query	421	AGATGGGGTCTCACTATGTTGCCAGGCTGGTCTCAAACACTGGGCTCAAGTGAACCTC	480
Sbjct	421	AGATGGGGTCTCACTATGTTGCCAGGCTGGTCTCAAACACTGGGCTCAAGTGAACCTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTTCT	485
Sbjct	481	CTTCT	485

Sequence 423 matched with Sequence 85

Query= Sequence ID - 423 nt: 387
Length=387

SEQ ID NO: 85 nt: 387

ALIGNMENTS

Identities = 387/387 (100%), Gaps = 0/387 (0%)

Query	1	TGTTTCTCNAGGGCGAGAGGCTGTCTTANAGCACCATTCTCTGGCCCTNGTCCCATGAGA	60
Sbjct	1	TGTTTCTCNAGGGCGAGAGGCTGTCTTANAGCACCATTCTCTGGCCCTNGTCCCATGAGA	60
Query	61	AGGAACCGCACTCAGGAGCCACACTCTCCCACTNCCCTTGCCCANAAAGACTCACAGAGGG	120
Sbjct	61	AGGAACCGCACTCAGGAGCCACACTCTCCCACTNCCCTTGCCCANAAAGACTCACAGAGGG	120
Query	121	CACGGAGCTGGCTGTGGTGAGAGGAGGTCCANCAAATTCCTGTCTGCANAAGGGTTCTGA	180
Sbjct	121	CACGGAGCTGGCTGTGGTGAGAGGAGGTCCANCAAATTCCTGTCTGCANAAGGGTTCTGA	180
Query	181	ACACCACCGCCTGGCAGCGTGCTGGAGGAGGGATTCTCTTTTCCTCACAGCAATTCTGA	240
Sbjct	181	ACACCACCGCCTGGCAGCGTGCTGGAGGAGGGATTCTCTTTTCCTCACAGCAATTCTGA	240
Query	241	CCAGAAACCTGTCAAATCAGGAATGGCTAAAATAAGACCAGGGTATGAATGACCATCAGC	300
Sbjct	241	CCAGAAACCTGTCAAATCAGGAATGGCTAAAATAAGACCAGGGTATGAATGACCATCAGC	300
Query	301	CACAGTAAAACCAAGGCACAGCTCTCCTGAGCCCACCCAAGCTGCTGTGGCCCAGACTGG	360
Sbjct	301	CACAGTAAAACCAAGGCACAGCTCTCCTGAGCCCACCCAAGCTGCTGTGGCCCAGACTGG	360
Query	361	TGACATCACCTCAGGGCaaaaaaaaa	387
Sbjct	361	TGACATCACCTCAGGGCAAAAAAAAAA	387

Sequence 424 matched with Sequence 86

Query= Sequence ID - 424 nt: 420
Length=420

SEQ ID NO: 86 nt: 420

ALIGNMENTS

Identities = 420/420 (100%), Gaps = 0/420 (0%)

Query	1	CGCAGAATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAGGGCCGTTCTGCCATCAAC	60
Sbjct	1	CGCAGAATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAGGGCCGTTCTGCCATCAAC	60
Query	61	GAAGTGGTAACCCGAGAATACACCATCAACATTACACAAGCGCATCCATGGAGTGGGCTTC	120
Sbjct	61	GAAGTGGTAACCCGAGAATACACCATCAACATTACACAAGCGCATCCATGGAGTGGGCTTC	120
Query	121	AAGAAGCGTGCACCTCGGGCACTCAAAGAGATTTCGGAATTTGCCATGAAGGAGATGGGA	180
Sbjct	121	AAGAAGCGTGCACCTCGGGCACTCAAAGAGATTTCGGAATTTGCCATGAAGGAGATGGGA	180
Query	181	ACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGG	240
Sbjct	181	ACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGG	240
Query	241	AATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTCA	300
Sbjct	241	AATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTCA	300
Query	301	CCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAG	360
Sbjct	301	CCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAG	360
Query	361	ACAGTCAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAATTG	420
Sbjct	361	ACAGTCAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAATTG	420

Sequence 425 matched with Sequence 87

Query= Sequence ID 425
Length=675

SEQ ID NO: 87

ALIGNMENTS

Identities = 675/675 (100%), Gaps = 0/675 (0%)

Query	1	GGAAACTGATGCCAGTCAGAACTCAGATCAAATGAAGGGTGAAGAGAACCAGAATTGA	60
Sbjct	1	GGAAACTGATGCCAGTCAGAACTCAGATCAAATGAAGGGTGAAGAGAACCAGAATTGA	60
Query	61	TCTCTCTGTAGGAGAATATAAATGACTTTTTTAAAGTACATATTTTCTGTGAAAGACAGT	120
Sbjct	61	TCTCTCTGTAGGAGAATATAAATGACTTTTTTAAAGTACATATTTTCTGTGAAAGACAGT	120
Query	121	TTTTTGTTTAATGCAAAAATGTTAACAATGTTTATATCATGTAGAAGTAAAAGATCGTGA	180
Sbjct	121	TTTTTGTTTAATGCAAAAATGTTAACAATGTTTATATCATGTAGAAGTAAAAGATCGTGA	180
Query	181	AACAGCACAGAGAACAGTAGTAAGACAGATTGAATTGCACTGTTGTAAGATGATGAACTT	240
Sbjct	181	AACAGCACAGAGAACAGTAGTAAGACAGATTGAATTGCACTGTTGTAAGATGATGAACTT	240
Query	241	ACAATATTAAGTGAAGGTAGACTGTGATAGATTAAGGATATATATTGTAATCCCTAGAGC	300
Sbjct	241	ACAATATTAAGTGAAGGTAGACTGTGATAGATTAAGGATATATATTGTAATCCCTAGAGC	300
Query	301	AATTGTCAAAGTGGTACAGGTAAAAAGCCAATAGAGGTGATAAAATGGAATACTAAAAAA	360
Sbjct	301	AATTGTCAAAGTGGTACAGGTAAAAAGCCAATAGAGGTGATAAAATGGAATACTAAAAAA	360
Query	361	TATCAGATGAATAATAAAGAAGACAGGAAATGAGGAACAGTGGAACAGAATGAATAAAAA	420
Sbjct	361	TATCAGATGAATAATAAAGAAGACAGGAAATGAGGAACAGTGGAACAGAATGAATAAAAA	420
Query	421	ACAAGACCATTAACTTAATCATTAATAATTACTTTAAATGGGTAAACATTATGGTTATA	480
Sbjct	421	ACAAGACCATTAACTTAATCATTAATAATTACTTTAAATGGGTAAACATTATGGTTATA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGGCAGAGATTTTCAGACTAGATAAAAGAGCAAGCTCCACTATATACTGTCTACAAGAGA  540
          |||
Sbjct   481  AGGCAGAGATTTTCAGACTAGATAAAAGAGCAAGCTCCACTATATACTGTCTACAAGAGA  540

Query  541  TATACTTTAAAGTGTATATTATATTTAAATATAAAGATTTGGAATAAAATAAACCTAAGAA  600
          |||
Sbjct   541  TATACTTTAAAGTGTATATTATATTTAAATATAAAGATTTGGAATAAAATAAACCTAAGAA  600

Query  601  TAAGCTTACTAGGGAAGTGAAAGATCTGTACAACAAGAATTACAAAACACTGCTGAACGA  660
          |||
Sbjct   601  TAAGCTTACTAGGGAAGTGAAAGATCTGTACAACAAGAATTACAAAACACTGCTGAACGA  660

Query  661  AATCATAGGTGACCA  675
          |||
Sbjct   661  AATCATAGGTGACCA  675
```

Sequence 426 matched with Sequence 88

Query= Sequence ID 426
Length=594

SEQ ID NO: 88

ALIGNMENTS

Identities = 594/594 (100%), Gaps = 0/594 (0%)

Query	1	GTCCCGGAATCGCGGCCGCGTCGACGTTTCCTCAAAATTTATCTTCCTGTTAATGTCAGG	60
Sbjct	1	GTCCCGGAATCGCGGCCGCGTCGACGTTTCCTCAAAATTTATCTTCCTGTTAATGTCAGG	60
Query	61	CATGTATCTCCTTAGCTTGCCACAAATAACTATATATACCACAGACCTTCCTTTGTAGGG	120
Sbjct	61	CATGTATCTCCTTAGCTTGCCACAAATAACTATATATACCACAGACCTTCCTTTGTAGGG	120
Query	121	CTAACAGTGTTCATTGTAAGTGGAGGCCTCATAGATACCTGGCCTTTTCCTACCTTATT	180
Sbjct	121	CTAACAGTGTTCATTGTAAGTGGAGGCCTCATAGATACCTGGCCTTTTCCTACCTTATT	180
Query	181	CCAAAGATGGTTGCATCTTATAAATAATGTCATTCTTCAGCAAATGGTATGGAAATGAGA	240
Sbjct	181	CCAAAGATGGTTGCATCTTATAAATAATGTCATTCTTCAGCAAATGGTATGGAAATGAGA	240
Query	241	TTGTAATGTCATTATTTCTCTTTAAATAATCAGGACAACCTCATGATACAAAGAGCTCTT	300
Sbjct	241	TTGTAATGTCATTATTTCTCTTTAAATAATCAGGACAACCTCATGATACAAAGAGCTCTT	300
Query	301	CTCTATAAAAGGTGGGACtttttttttAGTAATAGCAAAAATAAAATTGTACCTCCTTA	360
Sbjct	301	CTCTATAAAAGGTGGGACTTTTTTTTTAGTAATAGCAAAAATAAAATTGTACCTCCTTA	360
Query	361	ATCTTCTACAGAAAGATGGATTTTCATTTTCAACATTAAGAGGTAGTTTAAAGAAGCAGTA	420
Sbjct	361	ATCTTCTACAGAAAGATGGATTTTCATTTTCAACATTAAGAGGTAGTTTAAAGAAGCAGTA	420
Query	421	GAAGTCAGCCTGGGCAGCATGGTGAAACCCCGTCTCTACAAAAAAGTTAGCTGGGCTTAG	480
Sbjct	421	GAAGTCAGCCTGGGCAGCATGGTGAAACCCCGTCTCTACAAAAAAGTTAGCTGGGCTTAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TAGTTGCAATCCCAGCTACTCTGGAGGCTGAGGTTGGAGATCATCTGANCCTGGGGAGGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TAGTTGCAATCCCAGCTACTCTGGAGGCTGAGGTTGGAGATCATCTGANCCTGGGGAGGT  540

Query  541  CNAGGCTGCAATGATACANTGAGCCCTGATTGTGCCACTCCACCTGGTTGCAGA  594
          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CNAGGCTGCAATGATACANTGAGCCCTGATTGTGCCACTCCACCTGGTTGCAGA  594
```

Sequence 427 matched with Sequence 89

Query= Sequence ID 427
Length=530

SEQ ID NO: 89

ALIGNMENTS

Identities = 530/530 (100%), Gaps = 0/530 (0%)

Query	1	TTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGTAT	60
Sbjct	1	TTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGTAT	60
Query	61	GCATATACGAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACC	120
Sbjct	61	GCATATACGAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACC	120
Query	121	ATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAATGGGGCTGGAC	180
Sbjct	121	ATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAATGGGGCTGGAC	180
Query	181	ACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACGCAGA	240
Sbjct	181	ACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACGCAGA	240
Query	241	GAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGT	300
Sbjct	241	GAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGT	300
Query	301	GAACAAAGCACCTAAGATGCGCCGCCGACCTACAGAGCTCATGGTCGGATTAACCCATA	360
Sbjct	301	GAACAAAGCACCTAAGATGCGCCGCCGACCTACAGAGCTCATGGTCGGATTAACCCATA	360
Query	361	CATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGAAAAGGAACAGATTGTTCTTAA	420
Sbjct	361	CATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGAAAAGGAACAGATTGTTCTTAA	420
Query	421	ACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAACAAAA	480
Sbjct	421	ACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAACTGAAGAAACAAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ACTTATGGCACGGGAGTAAATTCAGCATTTAAATAAATGTAATTAAAAGG  530
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACTTATGGCACGGGAGTAAATTCAGCATTTAAATAAATGTAATTAAAAGG  530
```


Sequence 428 matched with Sequence 90

Query= Sequence ID 428
Length=381

SEQ ID NO: 90

ALIGNMENTS

Identities = 381/381 (100%), Gaps = 0/381 (0%)

Query	1	TGCAGGATCCGTCGACTCTAGATAACATGGCTAGAAAAGAGAATGAAAAAGTTGGAATTT	60
Sbjct	1	TGCAGGATCCGTCGACTCTAGATAACATGGCTAGAAAAGAGAATGAAAAAGTTGGAATTT	60
Query	61	TTAATTGCCATGGTATGGGGGGTAATCAGGTTTTCTTATACTGCCAACAAAGAAATTA	120
Sbjct	61	TTAATTGCCATGGTATGGGGGGTAATCAGGTTTTCTTATACTGCCAACAAAGAAATTA	120
Query	121	GAACAGATGACCTTTGCTTGGATGTTTCCAACTTAATGGCCAGTTACAATGCTCAAAT	180
Sbjct	121	GAACAGATGACCTTTGCTTGGATGTTTCCAACTTAATGGCCAGTTACAATGCTCAAAT	180
Query	181	GCCACCACCTAAAAGGCAACCAACTCTGGGAGTATGACCCAGTGAAATTAACCCTGCAGC	240
Sbjct	181	GCCACCACCTAAAAGGCAACCAACTCTGGGAGTATGACCCAGTGAAATTAACCCTGCAGC	240
Query	241	ATGTGAACAGTAATCAGTGCCTGGATAAAGCCACAGAAGAGGATAGCCAGGTGCCAGCA	300
Sbjct	241	ATGTGAACAGTAATCAGTGCCTGGATAAAGCCACAGAAGAGGATAGCCAGGTGCCAGCA	300
Query	301	TTAGAGACTGCAATGGAAGTCGGTCCCAGCAGTGGCTTCTTCGAAACGTCACCCTGCCAG	360
Sbjct	301	TTAGAGACTGCAATGGAAGTCGGTCCCAGCAGTGGCTTCTTCGAAACGTCACCCTGCCAG	360
Query	361	AAATATTCTGAGACCAAATTT	381
Sbjct	361	AAATATTCTGAGACCAAATTT	381

Sequence 429 matched with Sequence 91

Query= Sequence ID - 429 nt: 535
Length=535

SEQ ID NO: 91 nt: 535

ALIGNMENTS

Identities = 535/535 (100%), Gaps = 0/535 (0%)

Query	1	CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAATAATAAAATGCTTACACGAA	60
Sbjct	1	CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAATAATAAAATGCTTACACGAA	60
Query	61	AATTATTTATTGAGAATATTCATATAAAAAATTACCTAAAGCAAAGTaaaaaaaGTAAAT	120
Sbjct	61	AATTATTTATTGAGAATATTCATATAAAAAATTACCTAAAGCAAAGTAAAAAAGTAAAT	120
Query	121	CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTGTAGCTGTAACAAAAAGAAAG	180
Sbjct	121	CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTGTAGCTGTAACAAAAAGAAAG	180
Query	181	AAAACAACtttttttAAAGCCTCATTCTCTTTCTTTCAAATGTACCTTATTCCACAC	240
Sbjct	181	AAAACAACTTTTTTTAAAGCCTCATTCTCTTTCTTTCAAATGTACCTTATTCCACAC	240
Query	241	ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAAATAAGAT	300
Sbjct	241	ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAAATAAGAT	300
Query	301	GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAACTCCTCTTCACGATTG	360
Sbjct	301	GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAACTCCTCTTCACGATTG	360
Query	361	ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAAGTGGTCTTAAGTTGGAA	420
Sbjct	361	ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAAGTGGTCTTAAGTTGGAA	420
Query	421	AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA	480
Sbjct	421	AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTGTTCTAT	535
Sbjct	481	ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTGTTCTAT	535

Sequence 430 matched with Sequence 92

Query= Sequence ID 430
Length=619

SEQ ID NO: 92

ALIGNMENTS

Identities = 619/619 (100%), Gaps = 0/619 (0%)

Query	1	CAGGGGCTTCTGCTGAGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGtttttttCT	60
Sbjct	1	CAGGGGCTTCTGCTGAGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTTCT	60
Query	61	CTTTGAAAGATAGAGATTAATACAACACTTAAAAAATATAGTCAATAGGTTACTAAGAT	120
Sbjct	61	CTTTGAAAGATAGAGATTAATACAACACTTAAAAAATATAGTCAATAGGTTACTAAGAT	120
Query	121	ATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATAT	180
Sbjct	121	ATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATAT	180
Query	181	GAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAAACATGACGGA	240
Sbjct	181	GAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAAACATGACGGA	240
Query	241	GGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAAATTGAGAGAAAG	300
Sbjct	241	GGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAAATTGAGAGAAAG	300
Query	301	GACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGG	360
Sbjct	301	GACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGG	360
Query	361	TGACTTAAACAGCTTAAAGTTTAGTTTAAAGTTGTAGGTGATTAAAAATAATTTGAAGGC	420
Sbjct	361	TGACTTAAACAGCTTAAAGTTTAGTTTAAAGTTGTAGGTGATTAAAAATAATTTGAAGGC	420
Query	421	GATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAGACCTTGAAATCCATGACGCAG	480
Sbjct	421	GATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAGACCTTGAAATCCATGACGCAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAAATGGAA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAAATGGAA  540

Query  541  AGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAGTGGAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAGTGGAAA  600

Query  601  ACTGGAAGACAGAAGTACC  619
          |||||||||||||||
Sbjct   601  ACTGGAAGACAGAAGTACC  619
```

Sequence 431 matched with Sequence 93

Query= Sequence ID 431
Length=131

SEQ ID NO: 93

ALIGNMENTS

Identities = 131/131 (100%), Gaps = 0/131 (0%)

```
Query 1      CGCTGGGTGCCTGCAGCGCCTCCCTTGTCTCATATGGTGTGTCCAGCACTCTATTGTTGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1      CGCTGGGTGCCTGCAGCGCCTCCCTTGTCTCATATGGTGTGTCCAGCACTCTATTGTTGT  60

Query 61     AAAGTGTGNTTTGNCTGACCTAAATTNTCTTTACTAAACANATTTAATAGTTnaaaaaa  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61     AAAGTGTGNTTTGNCTGACCTAAATTNTCTTTACTAAACANATTTAATAGTTNAAAAAA  120

Query 121    aaaaaaNANCA  131
            |||||||||
Sbjct 121    AAAAAANANCA  131
```

Blast comparison trimmed “NANCA” from the 3’ end of both sequences and reported 126 identities. The report has been manually corrected for this. “NANCA” has been appended to both sequences and identity count has been increased to 131.

Sequence 432 matched with Sequence 94

Query= Sequence ID 432
Length=607

SEQ ID NO: 94

ALIGNMENTS

Identities = 607/607 (100%), Gaps = 0/607 (0%)

Query	1	TTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAAGGGTCCA	60
Sbjct	1	TTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAAGGGTCCA	60
Query	61	AGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACCAGAGACTCT	120
Sbjct	61	AGACTCCATTAAGTGCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACCAGAGACTCT	120
Query	121	CCTATCTCACGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAATGCTTATAGG	180
Sbjct	121	CCTATCTCACGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAATGCTTATAGG	180
Query	181	AAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAGTGCAACCCT	240
Sbjct	181	AAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAGTGCAACCCT	240
Query	241	TGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGGAAACACACC	300
Sbjct	241	TGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGGAAACACACC	300
Query	301	AGCTTCTGCTACCTTCATGCTCATTGTTaaaaaaGATTAACCAGTGTGAACATTCTGAT	360
Sbjct	301	AGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAGATTAACCAGTGTGAACATTCTGAT	360
Query	361	CTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAGAATAACCCCA	420
Sbjct	361	CTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTGGTAGAATAACCCCA	420
Query	421	AAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGG	480
Sbjct	421	AAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGC  540

Query  541  TATCCCACCCCAAATTTCAACCTGAGGTATATTTCAATGAAGGCAGGTAGCTGTGCTTCT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TATCCCACCCCAAATTTCAACCTGAGGTATATTTCAATGAAGGCAGGTAGCTGTGCTTCT  600

Query  601  CAGAGCA  607
          |||||
Sbjct   601  CAGAGCA  607
```


Sequence 433 matched with Sequence 95

Query= Sequence ID 433
Length=687

SEQ ID NO: 95

ALIGNMENTS

Identities = 687/687 (100%), Gaps = 0/687 (0%)

Query	1	TCCCGGAATCGCGCCGCGTCGACCCGCCGCCGAGGATTACAGCAgcctcccccttgagcc	60
Sbjct	1	TCCCGGAATCGCGCCGCGTCGACCCGCCGCCGAGGATTACAGCAGCTCCCCCTTGAGCC	60
Query	61	ccctcgcttcccgacgttccgttccccctgccgccttctcccgccaccgccgcgcg	120
Sbjct	61	CCCTCGCTTCCCGACGTTCCGTTCCCCCTGCCGCCTTCTCCCGCCACCGCCGCCGCCG	120
Query	121	ccttccgcaggccgTTTCCACCGAGGAAAAGGAATCGTATCGTATGTCCGCTATCCAGAA	180
Sbjct	121	CCTTCCGCAGGCCGTTTCCACCGAGGAAAAGGAATCGTATCGTATGTCCGCTATCCAGAA	180
Query	181	CCTCCACTCTTTCGACCCCTTTGCTGATGCAAGTAAGGGTGATGACCTGCTTCCTGCTGG	240
Sbjct	181	CCTCCACTCTTTCGACCCCTTTGCTGATGCAAGTAAGGGTGATGACCTGCTTCCTGCTGG	240
Query	241	CACTGAGGATTATATCCATATAAGAATTCAACAGAGAAACGGCAGGAAGACCCTTACTAC	300
Sbjct	241	CACTGAGGATTATATCCATATAAGAATTCAACAGAGAAACGGCAGGAAGACCCTTACTAC	300
Query	301	TGTCCAAGGGATCGCTGATGATTACGATAAAAAAGAACTAGTGAAGGCGTTTAAGAAAAA	360
Sbjct	301	TGTCCAAGGGATCGCTGATGATTACGATAAAAAAGAACTAGTGAAGGCGTTTAAGAAAAA	360
Query	361	GTTTGCCTGCAATGGTACTGTAATTGAGCATCCGGAATATGGAGAAGTAATTCAGCTACA	420
Sbjct	361	GTTTGCCTGCAATGGTACTGTAATTGAGCATCCGGAATATGGAGAAGTAATTCAGCTACA	420
Query	421	GGGTGACCAACGCAAGAACATATGCCAGTTCCTCGTAGAGATTGGACTGGCTAAGGACGA	480
Sbjct	421	GGGTGACCAACGCAAGAACATATGCCAGTTCCTCGTAGAGATTGGACTGGCTAAGGACGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TCAGCTGAAGGTTTCATGGGTTTTAAGTGCTTGTGGCTCACTGAAGCTTAAGTGAGGATTT  540
          |||
Sbjct  481  TCAGCTGAAGGTTTCATGGGTTTTAAGTGCTTGTGGCTCACTGAAGCTTAAGTGAGGATTT  540

Query  541  CCTTGCAATGAGTAGAATTTCCCTTCCTCCCTTGTCACAGGTTTAAAAACCTCACAGCTT  600
          |||
Sbjct  541  CCTTGCAATGAGTAGAATTTCCCTTCCTCCCTTGTCACAGGTTTAAAAACCTCACAGCTT  600

Query  601  GTATAATGTAACCATTTGGGGTCCGCTTTTAACTGGACTAGTGTAACNCTTCATGCAA  660
          |||
Sbjct  601  GTATAATGTAACCATTTGGGGTCCGCTTTTAACTGGACTAGTGTAACNCTTCATGCAA  660

Query  661  TAAACTGAAAAGACCATGCTGCTANTC  687
          |||
Sbjct  661  TAAACTGAAAAGACCATGCTGCTANTC  687
```

Blast comparison trimmed “NTC” from the 3’ end of both sequences and reported 684 identities. The report has been manually corrected for this. “NTC” has been appended to both sequences and identity count has been increased to 687.

Sequence 434 matched with Sequence 96

Query= Sequence ID 434
Length=462

SEQ ID NO: 96

ALIGNMENTS

Identities = 462/462 (100%), Gaps = 0/462 (0%)

Query	1	TTCGGACGCAAGAAGACAGCGACAGCTGTGGCGCACTGCAAACGCGGCAATGGTCTCATC	60
Sbjct	1	TTCGGACGCAAGAAGACAGCGACAGCTGTGGCGCACTGCAAACGCGGCAATGGTCTCATC	60
Query	61	AAGGTGAACGGGCGGCCCTGGAGATGATTGAGCCGCGCACGCTACAGTACAAGCTGCTG	120
Sbjct	61	AAGGTGAACGGGCGGCCCTGGAGATGATTGAGCCGCGCACGCTACAGTACAAGCTGCTG	120
Query	121	GAGCCAGTTCTGCTTCTCGGCAAGGAGCGATTTGCTGGTGTAGACATCCGTGTCCGTGTA	180
Sbjct	121	GAGCCAGTTCTGCTTCTCGGCAAGGAGCGATTTGCTGGTGTAGACATCCGTGTCCGTGTA	180
Query	181	AAGGGTGGTGGTCACGTGGCCCANATTTATGCTATCCGTCACTCCATCTCCAAAGCCCTG	240
Sbjct	181	AAGGGTGGTGGTCACGTGGCCCANATTTATGCTATCCGTCACTCCATCTCCAAAGCCCTG	240
Query	241	GTGGCCTATTACCANAAATATGTGGATGAGGCTTCCAAGAAGGAGATCAAAGACATCCTC	300
Sbjct	241	GTGGCCTATTACCANAAATATGTGGATGAGGCTTCCAAGAAGGAGATCAAAGACATCCTC	300
Query	301	ATCCAGTATGACCGGACCCTGCTGGTAGCTGACCCTCGTCGCTGCGAGTCCAAAAAGTTT	360
Sbjct	301	ATCCAGTATGACCGGACCCTGCTGGTAGCTGACCCTCGTCGCTGCGAGTCCAAAAAGTTT	360
Query	361	GGAGGCCCTGGTGCCCGCGCTCGCTACCAGAAATCCTACCGATAAGCCCATCGTGACTCA	420
Sbjct	361	GGAGGCCCTGGTGCCCGCGCTCGCTACCAGAAATCCTACCGATAAGCCCATCGTGACTCA	420
Query	421	AAACTCACTTGTATAATAAACAGTTTTTTGAGGGATTTTAAAA	462
Sbjct	421	AAACTCACTTGTATAATAAACAGTTTTTTGAGGGATTTTAAAA	462

Sequence 435 matched with Sequence 97

Query= Sequence ID 435
Length=535

SEQ ID NO: 97

ALIGNMENTS

Identities = 535/535 (100%), Gaps = 0/535 (0%)

Query	1	CTGCAATGTGCAATAGTTGCACCACTGCACTCCAGCCTGGGTGACAGAGTGAGAACCTAT	60
Sbjct	1	CTGCAATGTGCAATAGTTGCACCACTGCACTCCAGCCTGGGTGACAGAGTGAGAACCTAT	60
Query	61	CTCTTaaaaaaaaaaaaaaaaaaaaaGGAAGAAGAGACATGAGAGGGCCCAAGTCACTTGCT	120
Sbjct	61	CTCTTAAAAAAAAAAAAAAAAAAAAAAGGAAGAAGAGACATGAGAGGGCCCAAGTCACTTGCT	120
Query	121	CACTCACTTTCCGTGTACATGTACCAAGAAAAGGCCATGTGGGAAAGAGCAAGAAGGCAG	180
Sbjct	121	CACTCACTTTCCGTGTACATGTACCAAGAAAAGGCCATGTGGGAAAGAGCAAGAAGGCAG	180
Query	181	CCGCCTTCAAGACAGGAAGAGAGCCCTCACCAGAACTGAGCCAGAACCTTGAATTCCA	240
Sbjct	181	CCGCCTTCAAGACAGGAAGAGAGCCCTCACCAGAACTGAGCCAGAACCTTGAATTCCA	240
Query	241	GCCTCCANAAGTGTGAGAAAAGAAATTTTCTGTTGTTTCAGTCCCCCAGCTATGGCATT	300
Sbjct	241	GCCTCCANAAGTGTGAGAAAAGAAATTTTCTGTTGTTTCAGTCCCCCAGCTATGGCATT	300
Query	301	TGTTACGGCAGCCTGAGCTAATACTCCTACTTTGTCCTGCATTTACTTGGTCTTCCAGTT	360
Sbjct	301	TGTTACGGCAGCCTGAGCTAATACTCCTACTTTGTCCTGCATTTACTTGGTCTTCCAGTT	360
Query	361	AGTTTTTTAGACTTTGGGAATCAGAGCAGTCAGTTGTCAGATTTTAGCTTACAGTTGTCC	420
Sbjct	361	AGTTTTTTAGACTTTGGGAATCAGAGCAGTCAGTTGTCAGATTTTAGCTTACAGTTGTCC	420
Query	421	TACCTGTGCAACTGAAATTTCTTCCATTTTAAACCAGAGCAGAGTTTTAGAGTCAAAAAGA	480
Sbjct	421	TACCTGTGCAACTGAAATTTCTTCCATTTTAAACCAGAGCAGAGTTTTAGAGTCAAAAAGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AACCAGATCTTTTAGTGCAGAAGCTTTCCTGTATTANAAGTGAGGAAGTTGGT	535
Sbjct	481	AACCAGATCTTTTAGTGCAGAAGCTTTCCTGTATTANAAGTGAGGAAGTTGGT	535

Sequence 436 matched with Sequence 98

Query= Sequence ID 436
Length=512

SEQ ID NO: 98

ALIGNMENTS

Identities = 512/512 (100%), Gaps = 0/512 (0%)

Query	1	aaaaaaaCTCCAGAGAAGTTTATAGAAAGAGATGACATGTAAACCCTGCTGAAAAATAGT	60
Sbjct	1	AAAAAACTCCAGAGAAGTTTATAGAAAGAGATGACATGTAAACCCTGCTGAAAAATAGT	60
Query	61	TTCATTTGTTAGAATATAATTGTCTTCCACTaaaaaaagaaaaaaaaGCATTTAAGGC	120
Sbjct	61	TTCATTTGTTAGAATATAATTGTCTTCCACTAAAAAAGAAAAAAAAAGCATTTAAGGC	120
Query	121	TCTAAGATCTCTTGAAGTACCACTTTTCCTGAATCCCAGAGTTTTTATGTGCATTATTTT	180
Sbjct	121	TCTAAGATCTCTTGAAGTACCACTTTTCCTGAATCCCAGAGTTTTTATGTGCATTATTTT	180
Query	181	TATGCGTTTGTAGTTTGATATGTTGTATTTATAAGTAGTTTTAGCTTTCCATTATGAATT	240
Sbjct	181	TATGCGTTTGTAGTTTGATATGTTGTATTTATAAGTAGTTTTAGCTTTCCATTATGAATT	240
Query	241	CTTCTTTGACCCATGAGTTATTTAGGTAAGTGTTTAAAAATTTACAATAGTTTATATATG	300
Sbjct	241	CTTCTTTGACCCATGAGTTATTTAGGTAAGTGTTTAAAAATTTACAATAGTTTATATATG	300
Query	301	CAAATATTATGTTGTTAGAGTTGGTTTTTCATGTCATTTTTACATATACAGGGGCAGTTTC	360
Sbjct	301	CAAATATTATGTTGTTAGAGTTGGTTTTTCATGTCATTTTTACATATACAGGGGCAGTTTC	360
Query	361	CCCAACTAAATTGTATATTCCTTAAAGCAGCACTCTTAAATTTTATTTCTGTGTCAATTT	420
Sbjct	361	CCCAACTAAATTGTATATTCCTTAAAGCAGCACTCTTAAATTTTATTTCTGTGTCAATTT	420
Query	421	CTTGNCTGTGTTTCCTGGCATGGAATACATGGCATAAAATTTGTTATGTAATTAAATGAA	480
Sbjct	421	CTTGNCTGTGTTTCCTGGCATGGAATACATGGCATAAAATTTGTTATGTAATTAAATGAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATATTATTATACTTTCTATTTTCTAGAAAAAA  512
          |||||||||||||||||||||||||||
Sbjct  481  ATATTATTATACTTTCTATTTTCTAGAAAAAA  512
```


Sequence 438 matched with Sequence 99

Query= Sequence ID - 438 nt: 577
Length=577

SEQ ID NO: 99 nt: 577

ALIGNMENTS

Identities = 577/577 (100%), Gaps = 0/577 (0%)

Query	1	GTCGACAGGGATGACATAACTATTAGTGGCAGGTTAGTTGTTGGTCACTTTCAACTCTGG	60
Sbjct	1	GTCGACAGGGATGACATAACTATTAGTGGCAGGTTAGTTGTTGGTCACTTTCAACTCTGG	60
Query	61	GTTCAAGCGATTCTCCTACCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGCACCGCC	120
Sbjct	61	GTTCAAGCGATTCTCCTACCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGCACCGCC	120
Query	121	ACACCTAATTTTCTATTCTTAGTAGAGACGGGGTTTCTCCCTGTTGGTCAGGCTGGTCTC	180
Sbjct	121	ACACCTAATTTTCTATTCTTAGTAGAGACGGGGTTTCTCCCTGTTGGTCAGGCTGGTCTC	180
Query	181	GAACTCCCGACCTCAGGTGATCTGCCTGCCTCAGTCTCCCAAAGTCCTGGAACACAGAC	240
Sbjct	181	GAACTCCCGACCTCAGGTGATCTGCCTGCCTCAGTCTCCCAAAGTCCTGGAACACAGAC	240
Query	241	ATGAGCCACCACGCCTGGCCCTTTTAAATATTTCTGCTCATTGATGATGCACCCAGTC	300
Sbjct	241	ATGAGCCACCACGCCTGGCCCTTTTAAATATTTCTGCTCATTGATGATGCACCCAGTC	300
Query	301	ACCCAAGTGCTCTGATGGAGATGTATAAGGAGATGAATGCTGTTTTCATGGCTGCTAATA	360
Sbjct	301	ACCCAAGTGCTCTGATGGAGATGTATAAGGAGATGAATGCTGTTTTCATGGCTGCTAATA	360
Query	361	CAACATTCTATTCTGCAACCCCCAAATCAAGAAGTAATTTTGACTTTCAAGTCTTATTATT	420
Sbjct	361	CAACATTCTATTCTGCAACCCCCAAATCAAGAAGTAATTTTGACTTTCAAGTCTTATTATT	420
Query	421	TAAGAAATATATTTTGCAAGACTATAGCTGCCATAGACCGTGATTCCTCTGATGGATCAG	480
Sbjct	421	TAAGAAATATATTTTGCAAGACTATAGCTGCCATAGACCGTGATTCCTCTGATGGATCAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ACAAATAAAATGAAAACCTCCTGCAACGTATTCATCATTCTAGATCCCTGAGGAATCGC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ACAAATAAAATGAAAACCTCCTGCAACGTATTCATCATTCTAGATCCCTGAGGAATCGC  540

Query  541  CAACTGACTTNCACAATGGGTGAACTGGGTACAGT  577
          ||||||||||||||||||||||||
Sbjct   541  CAACTGACTTNCACAATGGGTGAACTGGGTACAGT  577
```

Sequence 441 matched with Sequence 100

Query= Sequence ID - 441 nt: 552
Length=552

SEQ ID NO: 100 nt: 552

ALIGNMENTS

Identities = 552/552 (100%), Gaps = 0/552 (0%)

Query	1	AAACAAAATTATTCTCTGAGAGGGAAAGGACATTTGAGGGAAACATCAAATTTCCCCATA	60
Sbjct	1	AAACAAAATTATTCTCTGAGAGGGAAAGGACATTTGAGGGAAACATCAAATTTCCCCATA	60
Query	61	AATAAATGAATGGAGTTTGCAGGAAGGTGAGGGTGAGCAGAGATGTGTGTGGACATCTCT	120
Sbjct	61	AATAAATGAATGGAGTTTGCAGGAAGGTGAGGGTGAGCAGAGATGTGTGTGGACATCTCT	120
Query	121	GACCATCCATCGCTGTATTCAAATGGATTGTTTTATTCCATTCTGGTCTCAGGCATGACC	180
Sbjct	121	GACCATCCATCGCTGTATTCAAATGGATTGTTTTATTCCATTCTGGTCTCAGGCATGACC	180
Query	181	ACGTCCAGTGAAGACATTTGAGGCAGCACATCTCAGGACCCAGGCAATAGACTGGCCCCA	240
Sbjct	181	ACGTCCAGTGAAGACATTTGAGGCAGCACATCTCAGGACCCAGGCAATAGACTGGCCCCA	240
Query	241	ACTCAGGCTGGACTAAGGTGTGATTAATTCTTTGTTTTTGTGTGGAACAGCTCACCTTG	300
Sbjct	241	ACTCAGGCTGGACTAAGGTGTGATTAATTCTTTGTTTTTGTGTGGAACAGCTCACCTTG	300
Query	301	TCAGACAGCCTCAGGGCATCTCTGAGACACAGGGGCAGAAAATGACATTCATCTTTTGAG	360
Sbjct	301	TCAGACAGCCTCAGGGCATCTCTGAGACACAGGGGCAGAAAATGACATTCATCTTTTGAG	360
Query	361	TCCTCATCCATGGAGTGCTGTGTTTGGGGGGCTGCATCTGCTGAAGCGAGAACCCCATTC	420
Sbjct	361	TCCTCATCCATGGAGTGCTGTGTTTGGGGGGCTGCATCTGCTGAAGCGAGAACCCCATTC	420
Query	421	TGCCACCCACCCAGGATGCCATTCTCCAGGACTTCTCCAACCTTACTATTAGACTAAACC	480
Sbjct	421	TGCCACCCACCCAGGATGCCATTCTCCAGGACTTCTCCAACCTTACTATTAGACTAAACC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGAACAAGCAACAAACTGTATTTATGCAAGCAAAATTGATGAGAAAATTATATTCAAATA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGAACAAGCAACAAACTGTATTTATGCAAGCAAAATTGATGAGAAAATTATATTCAAATA  540

Query  541  AAGCAAAAATTA  552
          |||||||||
Sbjct   541  AAGCAAAAATTA  552
```

Sequence 442 matched with Sequence 101

Query= Sequence ID - 442 nt: 606
Length=606

SEQ ID NO: 101 nt: 606

ALIGNMENTS

Identities = 606/606 (100%), Gaps = 0/606 (0%)

Query	1	TCGTGCCACTGCACTCCAGCCTGGACGACAGAGTGAGACTCCATCTCaaaataaataaat	60
Sbjct	1	TCGTGCCACTGCACTCCAGCCTGGACGACAGAGTGAGACTCCATCTCAAAATAAATAAAT	60
Query	61	aaataaataaataaataaataaataaaaaataaaaaataCTTCTGCTATGAAAAACCTA	120
Sbjct	61	AAATAAATAAATAAATAAATAAATAAAAAATAAAAAATACTTCTGCTATGAAAAACCTA	120
Query	121	GTTGGTATTTTGGCTTATTTAATACTATAGAAATATGGTGATCTCATCTTTAATAGAGTG	180
Sbjct	121	GTTGGTATTTTGGCTTATTTAATACTATAGAAATATGGTGATCTCATCTTTAATAGAGTG	180
Query	181	CTTTTAAGGTCCCCAGTGATAATCTCCTAAATCATGAACCTTAAGAATTTATAATGTTA	240
Sbjct	181	CTTTTAAGGTCCCCAGTGATAATCTCCTAAATCATGAACCTTAAGAATTTATAATGTTA	240
Query	241	ATATGAGGAAATGAAATCTGGATTATCTCACCACATATTATATAATTCATTAGTGACAGA	300
Sbjct	241	ATATGAGGAAATGAAATCTGGATTATCTCACCACATATTATATAATTCATTAGTGACAGA	300
Query	301	GCAAGAACTCCAGGTCACCTGTCTATTCCATGTTTTTCCTATCTGCCTTTAAATGTTGAG	360
Sbjct	301	GCAAGAACTCCAGGTCACCTGTCTATTCCATGTTTTTCCTATCTGCCTTTAAATGTTGAG	360
Query	361	ATACTACCCTTATCTCATGTGAATGGAGAACTGCCTAAAATGCTAAAACCTGACTCAGAG	420
Sbjct	361	ATACTACCCTTATCTCATGTGAATGGAGAACTGCCTAAAATGCTAAAACCTGACTCAGAG	420
Query	421	GCACCCAGACATAAGTGAAGTGTGATTAGAAAATCCTGGTCAGTTGAGTCTTAGCCAAAT	480
Sbjct	421	GCACCCAGACATAAGTGAAGTGTGATTAGAAAATCCTGGTCAGTTGAGTCTTAGCCAAAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTGTACCTACTGTGTCTGCCTCTATCAAGTCAATGAAAACATGATCTGAGAACTGTAAGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTGTACCTACTGTGTCTGCCTCTATCAAGTCAATGAAAACATGATCTGAGAACTGTAAGT  540

Query  541  CCATTTATGGAAGGGTTGATTANAGATATTTTGAAGTTNCAGTGATGAGCCCCCTTCTC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CCATTTATGGAAGGGTTGATTANAGATATTTTGAAGTTNCAGTGATGAGCCCCCTTCTC  600

Query  601  AAATAG  606
          |||||
Sbjct   601  AAATAG  606
```

Sequence 446 matched with Sequence 102

Query= Sequence ID 446
Length=341

SEQ ID NO: 102

ALIGNMENTS

Identities = 341/341 (100%), Gaps = 0/341 (0%)

```
Query 1   CGGACTCCTGTGCTAATTGTCAGCTTACATATCATTGTATAGAGACTGTTTATTCTGTAC 60
          |||
Sbjct 1   CGGACTCCTGTGCTAATTGTCAGCTTACATATCATTGTATAGAGACTGTTTATTCTGTAC 60

Query 61  CAAACTGATTTCAAAAGTACTACATNGAAAATAAACCGGTGACTGTTTTCTTCATAAAG 120
          |||
Sbjct 61  CAAACTGATTTCAAAAGTACTACATNGAAAATAAACCGGTGACTGTTTTCTTCATAAAG 120

Query 121 TTCTGCGTTTGGCATCTTCACTCTTTCCAAAATGTATCTGTACATCANAAATGTCACTAT 180
          |||
Sbjct 121 TTCTGCGTTTGGCATCTTCACTCTTTCCAAAATGTATCTGTACATCANAAATGTCACTAT 180

Query 181 TCCAAGTGTCTTTTTAGTGTGGCTTTAGTATGGCTTCCTTTTAATATTGNACATACATTG 240
          |||
Sbjct 181 TCCAAGTGTCTTTTTAGTGTGGCTTTAGTATGGCTTCCTTTTAATATTGNACATACATTG 240

Query 241 NATCTTTGTTTTATGGNAATAAGTAATAAAAATGTAGACTTCATATTTGTACAAAATGT 300
          |||
Sbjct 241 NATCTTTGTTTTATGGNAATAAGTAATAAAAATGTAGACTTCATATTTGTACAAAATGT 300

Query 301 CCTATGTACAGAATAAAAAAGTTCATAGAAACAGCCNANAA 341
          |||
Sbjct 301 CCTATGTACAGAATAAAAAAGTTCATAGAAACAGCCNANAA 341
```

Blast comparison trimmed “NANAA” from the 3’ end of both sequences and reported 336 identities. The report has been manually corrected for this. “NANAA” has been appended to both sequences and identity count has been increased to 341.

Sequence 447 matched with Sequence 103

Query= Sequence ID 447
Length=85

SEQ ID NO: 103

ALIGNMENTS

Identities = 85/85 (100%), Gaps = 0/85 (0%)

```
Query 1  AGGCCGAGGCAGGCAGATCNCNTGAGGTCAAGAGTTTGAGACCAGCNTAGCTAACATGGT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  AGGCCGAGGCAGGCAGATCNCNTGAGGTCAAGAGTTTGAGACCAGCNTAGCTAACATGGT 60

Query 61  GAAACCCCATCTCTACAAAAATATA 85
          ||||||||||||||||||||
Sbjct 61  GAAACCCCATCTCTACAAAAATATA 85
```


Sequence 448 matched with Sequence 104

Query= Sequence ID - 448 nt: 329
Length=329

SEQ ID NO: 104 nt: 329

ALIGNMENTS

Identities = 329/329 (100%), Gaps = 0/329 (0%)

Query	1	TACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAG	60
Sbjct	1	TACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAG	60
Query	61	AAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTG	120
Sbjct	61	AAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTG	120
Query	121	AAATGCCCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTTG	180
Sbjct	121	AAATGCCCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTTG	180
Query	181	TGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAAAGCAAGGCTTACAGAA	240
Sbjct	181	TGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAAAGCAAGGCTTACAGAA	240
Query	241	GGATGTTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTGAGTCAAGATGAGTGGGAAAC	300
Sbjct	241	GGATGTTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTGAGTCAAGATGAGTGGGAAAC	300
Query	301	CATCTCAATAAACACATTTTGGGTAAAA	329
Sbjct	301	CATCTCAATAAACACATTTTGGGTAAAA	329

Sequence 450 matched with Sequence 105

Query= Sequence ID 450
Length=504

SEQ ID NO: 105

ALIGNMENTS

Identities = 504/504 (100%), Gaps = 0/504 (0%)

Query	1	GAGCAGTGGCATGATCACACCTTACTGCGGCCTCCAACCCCTGAGCTTAAGTGATTCTCC	60
Sbjct	1	GAGCAGTGGCATGATCACACCTTACTGCGGCCTCCAACCCCTGAGCTTAAGTGATTCTCC	60
Query	61	CGCATTATCCTCCTGAGTAGCTGAGACTACAGGTGCATGCCACCATACACTACTAAATTT	120
Sbjct	61	CGCATTATCCTCCTGAGTAGCTGAGACTACAGGTGCATGCCACCATACACTACTAAATTT	120
Query	121	GGGTCGGGTGGTGGTGGTGATTTTTTAATATTTTTGTAGAGACAGGGTCTCACTGTGATG	180
Sbjct	121	GGGTCGGGTGGTGGTGGTGATTTTTTAATATTTTTGTAGAGACAGGGTCTCACTGTGATG	180
Query	181	CCCAGGCTGGTCTTGAACCTCTGGGCTCAAGCAGTCACCCACCTCAGCCTCCCAAAGCAC	240
Sbjct	181	CCCAGGCTGGTCTTGAACCTCTGGGCTCAAGCAGTCACCCACCTCAGCCTCCCAAAGCAC	240
Query	241	TGGGATTACAGGTGTGAGCCACCACACTGGCCAGCTTTGTTTTGTTTGTATGACTAAGCT	300
Sbjct	241	TGGGATTACAGGTGTGAGCCACCACACTGGCCAGCTTTGTTTTGTTTGTATGACTAAGCT	300
Query	301	GCTCTTGCTAAAAGGGCTTCTCTCTGAACCTCCCTACCTTTCTTCTGTTCCCTGGGCTA	360
Sbjct	301	GCTCTTGCTAAAAGGGCTTCTCTCTGAACCTCCCTACCTTTCTTCTGTTCCCTGGGCTA	360
Query	361	GGGCTCCATGTTGGCAGTCCTACTCCCAATTAACCTGGGGCTGTCTGGTTAACCTTTATA	420
Sbjct	361	GGGCTCCATGTTGGCAGTCCTACTCCCAATTAACCTGGGGCTGTCTGGTTAACCTTTATA	420
Query	421	AGATCTGCAGTCATTGGGAGACCCGGGGACCAGGAATATTGTTGTTGAGGGAGCTACCCT	480
Sbjct	421	AGATCTGCAGTCATTGGGAGACCCGGGGACCAGGAATATTGTTGTTGAGGGAGCTACCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGAAAGTGGATGGGTGGCCAAAGG	504
Sbjct	481	GGAAAGTGGATGGGTGGCCAAAGG	504

Sequence 452 matched with Sequence 106

Query= Sequence ID 452
Length=582

SEQ ID NO: 106

ALIGNMENTS

Identities = 582/582 (100%), Gaps = 0/582 (0%)

Query	1	TTTGGCTTTGCCTCTAGGCATTAGATGTTATCTTTGGAGGCATCCTTCTATGAGCATTCA	60
Sbjct	1	TTTGGCTTTGCCTCTAGGCATTAGATGTTATCTTTGGAGGCATCCTTCTATGAGCATTCA	60
Query	61	TTTTTGGACCAAGCCTGGATTTACAATTCTATTACTGGCCCAGACTTCATTTCTATCCAA	120
Sbjct	61	TTTTTGGACCAAGCCTGGATTTACAATTCTATTACTGGCCCAGACTTCATTTCTATCCAA	120
Query	121	TTTCATTCCACTGTGCTATAGTTTACAACATATAATTTGACTTATAAAATAATTCCTGACT	180
Sbjct	121	TTTCATTCCACTGTGCTATAGTTTACAACATATAATTTGACTTATAAAATAATTCCTGACT	180
Query	181	ATGGGTTTAAAGACTGAAAAATGGATCAATAGAACTTTGAAAATGTAAACATCTTGATTG	240
Sbjct	181	ATGGGTTTAAAGACTGAAAAATGGATCAATAGAACTTTGAAAATGTAAACATCTTGATTG	240
Query	241	CTTTTCTCAGTGTAGAAATGGACAATGTTTAGCTTAAAACTGCATGTTTTTAATGAGAT	300
Sbjct	241	CTTTTCTCAGTGTAGAAATGGACAATGTTTAGCTTAAAACTGCATGTTTTTAATGAGAT	300
Query	301	ACGGGGTTGAAAGACTTATTCCTGGAATTTATTGTTCTGGAGAAAGCCTGTTGCTATCTG	360
Sbjct	301	ACGGGGTTGAAAGACTTATTCCTGGAATTTATTGTTCTGGAGAAAGCCTGTTGCTATCTG	360
Query	361	CCATACCTTGTTTTACTTTGTGCAAAATGAGCTTCTTTTAAAGTAATGAGCTCTTTCCAT	420
Sbjct	361	CCATACCTTGTTTTACTTTGTGCAAAATGAGCTTCTTTTAAAGTAATGAGCTCTTTCCAT	420
Query	421	G TTCAGCTTAAATTGCTGTCTTAGACACTTCATCAGGGTTCCTGCTCTGCCTCATTCCC	480
Sbjct	421	G TTCAGCTTAAATTGCTGTCTTAGACACTTCATCAGGGTTCCTGCTCTGCCTCATTCCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCTTTTGCTCACTTGCAGCCTTTGACATAATCCTGGGAGGCAATTGGCATCATACATATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CCTTTTGCTCACTTGCAGCCTTTGACATAATCCTGGGAGGCAATTGGCATCATACATATT  540

Query  541  TTGCTTTGTAATCTCCTGCTTTGATTCTGACTGGGACCCAGC  582
          ||||||||||||||||||||||||||||||||
Sbjct   541  TTGCTTTGTAATCTCCTGCTTTGATTCTGACTGGGACCCAGC  582
```

Sequence 453 matched with Sequence 107

Query= Sequence ID - 453 nt: 747
Length=747

SEQ ID NO: 107 nt: 747

ALIGNMENTS

Identities = 747/747 (100%), Gaps = 0/747 (0%)

Query	1	GGATCTAAGACCAGCCTGGCAGCCACCAGATGGTGATTCTAGTCCTGGCTCAGTCAGTAA	60
Sbjct	1	GGATCTAAGACCAGCCTGGCAGCCACCAGATGGTGATTCTAGTCCTGGCTCAGTCAGTAA	60
Query	61	TAGGTCACTGACCCCAGAGAAATCAATTCAGCCTCCCAGGTCCTTGGATTCTTTCTGT	120
Sbjct	61	TAGGTCACTGACCCCAGAGAAATCAATTCAGCCTCCCAGGTCCTTGGATTCTTTCTGT	120
Query	121	GAAAATGAAAGCATAGGTAGGAATTTCCCATGGAACAGCTAGCAGAGGAGAAATATTA	180
Sbjct	121	GAAAATGAAAGCATAGGTAGGAATTTCCCATGGAACAGCTAGCAGAGGAGAAATATTA	180
Query	181	AGTCAGGAGACTCATGCTATAGTTTTCATACTTCATTACAACAATGTTGTTTAGGACAAG	240
Sbjct	181	AGTCAGGAGACTCATGCTATAGTTTTCATACTTCATTACAACAATGTTGTTTAGGACAAG	240
Query	241	TGAGTTAACCTGTTAGCTTCCTCTATATAAAATGGAAAGTCATTAAAAACCTACATAGCA	300
Sbjct	241	TGAGTTAACCTGTTAGCTTCCTCTATATAAAATGGAAAGTCATTAAAAACCTACATAGCA	300
Query	301	GGGTTCTTGTGAAGATCAAGTGATAATGTAGGAAGCATGTACAAATGTCACATTCTGCCG	360
Sbjct	301	GGGTTCTTGTGAAGATCAAGTGATAATGTAGGAAGCATGTACAAATGTCACATTCTGCCG	360
Query	361	TCACGTAATGGTCCTCACAGCTTGAGGTAGCATTTAGCATGTGTCATGATTTAGTACAAG	420
Sbjct	361	TCACGTAATGGTCCTCACAGCTTGAGGTAGCATTTAGCATGTGTCATGATTTAGTACAAG	420
Query	421	GGTTGGCAAACCTGTTGCTCTTGATTAAGTCTGGCTCATTGCCTGTTTTCAAAGaaaaa	480
Sbjct	421	GGTTGGCAAACCTGTTGCTCTTGATTAAGTCTGGCTCATTGCCTGTTTTCAAAGAAAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  aaTtgtatatgtgtgtatatatggtatatataggtacacacacatatgtgctatatatag  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AATTGTATATGTGTGTATATATGTTATATATAGGTACACACACATATGTGCTATATATAG  540

Query  541  catatatacacacataaatatataaacatgtacatatatagcattatatatataccgtgta  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CATATATACACACATAATATATAAACATGTACATATATAGCATTATATATATACCGTGTA  600

Query  601  taatatCTCCAGTCCTCATGACCAGCCATGCTTGTTTACATTTGCATACTCTATGA  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TAATATCTCCAGTCCTCATGACCAGCCATGCTTGTTTACATTTGCATACTCTATGA  660

Query  661  TTGCTTTTCATGCAACAATGGCAGAGTTGAGTGATTGTTTTGCACAGANACTGTATGGCCC  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  TTGCTTTTCATGCAACAATGGCAGAGTTGAGTGATTGTTTTGCACAGANACTGTATGGCCC  720

Query  721  ACTAAACCTAAAATATTAATCTCTGCC  747
          |||||||||||||||||||||||
Sbjct   721  ACTAAACCTAAAATATTAATCTCTGCC  747
```

Sequence 454 matched with Sequence 108

Query= Sequence ID 454
Length=522

SEQ ID NO: 108

ALIGNMENTS

Identities = 522/522 (100%), Gaps = 0/522 (0%)

Query	1	CTCCTGCCGGGCTCGTGGCGGCTTCTGTCCGCTCCGCGGAGGGAAGCGCCTTCCCCACAG	60
Sbjct	1	CTCCTGCCGGGCTCGTGGCGGCTTCTGTCCGCTCCGCGGAGGGAAGCGCCTTCCCCACAG	60
Query	61	GACATCAATGCAAGCTTGAATAAGAAAAACAAATTCTTCCTCCTAAGCCATGGCATATCA	120
Sbjct	61	GACATCAATGCAAGCTTGAATAAGAAAAACAAATTCTTCCTCCTAAGCCATGGCATATCA	120
Query	121	GTTATACAGAAATACTACTTTGGGAAACAGTCTTCAGGAGAGCCTAGATGAGCTCATACA	180
Sbjct	121	GTTATACAGAAATACTACTTTGGGAAACAGTCTTCAGGAGAGCCTAGATGAGCTCATACA	180
Query	181	GTCTCAACAGATCACCCCCCAACTTGCCCTTCAAGTTCTACTTCAGTTTGATAAGGCTAT	240
Sbjct	181	GTCTCAACAGATCACCCCCCAACTTGCCCTTCAAGTTCTACTTCAGTTTGATAAGGCTAT	240
Query	241	AAATGCAGCACTGGCTCAGAGGGTCAGGAACAGAGTCAATTTTCAGGGGCTCTCTAAATAC	300
Sbjct	241	AAATGCAGCACTGGCTCAGAGGGTCAGGAACAGAGTCAATTTTCAGGGGCTCTCTAAATAC	300
Query	301	GTACAGATTCTGCGATAATGTGTGGACTTTTGTACTGAATGATGTTGAATTCAGAGAGGT	360
Sbjct	301	GTACAGATTCTGCGATAATGTGTGGACTTTTGTACTGAATGATGTTGAATTCAGAGAGGT	360
Query	361	GACAGAACTTATTAAAGTGGATAAAGTGAAAATTGTAGCCTGTGATGGTAAAAATACTGG	420
Sbjct	361	GACAGAACTTATTAAAGTGGATAAAGTGAAAATTGTAGCCTGTGATGGTAAAAATACTGG	420
Query	421	CTCCAATACTACAGAATGAATAGAAAAAATATGACTTTTTTACACCATCTTCTGTTATTC	480
Sbjct	421	CTCCAATACTACAGAATGAATAGAAAAAATATGACTTTTTTACACCATCTTCTGTTATTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATTGCTTTTGAAGAGAAGCATAGAAGAGACTTTTTATTATT	522
Sbjct	481	ATTGCTTTTGAAGAGAAGCATAGAAGAGACTTTTTATTATT	522

Sequence 458 matched with Sequence 109

Query= Sequence ID - 458 nt: 682
Length=682

SEQ ID NO: 109 nt: 682

ALIGNMENTS

Identities = 682/682 (100%), Gaps = 0/682 (0%)

Query	1	TGCCACTGAAGATCCTGGTGTGCGCCATGGGCCGCCGCCGCCGCCGTTGTTACCGGTATTG	60
Sbjct	1	TGCCACTGAAGATCCTGGTGTGCGCCATGGGCCGCCGCCGCCGCCGTTGTTACCGGTATTG	60
Query	61	TAAGAACAAGCCGTACCCAAAGTCTCGCTTCTGCCGAGGTGTCCCTGATGCCAAGATTCTG	120
Sbjct	61	TAAGAACAAGCCGTACCCAAAGTCTCGCTTCTGCCGAGGTGTCCCTGATGCCAAGATTCTG	120
Query	121	CATTTTTGACCTGGGGCGGAAAAAGGCAAAAGTGGATGAGTTTCCGCTTTGTGGCCACAT	180
Sbjct	121	CATTTTTGACCTGGGGCGGAAAAAGGCAAAAGTGGATGAGTTTCCGCTTTGTGGCCACAT	180
Query	181	GGTGTCTAGATGAATATGAGCAGCTGTCTCTGAAGCCCTGGAGGCTGCCGAATTTGTGC	240
Sbjct	181	GGTGTCTAGATGAATATGAGCAGCTGTCTCTGAAGCCCTGGAGGCTGCCGAATTTGTGC	240
Query	241	CAATAAGTACATGGTAAAAAGTTGTGGCAAAGATGGCTTCCATATCCGGGTGCGGCTCCA	300
Sbjct	241	CAATAAGTACATGGTAAAAAGTTGTGGCAAAGATGGCTTCCATATCCGGGTGCGGCTCCA	300
Query	301	CCCCTTCCACGTCATCCGCATCAACAAGATGTTGTCCTGTGCTGGGGCTGACAGGCTCCA	360
Sbjct	301	CCCCTTCCACGTCATCCGCATCAACAAGATGTTGTCCTGTGCTGGGGCTGACAGGCTCCA	360
Query	361	AACAGGCATGCGAGGTGCCTTTGGAAAGCCCCAGGGCACTGTGGCCAGGGTTCACATTGG	420
Sbjct	361	AACAGGCATGCGAGGTGCCTTTGGAAAGCCCCAGGGCACTGTGGCCAGGGTTCACATTGG	420
Query	421	CCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAGGAGCATGTGATTGAGGCCCT	480
Sbjct	421	CCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAGGAGCATGTGATTGAGGCCCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCGCAGGGCCAAGTTCAAGTTTCTGGCCGCGAGAAGATCCACATCTCAAAGAAGTGGGGCT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCGCAGGGCCAAGTTCAAGTTTCTGGCCGCGAGAAGATCCACATCTCAAAGAAGTGGGGCT  540

Query  541  TCACCAAGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAAAAGCGGCTCATCCCAN  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TCACCAAGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAAAAGCGGCTCATCCCAN  600

Query  601  ATGGCTGTGGGGTCAAGTACATCCCCAATCGTGGCCCTCTGGACAAGTGGCGGCCCTGCA  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  ATGGCTGTGGGGTCAAGTACATCCCCAATCGTGGCCCTCTGGACAAGTGGCGGCCCTGCA  660

Query  661  CTCATGAAGGCTTTCAATGTGC  682
          ||||||||||||||||
Sbjct   661  CTCATGAAGGCTTTCAATGTGC  682
```

Sequence 459 matched with Sequence 110

Query= Sequence ID 459
Length=668

SEQ ID NO: 110

ALIGNMENTS

Identities = 668/668 (100%), Gaps = 0/668 (0%)

Query	1	TCCCGGAATCGCGGCCGCTCGACCTTGTCTTGAGCGTCAACCTTCTTCCCTGAAGTG	60
Sbjct	1	TCCCGGAATCGCGGCCGCTCGACCTTGTCTTGAGCGTCAACCTTCTTCCCTGAAGTG	60
Query	61	GCTGGGGTTCCTGTTTCCTTCTTTGATTGACAACTTGTGTTAACCCTCGCACATCTCTGG	120
Sbjct	61	GCTGGGGTTCCTGTTTCCTTCTTTGATTGACAACTTGTGTTAACCCTCGCACATCTCTGG	120
Query	121	GCCAATTTTGTCTGTAAGTCTTCCGGAGACCCCTGGAATTTAAATCATTAGCACCGCG	180
Sbjct	121	GCCAATTTTGTCTGTAAGTCTTCCGGAGACCCCTGGAATTTAAATCATTAGCACCGCG	180
Query	181	CCCTTCCCCGAAGAGTCTTCGAAGGGTTGCCGCTTTTCGGTGGCGCAGTTCTCGCGAGAA	240
Sbjct	181	CCCTTCCCCGAAGAGTCTTCGAAGGGTTGCCGCTTTTCGGTGGCGCAGTTCTCGCGAGAA	240
Query	241	GGTGACTTTCTTTCTCGGTATTTCTGGTTTCCAGAATCCTTAGCGCGAGGCGGAAAAAA	300
Sbjct	241	GGTGACTTTCTTTCTCGGTATTTCTGGTTTCCAGAATCCTTAGCGCGAGGCGGAAAAAA	300
Query	301	TATTTCTCCCAGCTTGTGTTGATGCCGCGATTTTGACTGAGACTTCTTCCCACGATTTCT	360
Sbjct	301	TATTTCTCCCAGCTTGTGTTGATGCCGCGATTTTGACTGAGACTTCTTCCCACGATTTCT	360
Query	361	GTTTTTGCTTCTCCAAGGAAAAATGGCAGCTCCCGAGCAGCCGCTTGCATATCAAGGGGA	420
Sbjct	361	GTTTTTGCTTCTCCAAGGAAAAATGGCAGCTCCCGAGCAGCCGCTTGCATATCAAGGGGA	420
Query	421	TGCACGAGCTCCTCCTCGCTTTCCTCGCTTCGGGGCGACCGAACCCTTCTGGTCAGGCAC	480
Sbjct	421	TGCACGAGCTCCTCCTCGCTTTCCTCGCTTCGGGGCGACCGAACCCTTCTGGTCAGGCAC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGCCGGCTGAGCTTACTGCTGAGGAGAAAGAGGACTTGCTGAAGTACTTCGGGGCTCAG	540
Sbjct	481	CTGCCGGCTGAGCTTACTGCTGAGGAGAAAGAGGACTTGCTGAAGTACTTCGGGGCTCAG	540
Query	541	TCTGTGCGGGTCCTGTCAGATAAGGGGCGACTGAAACATACAGCTTTTGCCACATTCCCT	600
Sbjct	541	TCTGTGCGGGTCCTGTCAGATAAGGGGCGACTGAAACATACAGCTTTTGCCACATTCCCT	600
Query	601	AATGAAAAAGCAGCTNTAAAGGCATTGACAACTNCATCAACTGAACTTTTAGTCATAC	660
Sbjct	601	AATGAAAAAGCAGCTNTAAAGGCATTGACAACTNCATCAACTGAACTTTTAGTCATAC	660
Query	661	TTTAATCG	668
Sbjct	661	TTTAATCG	668

Sequence 460 matched with Sequence 111

Query= Sequence ID - 460 nt: 536
Length=536

SEQ ID NO: 111 nt: 536

ALIGNMENTS

Identities = 536/536 (100%), Gaps = 0/536 (0%)

Query	1	CAGAGATCAAAATAGGCCTTACACAGTGCACGCGAATTTAAAAGATTACCCCATTCAGG	60
Sbjct	1	CAGAGATCAAAATAGGCCTTACACAGTGCACGCGAATTTAAAAGATTACCCCATTCAGG	60
Query	61	TGTATGGATTTTGCAGTATTAAAGATGCTGCCTGGAATAGGTCATTATCTTCTCCAAGTA	120
Sbjct	61	TGTATGGATTTTGCAGTATTAAAGATGCTGCCTGGAATAGGTCATTATCTTCTCCAAGTA	120
Query	121	CTCTGTTAAGTCAATGAGTCACATAGAGTATAAGGTTTATTATCTGCTTTTCTTTCATTA	180
Sbjct	121	CTCTGTTAAGTCAATGAGTCACATAGAGTATAAGGTTTATTATCTGCTTTTCTTTCATTA	180
Query	181	AATAAATCTTTATTGAATTTCTACTACATTaaaaaaccaaaccaaaacaaacaaa	240
Sbjct	181	AATAAATCTTTATTGAATTTCTACTACATTAaaaaaaccaaaccaaaacaaacaaa	240
Query	241	aaaaacaCTTCCCTGAGCCATAAAGGAGAAGGTAGTTTTGACTGGAACCTTGAAGGATGG	300
Sbjct	241	AAAAACACTTCCCTGAGCCATAAAGGAGAAGGTAGTTTTGACTGGAACCTTGAAGGATGG	300
Query	301	GTAAACTTTTCAGCAGATAAAGATTGAGAGAAGACCTTCCAGGTAGAGAAAGCAGTGTGGG	360
Sbjct	301	GTAAACTTTTCAGCAGATAAAGATTGAGAGAAGACCTTCCAGGTAGAGAAAGCAGTGTGGG	360
Query	361	CACAGGCAAAGATGGAAGAACACACGTGGCTGTGGGAAACACAGCTAGAAGCCAGTGCGG	420
Sbjct	361	CACAGGCAAAGATGGAAGAACACACGTGGCTGTGGGAAACACAGCTAGAAGCCAGTGCGG	420
Query	421	ATAGAGAGTAGGCTATGATGTGCAAAGGTTANACACTGGGAGAGACAGGTCCATGAGAGT	480
Sbjct	421	ATAGAGAGTAGGCTATGATGTGCAAAGGTTANACACTGGGAGAGACAGGTCCATGAGAGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGCTTGGA	CTAACACAGGGAGGGTTT	GGAATCCCAACTGGGGAACCTANAAATCAA	536
Sbjct	481	AGCTTGGA	CTAACACAGGGAGGGTTT	GGAATCCCAACTGGGGAACCTANAAATCAA	536

Sequence 461 matched with Sequence 112

Query= Sequence ID 461
Length=368

SEQ ID NO: 112

ALIGNMENTS

Identities = 368/368 (100%), Gaps = 0/368 (0%)

Query	1	TAGGAGGCTTATTCAGTATTCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGC	60
Sbjct	1	TAGGAGGCTTATTCAGTATTCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGC	60
Query	61	CAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTCCACAACACTT	120
Sbjct	61	CAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTCCACAACACTT	120
Query	121	TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCACATG	180
Sbjct	121	TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCACATG	180
Query	181	AAACATCCTATCATCTGTAGGCTCATTCACTTTCTCTAACAGCAGTAATATTAATAATTTT	240
Sbjct	181	AAACATCCTATCATCTGTAGGCTCATTCACTTTCTCTAACAGCAGTAATATTAATAATTTT	240
Query	241	CATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTAATAGTAGAAGAACCCTCCAT	300
Sbjct	241	CATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTAATAGTAGAAGAACCCTCCAT	300
Query	301	AAACCTGGAGTGACTATATGGATGCCCCCACCCTACCACACATTCTGAAGAACCCGTATA	360
Sbjct	301	AAACCTGGAGTGACTATATGGATGCCCCCACCCTACCACACATTCTGAAGAACCCGTATA	360
Query	361	CATAAAAT	368
Sbjct	361	CATAAAAT	368

Sequence 462 matched with Sequence 113

Query= Sequence ID 462
Length=338

SEQ ID NO: 113

ALIGNMENTS

Identities = 338/338 (100%), Gaps = 0/338 (0%)

Query	1	TCTTTATCAAGTTGAGAAAGTTCCTCCCCTCTATTCCTAGTTTGCTAAGAGTCCTTCTAT	60
Sbjct	1	TCTTTATCAAGTTGAGAAAGTTCCTCCCCTCTATTCCTAGTTTGCTAAGAGTCCTTCTAT	60
Query	61	CCTATTTCTTAATGGTTTAGTAGATGACTCTGTGGTACTTTGAAGGTTGTTGCAGAATT	120
Sbjct	61	CCTATTTCTTAATGGTTTAGTAGATGACTCTGTGGTACTTTGAAGGTTGTTGCAGAATT	120
Query	121	TCCATGCCATAGGCAATTTACCTTTCCTTGACATTTGAAGGATTGATGTTGGTGCCAAGT	180
Sbjct	121	TCCATGCCATAGGCAATTTACCTTTCCTTGACATTTGAAGGATTGATGTTGGTGCCAAGT	180
Query	181	ATAGAATCTTCACAGAGTCCTCCTGTAGCTTCTAAAGGTTTAGCTTGAAAAATGTTAATTG	240
Sbjct	181	ATAGAATCTTCACAGAGTCCTCCTGTAGCTTCTAAAGGTTTAGCTTGAAAAATGTTAATTG	240
Query	241	CTTAACGCTAGTAAGTGAGTGAAAAAGCTGGGGATAAATTTTGTATCTTGCTTATATTTT	300
Sbjct	241	CTTAACGCTAGTAAGTGAGTGAAAAAGCTGGGGATAAATTTTGTATCTTGCTTATATTTT	300
Query	301	AGTTCCACCTCTGTCCNGACNAAACCCCATATATAA	338
Sbjct	301	AGTTCCACCTCTGTCCNGACNAAACCCCATATATAA	338

Sequence 463 matched with Sequence 114

Query= Sequence ID 463
Length=383

SEQ ID NO: 114

ALIGNMENTS

Identities = 383/383 (100%), Gaps = 0/383 (0%)

Query	1	TAGTTTACATATCCCAACCTTTAAAAATATTCCTCTTATTAGCTTTATATTCACCTTTATA	60
Sbjct	1	TAGTTTACATATCCCAACCTTTAAAAATATTCCTCTTATTAGCTTTATATTCACCTTTATA	60
Query	61	GAAGTTGAGTTTTAATTAAAAATCTTGGCATCCTGAAGTATGTCACATAGCATGTGCTCC	120
Sbjct	61	GAAGTTGAGTTTTAATTAAAAATCTTGGCATCCTGAAGTATGTCACATAGCATGTGCTCC	120
Query	121	TTATAAATATGTTGATATCTCAGAAGACAGCATCCCGGTTTTTCATTTTATAAAGTACCAT	180
Sbjct	121	TTATAAATATGTTGATATCTCAGAAGACAGCATCCCGGTTTTTCATTTTATAAAGTACCAT	180
Query	181	ACTTAAGAATGCTGTAATACTTATCTTTTATAACATGTTTCCTTCGCTTTGCTTGNCCTT	240
Sbjct	181	ACTTAAGAATGCTGTAATACTTATCTTTTATAACATGTTTCCTTCGCTTTGCTTGNCCTT	240
Query	241	TATGNCATCAGTTTTAACTGTTTACTTCATTTAACAGNTTACATCATNCAACAGTTTACT	300
Sbjct	241	TATGNCATCAGTTTTAACTGTTTACTTCATTTAACAGNTTACATCATNCAACAGTTTACT	300
Query	301	TCATTAAACAGTAGGTGGAAAAATAGATGCCAGTCTATGAAAATCTTCCCATCTATATCA	360
Sbjct	301	TCATTAAACAGTAGGTGGAAAAATAGATGCCAGTCTATGAAAATCTTCCCATCTATATCA	360
Query	361	AAATACTTTCAAGGATATACTTT	383
Sbjct	361	AAATACTTTCAAGGATATACTTT	383

Sequence 464 matched with Sequence 115

Query= Sequence ID - 464 nt: 615
Length=615

SEQ ID NO: 115 nt: 615

ALIGNMENTS

Identities = 615/615 (100%), Gaps = 0/615 (0%)

Query	1	CGACTTTCAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCCTCTTTATCTCC	60
Sbjct	1	CGACTTTCAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCCTCTTTATCTCC	60
Query	61	TGACACAAAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTAGAAGAAATGGA	120
Sbjct	61	TGACACAAAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTAGAAGAAATGGA	120
Query	121	AGCTTCTCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCAAGATTTCCAAAA	180
Sbjct	121	AGCTTCTCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCAAGATTTCCAAAA	180
Query	181	CAAAACCTATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTCCCACCATTAAAAACACC	240
Sbjct	181	CAAAACCTATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTCCCACCATTAAAAACACC	240
Query	241	TGAGGCTGGAAGTGTATTACAAGTCCGATGAAATTGAATTAGAAGGTGCTACACAGTG	300
Sbjct	241	TGAGGCTGGAAGTGTATTACAAGTCCGATGAAATTGAATTAGAAGGTGCTACACAGTG	300
Query	301	GCCACACTCTACTTCTGCTTCTGCCACCTATGGGGTCGAGGCAGGTGTGGTGCCTTGGCT	360
Sbjct	301	GCCACACTCTACTTCTGCTTCTGCCACCTATGGGGTCGAGGCAGGTGTGGTGCCTTGGCT	360
Query	361	AAGTCCACAGACTTCTGAGAGGCCACGCTTTCTTCTTCTCCAGAAATAAACCTGAAAC	420
Sbjct	361	AAGTCCACAGACTTCTGAGAGGCCACGCTTTCTTCTTCTCCAGAAATAAACCTGAAAC	420
Query	421	TCAAGCAGCTTTAATCAGAGGGCAGGATTCCACGATAGCAGCATCAGAACAGCAAGTGGC	480
Sbjct	421	TCAAGCAGCTTTAATCAGAGGGCAGGATTCCACGATAGCAGCATCAGAACAGCAAGTGGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGCGAGAATTCTTGATTCCAATGATCAGGCAACAGTAAACCCTGTGGAATTTAATACTGA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGCGAGAATTCTTGATTCCAATGATCAGGCAACAGTAAACCCTGTGGAATTTAATACTGA  540

Query  541  GGGTGCAACACCCCATTTTCCCTTCTGGGAGACTTCTAATGAAACANATTCCTGATTGGC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GGGTGCAACACCCCATTTTCCCTTCTGGGAGACTTCTAATGAAACANATTCCTGATTGGC  600

Query  601  ATTAATGAANAGTCA  615
          |||||||||||||
Sbjct   601  ATTAATGAANAGTCA  615
```

Sequence 469 matched with Sequence 116

Query= Sequence ID 469
Length=161

SEQ ID NO: 116

ALIGNMENTS

Identities = 161/161 (100%), Gaps = 0/161 (0%)

```
Query  1      GATTTTAAAAATACATATAGCAAAAATATTACAGGGTCAGGGGAGACAATTAGAATGAT  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      GATTTTAAAAATACATATAGCAAAAATATTACAGGGTCAGGGGAGACAATTAGAATGAT  60

Query  61     ATAATTCAAAGTGGATTaaaaaaaaaCTGTCACCCAGAATACAATACCCAGCAAAGTTG  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61     ATAATTCAAAGTGGATTAAAAAAAAAACTGTCACCCAGAATACAATACCCAGCAAAGTTG  120

Query  121    TCCTTCATAAATGAAAGAAAAATNAAATCTTTNCCNAACNA  161
          |||||||||||||||||||||||||||||||||||
Sbjct  121    TCCTTCATAAATGAAAGAAAAATNAAATCTTTNCCNAACNA  161
```

Blast comparison trimmed “NA” from the 3’ end of both sequences and reported 159 identities. The report has been manually corrected for this. “NA” has been appended to both sequences and identity count has been increased to 161.

Sequence 471 matched with Sequence 117

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 471
Length=28

SEQ ID NO: 117

56.0 8e-15

ALIGNMENTS

Identities = 28/28 (100%), Gaps = 0/28 (0%)

```
Query    1  TCCCGGGAATCTGCAGGATCCGTCGACT   28
          |||
Sbjct   28  TCCCGGGAATCTGCAGGATCCGTCGACT    1
```

Blast comparison trimmed "ATCTGCAGGATCCGTCGACT" from the 3' end of the query sequence and the 5' end of the subject sequence and reported 8 identities. The report has been manually corrected for this. "ATCTGCAGGATCCGTCGACT" has been appended to the 3' end of the query sequence and 5' end of the subject sequence and identity count has been increased to 28.

Sequence 472 matched with Sequence 118

Query= Sequence ID 472
Length=258

SEQ ID NO: 118

ALIGNMENTS

Identities = 258/258 (100%), Gaps = 0/258 (0%)

Query	1	GACAGTGCCCAGGGCTCTGATATGTCTNTCACANCTTGNAAGTGTGAGACAGCTGCCTT	60
Sbjct	1	GACAGTGCCCAGGGCTCTGATATGTCTNTCACANCTTGNAAGTGTGAGACAGCTGCCTT	60
Query	61	GTGTGGGACTGAAAGGCAAGATTTGTTCTGCCCTTCCCTTTGTGACTTGAAGAACCCTG	120
Sbjct	61	GTGTGGGACTGAAAGGCAAGATTTGTTCTGCCCTTCCCTTTGTGACTTGAAGAACCCTG	120
Query	121	ACTTTGTTTCTGCAAAGGCACCTGCATGTGTCTGTGTTCTTGTAGGCATAATGTGAGGAG	180
Sbjct	121	ACTTTGTTTCTGCAAAGGCACCTGCATGTGTCTGTGTTCTTGTAGGCATAATGTGAGGAG	180
Query	181	GTGGGGANACCACCCACCCCATGTCCACCATGACCCTCTTNCCACNCTNACCTGTGCT	240
Sbjct	181	GTGGGGANACCACCCACCCCATGTCCACCATGACCCTCTTNCCACNCTNACCTGTGCT	240
Query	241	CCCTCCCAATCATNTTT	258
Sbjct	241	CCCTCCCAATCATNTTT	258

Sequence 473 matched with Sequence 119

Query= Sequence ID - 473 nt: 694
Length=694

SEQ ID NO: 119 nt: 694

ALIGNMENTS

Identities = 694/694 (100%), Gaps = 0/694 (0%)

Query	1	TGGGCTTTGGGCTGGCTGCAGTCTGTCTGAGGGCGGCCGAAGTGGCTGGCTCATTTAAGA	60
Sbjct	1	TGGGCTTTGGGCTGGCTGCAGTCTGTCTGAGGGCGGCCGAAGTGGCTGGCTCATTTAAGA	60
Query	61	TGAGGCTTCTGCTGCTTCTCCTAGNGGCGGCGTCTGCGATGGTCCGAGCGAGGCCTCGG	120
Sbjct	61	TGAGGCTTCTGCTGCTTCTCCTAGNGGCGGCGTCTGCGATGGTCCGAGCGAGGCCTCGG	120
Query	121	CCAATCTGGGCGGCGTGCCAGCAAGAGATTAAAGATGCAGTACGCCACGGGGCCGCTGC	180
Sbjct	121	CCAATCTGGGCGGCGTGCCAGCAAGAGATTAAAGATGCAGTACGCCACGGGGCCGCTGC	180
Query	181	TCAAGTTCCAGATTTGTGTTTCCTGAGGTTATAGGCGGGTGTTTGAGGAGTACATGCGGG	240
Sbjct	181	TCAAGTTCCAGATTTGTGTTTCCTGAGGTTATAGGCGGGTGTTTGAGGAGTACATGCGGG	240
Query	241	TTATTAGCCAGCGGTACCCAGACATCCGCATTGAAGGAGAGAATTACCTCCCTCAACCAA	300
Sbjct	241	TTATTAGCCAGCGGTACCCAGACATCCGCATTGAAGGAGAGAATTACCTCCCTCAACCAA	300
Query	301	TATATAGACACATAGCATCTTTCCTGTGCTGCTTCAAAGTATTAATAGGCTTAATAA	360
Sbjct	301	TATATAGACACATAGCATCTTTCCTGTGCTGCTTCAAAGTATTAATAGGCTTAATAA	360
Query	361	TTGTTGGCAAGGATCCTTTTGCTTTCTTTGGCATGCAAGCTCCTAGCATCTGGCAGTGGG	420
Sbjct	361	TTGTTGGCAAGGATCCTTTTGCTTTCTTTGGCATGCAAGCTCCTAGCATCTGGCAGTGGG	420
Query	421	GCCAAGAAAATAAGGTTTATGCATGTATGATGGTTTTCTTCTTGAGCAACATGATTGAGA	480
Sbjct	421	GCCAAGAAAATAAGGTTTATGCATGTATGATGGTTTTCTTCTTGAGCAACATGATTGAGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ACCAGTGTATGTCAACAGGTGCATTTGAGATAACTTTAAATGATGTACCTGTGTGGTCTA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ACCAGTGTATGTCAACAGGTGCATTTGAGATAACTTTAAATGATGTACCTGTGTGGTCTA  540

Query  541  AGCTGGAATCTGGTCACCTTCCATCCATGCAACAACCTTGTTCAAATTCTTGACAATGAAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AGCTGGAATCTGGTCACCTTCCATCCATGCAACAACCTTGTTCAAATTCTTGACAATGAAA  600

Query  601  TGAAACTCAATGTGCATATGGGATTCAATCCCCACCATCGATCATAGCACCCCCTATCAG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TGAAACTCAATGTGCATATGGGATTCAATCCCCACCATCGATCATAGCACCCCCTATCAG  660

Query  661  CACTGNAAACTCTTTTGCATTAAGGGATCATTGC  694
          ||||||||||||||||||||||||
Sbjct   661  CACTGNAAACTCTTTTGCATTAAGGGATCATTGC  694
```

Sequence 474 matched with Sequence 120

Query= Sequence ID 474
Length=337

SEQ ID NO: 120

ALIGNMENTS

Identities = 337/337 (100%), Gaps = 0/337 (0%)

```
Query 1  GGCAGCGCGGGAGCCCGTCGGCGCCGGCGGGCGGGCCGGTTTCGAAGTTGATGCAATCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  GGCAGCGCGGGAGCCCGTCGGCGCCGGCGGGCGGGCCGGTTTCGAAGTTGATGCAATCG 60

Query 61 GTTTAAACATGGCTGAACGCGTGTGTACACGGGACTGACGCAACCCACGTGTAAGTGTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GTTTAAACATGGCTGAACGCGTGTGTACACGGGACTGACGCAACCCACGTGTAAGTGTCA 120

Query 121 GCCGGGCCCTGAGTAATCGCTTAAAGATGTTCCCTACGGGCTtggttgctgttgatgttttg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 GCCGGGCCCTGAGTAATCGCTTAAAGATGTTCCCTACGGGCTTGTGCTGTTGATGTTTTG 180

Query 181 ttttgttttgttttttggtcttttttgTATTATAAAAAATAATCTATTTCTATGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 TTTTGTTTTGTTTTTTGGTCTTTTTTGTATTATAAAAAATAATCTATTTCTATGAGAAA 240

Query 241 AGAGGCGTCTGTATATTTTGGGAATCTTTTCCGTTTCAAGCATTAAGAACAACCTTTTAATA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AGAGGCGTCTGTATATTTTGGGAATCTTTTCCGTTTCAAGCATTAAGAACAACCTTTTAATA 300

Query 301 AACttttttttGATAATGGTTaaaaaaaaaaaaaaaaa 337
          ||||||||||||||||||||||||||||
Sbjct 301 AACTTTTTTTTGATAATGGTTAAAAAAAAAAAAAAAAA 337
```

Sequence 475 matched with Sequence 121

Query= Sequence ID 475
Length=210

SEQ ID NO: 121

ALIGNMENTS

Identities = 210/210 (100%), Gaps = 0/210 (0%)

Query	1	CATAATAAAAAACAATCAACAAACAGGGAATGGAAAGAACTTCCTCAGCATGGTGAAGG	60
Sbjct	1	CATAATAAAAAACAATCAACAAACAGGGAATGGAAAGAACTTCCTCAGCATGGTGAAGG	60
Query	61	CCACATATGAAAATCCCACAGCTAACATCATACTCAATGATGAAAGACTGAAAGCTTTTC	120
Sbjct	61	CCACATATGAAAATCCCACAGCTAACATCATACTCAATGATGAAAGACTGAAAGCTTTTC	120
Query	121	TCCTGAGATCAGGAACAAGACAAAGATGTCACCTTTTGTCACTTCTATTCAACTCATTAT	180
Sbjct	121	TCCTGAGATCAGGAACAAGACAAAGATGTCACCTTTTGTCACTTCTATTCAACTCATTAT	180
Query	181	TGGAAGTTTTTGGCAGAGCAATTAGGTAAG	210
Sbjct	181	TGGAAGTTTTTGGCAGAGCAATTAGGTAAG	210

Sequence 476 matched with Sequence 122

Query= Sequence ID - 476 nt: 476
Length=476

SEQ ID NO: 122 nt: 476

ALIGNMENTS

Identities = 476/476 (100%), Gaps = 0/476 (0%)

Query	1	CAGAATCTTTTCATAGGCTGAATGTTGCTCCACAATGTGTCCTTTGACTATCTCTGGCTA	60
Sbjct	1	CAGAATCTTTTCATAGGCTGAATGTTGCTCCACAATGTGTCCTTTGACTATCTCTGGCTA	60
Query	61	ATTATTATTTTAATCTCTTCTCAGCTTTTCCAAGAACATAACGTTAACCAAAGATCTTAG	120
Sbjct	61	ATTATTATTTTAATCTCTTCTCAGCTTTTCCAAGAACATAACGTTAACCAAAGATCTTAG	120
Query	121	GCCATTCACTCTTTTGTAATAATGTGGATGTGAAACGAGGCAACAAATCCTGA	180
Sbjct	121	GCCATTCACTCTTTTGTAATAATGTGGATGTGAAACGAGGCAACAAATCCTGA	180
Query	181	AGTAGAAAGTTATTCCTGGCCAGGCACGGTGGCTCACGCCTGTAATCCTGGCACTTTGGG	240
Sbjct	181	AGTAGAAAGTTATTCCTGGCCAGGCACGGTGGCTCACGCCTGTAATCCTGGCACTTTGGG	240
Query	241	AGGCCGAGGTGGTGGATCATGAGGACAGGAGATCGAGACCATCCTGGCCAACATGATGA	300
Sbjct	241	AGGCCGAGGTGGTGGATCATGAGGACAGGAGATCGAGACCATCCTGGCCAACATGATGA	300
Query	301	AACCCCATCTCTACTAAATAACAAAAATTAGCTGGGCATGGTGACGCGTGCCTGTAGTC	360
Sbjct	301	AACCCCATCTCTACTAAATAACAAAAATTAGCTGGGCATGGTGACGCGTGCCTGTAGTC	360
Query	361	CCAGTTACTCGGAGGCTGAGGCAGGGAATTGCTTGAACCTCGGAGGTGGGAGGTTGCA	420
Sbjct	361	CCAGTTACTCGGAGGCTGAGGCAGGGAATTGCTTGAACCTCGGAGGTGGGAGGTTGCA	420
Query	421	GTGTGCCGAGATCACGCTACTGCACTCCAGCCTGGCAACAGAGCAAGACTCCATCT	476
Sbjct	421	GTGTGCCGAGATCACGCTACTGCACTCCAGCCTGGCAACAGAGCAAGACTCCATCT	476

Sequence 477 matched with Sequence 123

Query= Sequence ID 477
Length=250

SEQ ID NO: 123

ALIGNMENTS

Identities = 250/250 (100%), Gaps = 0/250 (0%)

Query	1	AAACAGAAAGTTTCTTCTAAAGGCATGATTCAGTTAAGTCATTCTTAAGTGTTAAAAAAT	60
Sbjct	1	AAACAGAAAGTTTCTTCTAAAGGCATGATTCAGTTAAGTCATTCTTAAGTGTTAAAAAAT	60
Query	61	TGTGAAAAATGTGCCTGTAATCCCAACACTTTGGGAGGCCGAGGCAGGCAGATCACGAGG	120
Sbjct	61	TGTGAAAAATGTGCCTGTAATCCCAACACTTTGGGAGGCCGAGGCAGGCAGATCACGAGG	120
Query	121	TCAGGAGATCAAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACGAAAAATACCA	180
Sbjct	121	TCAGGAGATCAAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACGAAAAATACCA	180
Query	181	AAAACATTAGCCGGGCGTGGTTGTGGGCGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGG	240
Sbjct	181	AAAACATTAGCCGGGCGTGGTTGTGGGCGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGG	240
Query	241	CAGGAGAATG	250
Sbjct	241	CAGGAGAATG	250

Sequence 478 matched with Sequence 124

Query= Sequence ID 478
Length=523

SEQ ID NO: 124

ALIGNMENTS

Identities = 523/523 (100%), Gaps = 0/523 (0%)

Query	1	TTCTTGGGATATTGATGACTACTGTCTGAGAGGTGCTGTGGGGAGATTTTCAGGATTGTG	60
Sbjct	1	TTCTTGGGATATTGATGACTACTGTCTGAGAGGTGCTGTGGGGAGATTTTCAGGATTGTG	60
Query	61	TGGTCTTTGAGGGGGGTGtttttttAAGACAACATTGACCACTGTCCACTGTCCACATGA	120
Sbjct	61	TGGTCTTTGAGGGGGGTGTTTTTTAAGACAACATTGACCACTGTCCACTGTCCACATGA	120
Query	121	TCATTGTAAAATTGCAATGCCGCATGCTAGTTGGTTACATAAGACATAATTCCAGTGATT	180
Sbjct	121	TCATTGTAAAATTGCAATGCCGCATGCTAGTTGGTTACATAAGACATAATTCCAGTGATT	180
Query	181	GAAGGTGGTTACACTGTATGGTGGTGTGTTCAAGATGGCACTGGCATCTTTGAGCAGAGC	240
Sbjct	181	GAAGGTGGTTACACTGTATGGTGGTGTGTTCAAGATGGCACTGGCATCTTTGAGCAGAGC	240
Query	241	CTGGCTATGCAGCATCATTGAGTTTTTTAAACACCCTANAGGTCTGGTTGTTGTTGCTG	300
Sbjct	241	CTGGCTATGCAGCATCATTGAGTTTTTTAAACACCCTANAGGTCTGGTTGTTGTTGCTG	300
Query	301	TTGTCCTTTCCTGTGAAAGTCACaananaaGTTACAGTCCAGGTGAACCTGGAGTTTATA	360
Sbjct	301	TTGTCCTTTCCTGTGAAAGTCACANANAAGTTACAGTCCAGGTGAACCTGGAGTTTATA	360
Query	361	GGTTGGTTTTGTTTCTGntatatatatatatatatatatttttttttttttAACATTT	420
Sbjct	361	GGTTGGTTTTGTTTCTGNTATATATATATATATATATATATTTTTTTTTTTTAAACATTT	420
Query	421	ACCTGTAGTGCTGTAGCTGTTGATACTATCACCTGCATGCTATTTCTAGTGAGTGCTAAA	480
Sbjct	421	ACCTGTAGTGCTGTAGCTGTTGATACTATCACCTGCATGCTATTTCTAGTGAGTGCTAAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TACAGTATGGTCCAATGACAATAACAGCCCATGGTACTGCCAG	523
Sbjct	481	TACAGTATGGTCCAATGACAATAACAGCCCATGGTACTGCCAG	523

Sequence 479 matched with Sequence 125

Query= Sequence ID 479
Length=487

SEQ ID NO: 125

ALIGNMENTS

Identities = 487/487 (100%), Gaps = 0/487 (0%)

Query	1	CATCAGTCTGTTATCCATGCTGACTTTCCGAAGACTTGCAGCTACTGCATTGATATCTTT	60
Sbjct	1	CATCAGTCTGTTATCCATGCTGACTTTCCGAAGACTTGCAGCTACTGCATTGATATCTTT	60
Query	61	CCTGCCAATAAGCAAAGTGTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAA	120
Sbjct	61	CCTGCCAATAAGCAAAGTGTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAA	120
Query	121	GAGCTTTCAGAATATGTTTCGGAATCAGCAAACCATCGGAGCTCGTAAGGAGCTCCAGAAA	180
Sbjct	121	GAGCTTTCAGAATATGTTTCGGAATCAGCAAACCATCGGAGCTCGTAAGGAGCTCCAGAAA	180
Query	181	GAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATATAATTTTATATGTCAAG	240
Sbjct	181	GAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATATAATTTTATATGTCAAG	240
Query	241	GAGGAGATGaaaaaaaaCAACATCCCAGAGCCAGTTGTCATCGGAATAGTCTGGTCAAGT	300
Sbjct	241	GAGGAGATGAAAAAAAAACAACATCCCAGAGCCAGTTGTCATCGGAATAGTCTGGTCAAGT	300
Query	301	GTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAG	360
Sbjct	301	GTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAG	360
Query	361	CACTTGAAGCAATACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTG	420
Sbjct	361	CACTTGAAGCAATACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTG	420
Query	421	ACTCTGTTACTGAAGATTAGGGAGTATTGCTATGACAACATTCATTTTCATGAAAGCCTTC	480
Sbjct	421	ACTCTGTTACTGAAGATTAGGGAGTATTGCTATGACAACATTCATTTTCATGAAAGCCTTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CANAAAA	487
Sbjct	481	CANAAAA	487

Sequence 481 matched with Sequence 126

Query= Sequence ID 481
Length=274

SEQ ID NO: 126

ALIGNMENTS

Identities = 274/274 (100%), Gaps = 0/274 (0%)

Query	1	CACACTTTCATGATAAAACAGAACCTAGGAATGAAAAGAAATTATAGCAACATAATAAA	60
Sbjct	1	CACACTTTCATGATAAAACAGAACCTAGGAATGAAAAGAAATTATAGCAACATAATAAA	60
Query	61	GACCATATATGAGAAGCCACAGCTAACATACTGTATGGTGAAAACTGAAAGCTCTTCC	120
Sbjct	61	GACCATATATGAGAAGCCACAGCTAACATACTGTATGGTGAAAACTGAAAGCTCTTCC	120
Query	121	TCTAAGATCAGGAACAAGGCAAGGATGCCCATTCTTGCCACTTCTATCGAACGTAGTACT	180
Sbjct	121	TCTAAGATCAGGAACAAGGCAAGGATGCCCATTCTTGCCACTTCTATCGAACGTAGTACT	180
Query	181	GGAAGCCCTAGCCAGAACAAGCTAGGCAATAGAAAAGAAATTAAAGGCATCCATNTCAGAAA	240
Sbjct	181	GGAAGCCCTAGCCAGAACAAGCTAGGCAATAGAAAAGAAATTAAAGGCATCCATNTCAGAAA	240
Query	241	GGAAGAANCAAAATGCTGTCTGTTTAANATGACA	274
Sbjct	241	GGAAGAANCAAAATGCTGTCTGTTTAANATGACA	274

Sequence 482 matched with Sequence 127

Length=130

Identities = 130/130 (100%), Gaps = 0/130 (0%)

Query	1	TTTCTATanaaaaaaatttttttaaataattgtaaagttagatttaaaattgtaaaatat	60
Sbjct	1	TTTCTATANAAAAAATTTTAAATAATTGTAAAGTTAGATTAAAAATTGTAAATAT	60
Query	61	aaaatcacaaggaatgtaccaataaaatgtaaatgcnccataaaaaaaaaaaaaaaaaa	120
Sbjct	61	AAAATCACAAAGGAATGTACCAATAAAATGTAAATGCNCCATAAAAAAAAAAAAAAAAAA	120
Query	121	aaaaaaaaa	130
Sbjct	121	AAAAAAAAA	130

Sequence 483 matched with Sequence 128

Query= Sequence ID 483
Length=519

SEQ ID NO: 128

ALIGNMENTS

Identities = 519/519 (100%), Gaps = 0/519 (0%)

```
Query 1      CGNTAACGTGCAATCCGCCGCACGCCAGCAAACCTGGACAACTCCGGGATCTCATCGAAGCGA 63
|||||
Sbjct 1      CGNTAACGTGCAATCCGCCGCACGCCAGCAAACCTGGACAACTCCGGGATCTCATCGAAGCGA 63

Query 64     TTGAGCACCAGTACCAGAGTAATACCGGACTGATGTAACGAGGCGAGTCGCTCATCCAGC 123
|||||
Sbjct 64     TTGAGCACCAGTACCAGAGTAATACCGGACTGATGTAACGAGGCGAGTCGCTCATCCAGC 123

Query 124    TTGCTGACGTGAGGCAACATCCAGGCCATCGAACGGNTCATCAAGAATCAACAAGTCAGG 183
|||||
Sbjct 124    TTGCTGACGTGAGGCAACATCCAGGCCATCGAACGGNTCATCAAGAATCAACAAGTCAGG 183

Query 184    CTCCGACATCAGCGCCTGACACAGCAGGGTTTTTCGCGTCTCGCCAGTGGAAGGTATTT 243
|||||
Sbjct 184    CTCCGACATCAGCGCCTGACACAGCAGGGTTTTTCGCGTCTCGCCAGTGGAAGGTATTT 243

Query 244    AAAGCGTCNGTCGAGGAGGGCGGTAATACCGAACTGCTGCGCCAGTTGCATGCAACGCGG 303
|||||
Sbjct 244    AAAGCGTCNGTCGAGGAGGGCGGTAATACCGAACTGCTGCGCCAGTTGCATGCAACGCGG 303

Query 304    TGCATCCTTTACTTCATCCTGAATGATCTCAGCCGTAGTGCGTCCGGTGCCATCTTCGCC 363
|||||
Sbjct 304    TGCATCCTTTACTTCATCCTGAATGATCTCAGCCGTAGTGCGTCCGGTGCCATCTTCGCC 363

Query 364    AGGGCCGAGCATATCGGTGTTATTCGCTGCCATTGCTCGCTGACGAGTTTTTGCAATTG 423
|||||
Sbjct 364    AGGGCCGAGCATATCGGTGTTATTCGCTGCCATTGCTCGCTGACGAGTTTTTGCAATTG 423

Query 424    CTCGAAGGAGAGACGAGTGATGTGGGAAAACCTGGCTTTGCCGTTACCTTTCAAAAGCGG 483
|||||
Sbjct 424    CTCGAAGGAGAGACGAGTGATGTGGGAAAACCTGGCTTTGCCGTTACCTTTCAAAAGCGG 483
```

PATENT SEQUENCE ALIGNMENT

```
Query  484  GAAGTTCCCCCGCCAGCGCGGGGCCAGGGCCCGAT  519
          |||
Sbjct  484  GAAGTTCCCCCGCCAGCGCGGGGCCAGGGCCCGAT  519
```

Blast comparison trimmed “CGN” from the 5’ end of both sequences and reported 516 identities. The report has been manually corrected for this. “CGN” has been prepended to both sequences and identity count has been increased to 519.

Sequence 484 matched with Sequence 129

Query= Sequence ID 484
Length=272

SEQ ID NO: 129

ALIGNMENTS

Identities = 272/272 (100%), Gaps = 0/272 (0%)

Query	1	tttttttttttttATTCTatttaaaaaatgttnntgaaaaagataacttaaattttaagat	60
Sbjct	1	TTTTTTTTTTTTTATTCTATTAATAAATGTTNNTGAAAAAGATACTTAAATTTTAAAGAT	60
Query	61	aactnaattcctaangattttaaaatAATCCAAGCAGAGATGAAAGANCAAATGCAAATGC	120
Sbjct	61	AACTNAATTCCTAANGATTTAAATAATCCAAGCAGAGATGAAAGANCAAATGCAAATGC	120
Query	121	NTAAAAAGACCCCANAGCATTGTTTagcaaaaagcaaataatagttagccaagcatatatat	180
Sbjct	121	NTAAAAAGACCCCANAGCATTGTTAGCAAAAAGCAAATATAGTTAGCCAAGCATATATAT	180
Query	181	ntcataaaagcaataanaaggcntaaagcaagTTTGGGGAGAGCTTATTTAAAACTTGTA	240
Sbjct	181	NTCATAAAAGCAATAANAAGGCNTAAAGCAAGTTTGGGGAGAGCTTATTTAAAACTTGTA	240
Query	241	AAAATCATTGTAATTTTAAAAAGTTTCAAAC	272
Sbjct	241	AAAATCATTGTAATTTTAAAAAGTTTCAAAC	272

Sequence 485 matched with Sequence 130

Query= Sequence ID - 485 nt: 551
Length=551

SEQ ID NO: 130 nt: 551

ALIGNMENTS

Identities = 551/551 (100%), Gaps = 0/551 (0%)

Query	1	TTTGGAAACACAAAGTTCCCTTTT	60
Sbjct	1	TTTGGAAACACAAAGTTCCCTTTT	60
Query	61	AAGATAGAGACAGAGTGATTGCAAAATAATGGAGGATCATATTTATATATGAATTTTCA	120
Sbjct	61	AAGATAGAGACAGAGTGATTGCAAAATAATGGAGGATCATATTTATATATGAATTTTCA	120
Query	121	CTTATTTGAACTTTCAGATATCANCTTNAAAANCTTTGGTTTAAGTAAAGTNTNTTAATG	180
Sbjct	121	CTTATTTGAACTTTCAGATATCANCTTNAAAANCTTTGGTTTAAGTAAAGTNTNTTAATG	180
Query	181	AGACTCCTTGGATGAAAGTAACCAAAACCAGTAAAAATAAGGTAATAAGGATGTAATAGT	240
Sbjct	181	AGACTCCTTGGATGAAAGTAACCAAAACCAGTAAAAATAAGGTAATAAGGATGTAATAGT	240
Query	241	TTCTTATGGACACTCAACAGCTAGAATGCAGTTAGTCTCAGAAAAGAATTAGAACAAATA	300
Sbjct	241	TTCTTATGGACACTCAACAGCTAGAATGCAGTTAGTCTCAGAAAAGAATTAGAACAAATA	300
Query	301	ACTGGAAGGCCATCAGGAGTCCAAAACCATCACTCtttttatattttatattttatattttC	360
Sbjct	301	ACTGGAAGGCCATCAGGAGTCCAAAACCATCACTCTTTTATATTTTATATTTTATTTTTC	360
Query	361	TCTCTTCANATGAGCATTCTCTTTCTATGTCCATATGGTANAAGGCGGCAGCTCCATAGA	420
Sbjct	361	TCTCTTCANATGAGCATTCTCTTTCTATGTCCATATGGTANAAGGCGGCAGCTCCATAGA	420
Query	421	TTATGGCTTCAGATGTTACAGTTCCGCTNAATGCAGGGACAGACTTGCTATCTTTTCAGTC	480
Sbjct	421	TTATGGCTTCAGATGTTACAGTTCCGCTNAATGCAGGGACAGACTTGCTATCTTTTCAGTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCCTTACATATCCTGGGGAGAGAGCAAATGATTGACTGGCTTGAGTCAGGTGCCC GTTCC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCCTTACATATCCTGGGGAGAGAGCAAATGATTGACTGGCTTGAGTCAGGTGCCC GTTCC  540

Query  541  CTTTCCAATCT  551
          |||||||||
Sbjct  541  CTTTCCAATCT  551
```

Sequence 487 matched with Sequence 131

Query= Sequence ID - 487 nt:224
Length=224

SEQ ID NO: 131 nt:224

ALIGNMENTS

Identities = 224/224 (100%), Gaps = 0/224 (0%)

Query	1	GTTTGNTTGTGACCATCTGTACTTGTAATTTCTTTACNTTCATTGGTATGAAAAATATGT	60
Sbjct	1	GTTTGNTTGTGACCATCTGTACTTGTAATTTCTTTACNTTCATTGGTATGAAAAATATGT	60
Query	61	TCTTAGAAGCANGAAAAAGAATTCAGNTTGTCTTTGTATACTAAATTAAATGCTGTAATT	120
Sbjct	61	TCTTAGAAGCANGAAAAAGAATTCAGNTTGTCTTTGTATACTAAATTAAATGCTGTAATT	120
Query	121	TTGATAAAATGAAAAATCTGCTTTATTTGCAACAATTGGTTTCTTCCTTGACGTCAGCCT	180
Sbjct	121	TTGATAAAATGAAAAATCTGCTTTATTTGCAACAATTGGTTTCTTCCTTGACGTCAGCCT	180
Query	181	CACTCTTGGACTTTGGTATTCAGCCNGNCACCCCTGGGAATTCC	224
Sbjct	181	CACTCTTGGACTTTGGTATTCAGCCNGNCACCCCTGGGAATTCC	224

Sequence 488 matched with Sequence 132

Query= Sequence ID - 488 nt: 349
Length=349

SEQ ID NO: 132 nt: 349

ALIGNMENTS

Identities = 349/349 (100%), Gaps = 0/349 (0%)

```
Query 1   GTGCCTCCCTGTGTGAGTAGCCTAAGGTGCATTGAAAAAGACTGGGATGTGTTTTAtttt 60
          |||
Sbjct 1   GTGCCTCCCTGTGTGAGTAGCCTAAGGTGCATTGAAAAAGACTGGGATGTGTTTTATTTT 60

Query 61  tttGTATTAGATAGCATTAACTTACTGTTGAAGTATTTTGGTGGAGTATTAGTGACAA 120
          |||
Sbjct 61  TTTGTATTAGATAGCATTAACTTACTGTTGAAGTATTTTGGTGGAGTATTAGTGACAA 120

Query 121 GCCATTGAGTCTTAAGCCTTACGGCTTCCTATAAAATCACTAATTCGTGTGTGTTTGTG 180
          |||
Sbjct 121 GCCATTGAGTCTTAAGCCTTACGGCTTCCTATAAAATCACTAATTCGTGTGTGTTTGTG 180

Query 181 TGTAGGTTACGTTATATATAGGATTCGTGTTGCGCGTGGTGGCCGAAAAACGCCAGTTCC 240
          |||
Sbjct 181 TGTAGGTTACGTTATATATAGGATTCGTGTTGCGCGTGGTGGCCGAAAAACGCCAGTTCC 240

Query 241 TAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGTGTTAACCAGCTAAAGTTTGCTCG 300
          |||
Sbjct 241 TAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGTGTTAACCAGCTAAAGTTTGCTCG 300

Query 301 AAGCCTTCAGTCCGTTGCAGAGGANCGAGCTGGACNCCCTGGGGGGCTC 349
          |||
Sbjct 301 AAGCCTTCAGTCCGTTGCAGAGGANCGAGCTGGACNCCCTGGGGGGCTC 349
```

Sequence 489 matched with Sequence 133

Query= Sequence ID 489
Length=635

SEQ ID NO: 133

ALIGNMENTS

Identities = 635/635 (100%), Gaps = 0/635 (0%)

Query	1	TTAACAGCTGCATAGAGTTTTAAAAGTACATTATATTTTGTTCAGACAAGTAAAATATCTG	60
Sbjct	1	TTAACAGCTGCATAGAGTTTTAAAAGTACATTATATTTTGTTCAGACAAGTAAAATATCTG	60
Query	61	TTTTTCACGCaaaaaaaGCCATGAAATACGTAATTTTTTAAAGACAAAAAATCATCTTTT	120
Sbjct	61	TTTTTCACGCAAAAAAGCCATGAAATACGTAATTTTTTAAAGACAAAAAATCATCTTTT	120
Query	121	GAGTTTGCTCTTTGGTTTTTCTTCATTCTTTTGAGGATTGGGAAAACAGAAAGATTCTT	180
Sbjct	121	GAGTTTGCTCTTTGGTTTTTCTTCATTCTTTTGAGGATTGGGAAAACAGAAAGATTCTT	180
Query	181	TGATTTGGGTAATGAAGAGGTAATTTGGGACAGTGTGGTGGTACCAGGAAGAAAGAGGAT	240
Sbjct	181	TGATTTGGGTAATGAAGAGGTAATTTGGGACAGTGTGGTGGTACCAGGAAGAAAGAGGAT	240
Query	241	TGGAAAGGCCAGTACTGTTTTAGTTGCTCGGCACTGTTGGTTTTGTTTTAATGTGGTTGC	300
Sbjct	241	TGGAAAGGCCAGTACTGTTTTAGTTGCTCGGCACTGTTGGTTTTGTTTTAATGTGGTTGC	300
Query	301	CCTGTCCACTACATGGTTCTATCAGTAGTGTAATCCATTTTCAATGTAAAGCTCTTTTAG	360
Sbjct	301	CCTGTCCACTACATGGTTCTATCAGTAGTGTAATCCATTTTCAATGTAAAGCTCTTTTAG	360
Query	361	TTTTTGTTCATAGACATAAAATTAATATTTTGAGAGGCATCCCTCACCTGTTTCAATTTCTTCT	420
Sbjct	361	TTTTTGTTCATAGACATAAAATTAATATTTTGAGAGGCATCCCTCACCTGTTTCAATTTCTTCT	420
Query	421	GTGTTGAAATGAAGTACTTAAAATTACCGTTATACATGAACTTTGTGGACTGTAAGATTT	480
Sbjct	421	GTGTTGAAATGAAGTACTTAAAATTACCGTTATACATGAACTTTGTGGACTGTAAGATTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTATATATGTTCAAATGCCTTTTAGCTGGCTTTTAAATTAATATGCCTGTTTGAGTGC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTTATATATGTTCAAATGCCTTTTAGCTGGCTTTTAAATTAATATGCCTGTTTGAGTGC  540

Query  541  TTAATACAATGTAATGNGGATTGTAAATCATACCTATTTTAAATCATTCCTTCCTGTATA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TTAATACAATGTAATGNGGATTGTAAATCATACCTATTTTAAATCATTCCTTCCTGTATA  600

Query  601  TTTGNACTCAGAGAGCCTTATTTTATTCTTCCAGC   635
          ||||||||||||||||||||||||||||
Sbjct   601  TTTGNACTCAGAGAGCCTTATTTTATTCTTCCAGC   635
```

Sequence 491 matched with Sequence 134

Query= Sequence ID - 491 nt: 382
Length=382

SEQ ID NO: 134 nt: 382

ALIGNMENTS

Identities = 382/382 (100%), Gaps = 0/382 (0%)

Query	1	TTTTCTTAGAACTTTATTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA	60
Sbjct	1	TTTTCTTAGAACTTTATTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA	60
Query	61	CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA	120
Sbjct	61	CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA	120
Query	121	ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAATTAGCTGGGCGTGGTGGCGCATG	180
Sbjct	121	ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAATTAGCTGGGCGTGGTGGCGCATG	180
Query	181	CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG	240
Sbjct	181	CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG	240
Query	241	AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC	300
Sbjct	241	AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC	300
Query	301	CATCTCaaaaaaaaaaaaaaaaaaaaCAACCTTTATTTTTCTGATTTTAAAAGTAATAACT	360
Sbjct	301	CATCTCAAAAAAAAAAAAAAAAAAAAAACCTTTATTTTTCTGATTTTAAAAGTAATAACT	360
Query	361	AGTTTGTAGAAACATTAAAAAGT	382
Sbjct	361	AGTTTGTAGAAACATTAAAAAGT	382

Sequence 492 matched with Sequence 135

Query= Sequence ID 492
Length=503

SEQ ID NO: 135

ALIGNMENTS

Identities = 503/503 (100%), Gaps = 0/503 (0%)

Query	1	ACCCTAAACATAACTTAAAAATTTGTTNGGAATTTGAAAGTACAGAATTTTCCTGTAATTG	60
Sbjct	1	ACCCTAAACATAACTTAAAAATTTGTTNGGAATTTGAAAGTACAGAATTTTCCTGTAATTG	60
Query	61	AGACTNNTTTAACTTTTGTGGTTGGAGAAGGTATTCTATTTTTTGAAAAATATCTGTAAGT	120
Sbjct	61	AGACTNNTTTAACTTTTGTGGTTGGAGAAGGTATTCTATTTTTTGAAAAATATCTGTAAGT	120
Query	121	TTTATCTAAATAGTAAACTCTAAGTATTCTTCCCCTTTACTTACAGCCACCCTGGGAATC	180
Sbjct	121	TTTATCTAAATAGTAAACTCTAAGTATTCTTCCCCTTTACTTACAGCCACCCTGGGAATC	180
Query	181	TGAGACTAGAGAAAATAAAGTTTGTCTCTTGTTCTAAGGAGGGTCTGGTTTAGAAATCTG	240
Sbjct	181	TGAGACTAGAGAAAATAAAGTTTGTCTCTTGTTCTAAGGAGGGTCTGGTTTAGAAATCTG	240
Query	241	ATTTAGACATAGAAAAATTGCAAGAAGCTTGAGGTGATTGGAAGATACGATTTTGTTATC	300
Sbjct	241	ATTTAGACATAGAAAAATTGCAAGAAGCTTGAGGTGATTGGAAGATACGATTTTGTTATC	300
Query	301	AAAGNATGTTTCTGTTTTATAGATTTTATTCATCTACAACCTCCTTATTAATATATTTAAG	360
Sbjct	301	AAAGNATGTTTCTGTTTTATAGATTTTATTCATCTACAACCTCCTTATTAATATATTTAAG	360
Query	361	AAGTCATTAACCCACCATTGATTACTTGATATAAAAGGAGAANC GGTTGTTAAAAGGTGAA	420
Sbjct	361	AAGTCATTAACCCACCATTGATTACTTGATATAAAAGGAGAANC GGTTGTTAAAAGGTGAA	420
Query	421	ATANAAtttttaattttttttttttaagtttaggatttttttttAAAATCTAAGAGTTT	480
Sbjct	421	ATANAATTTTAAATTTTTTTTTTTTAAAGTTTAGGATTTTTTTTTTAAATCTAAGAGTTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGTCATTTGGGGACAATCAGAA	503
Sbjct	481	CTGTCATTTGGGGACAATCAGAA	503

Sequence 493 matched with Sequence 136

Query= Sequence ID 493
Length=576

SEQ ID NO: 136

ALIGNMENTS

Identities = 576/576 (100%), Gaps = 0/576 (0%)

Query	1	TGGGAATCATAATTNGTTAACTGAAGCTNATAAGATGAGAGCATT	CANAGAGAAAAGAAC	60
Sbjct	1	TGGGAATCATAATTNGTTAACTGAAGCTNATAAGATGAGAGCATT	CANAGAGAAAAGAAC	60
Query	61	GGAAAGATTGAATATCAGTTTCCCTTCTTTaaaaaaaTTGTGGATATGTGATCTAGCTTC		120
Sbjct	61	GGAAAGATTGAATATCAGTTTCCCTTCTTTAAAAAAATTGTGGATATGTGATCTAGCTTC		120
Query	121	TTGAGCATCACAGTGAAGTGGCTCGTGGTAATTGATCGCTATGCTGACAATCTTATC		180
Sbjct	121	TTGAGCATCACAGTGAAGTGGCTCGTGGTAATTGATCGCTATGCTGACAATCTTATC		180
Query	181	TCCACCTATGTCATTCAATTTTCTAAGAGGCAAAATCCTTAATCAGGAGGAGAGTTTAGC		240
Sbjct	181	TCCACCTATGTCATTCAATTTTCTAAGAGGCAAAATCCTTAATCAGGAGGAGAGTTTAGC		240
Query	241	TCTAGCTAAATTTCCCTTGTCAGCATGCTCCTGCTCCCCAACTTGTGGAAACAGCTAA		300
Sbjct	241	TCTAGCTAAATTTCCCTTGTCAGCATGCTCCTGCTCCCCAACTTGTGGAAACAGCTAA		300
Query	301	AGGATTGGACTAGGAGCANAAGTTTGAATGGTTAAATGTAGCAACATGTGTTTCCTGA		360
Sbjct	301	AGGATTGGACTAGGAGCANAAGTTTGAATGGTTAAATGTAGCAACATGTGTTTCCTGA		360
Query	361	AACAAAATTCCACTATAATaaaaaaaGCATTTGAATGCTCCCTTGTAATTCTGTTGGAGC		420
Sbjct	361	AACAAAATTCCACTATAATAAAAAAAGCATTTGAATGCTCCCTTGTAATTCTGTTGGAGC		420
Query	421	TTGTTGCCTTTTTTATGACACAACCATAATCAGTGATAGACAGTAGCATAAAGAAGCAAG		480
Sbjct	421	TTGTTGCCTTTTTTATGACACAACCATAATCAGTGATAGACAGTAGCATAAAGAAGCAAG		480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGCAAAGCAATTAAGTAATAATAGCACTACAAAAATGTGTGCTGTACTTACCAAACACGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGCAAAGCAATTAAGTAATAATAGCACTACAAAAATGTGTGCTGTACTTACCAAACACGA  540

Query  541  CATTTATGAATTATTANATAGGAATAAGGGGATGGT  576
          ||||||||||||||||||||||||||||||||
Sbjct   541  CATTTATGAATTATTANATAGGAATAAGGGGATGGT  576
```

Sequence 494 matched with Sequence 137

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 494
Length=22

SEQ ID NO: 137

44.1 2e-11

ALIGNMENTS

Identities = 22/22 (100%), Gaps = 0/22 (0%)

Query	1	GACCCAGCCATCTAAATAAGTT	22
Sbjct	1	GACCCAGCCATCTAAATAAGTT	22

Sequence 495 matched with Sequence 138

Query	1	TTTC
Sbjct	1	TTTC

Sequence 496 matched with Sequence 139

Query= Sequence ID 496
Length=431

SEQ ID NO: 139

ALIGNMENTS

Identities = 431/431 (100%), Gaps = 0/431 (0%)

Query	1	CTCGCTGGCGGGAGGCCACGGGCTTTCCACAGCGCGGGGAACGGGAGGCTGCAGGATGG	60
Sbjct	1	CTCGCTGGCGGGAGGCCACGGGCTTTCCACAGCGCGGGGAACGGGAGGCTGCAGGATGG	60
Query	61	TCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCAACGCGGTGCGCGACC	120
Sbjct	61	TCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCAACGCGGTGCGCGACC	120
Query	121	GGGAGCTGGACCTCCGGGGGTGATCTGGACCCTCTGGCATCTCTCAAATCGCTGACTTAC	180
Sbjct	121	GGGAGCTGGACCTCCGGGGGTGATCTGGACCCTCTGGCATCTCTCAAATCGCTGACTTAC	180
Query	181	CTAAGTATCCTAAGAAATCCGCTAACCAATAAGAAGCATTACAGATTGTATGTGATTTAT	240
Sbjct	181	CTAAGTATCCTAAGAAATCCGCTAACCAATAAGAAGCATTACAGATTGTATGTGATTTAT	240
Query	241	AAAGTTCGCAAGTCATAGTACTGGATTTCCAGAAAGTGAACTAAAATTTTAATCCAGG	300
Sbjct	241	AAAGTTCGCAAGTCATAGTACTGGATTTCCAGAAAGTGAACTAAAATTTTAATCCAGG	300
Query	301	TGCTGGTTTGCCAAGTGACAAAAAGAAAGGTGGGCCATCTCCAGGGGATGTAAAAGCAAT	360
Sbjct	301	TGCTGGTTTGCCAAGTGACAAAAAGAAAGGTGGGCCATCTCCAGGGGATGTAAAAGCAAT	360
Query	361	CAAGAATGCCATAGCAAATGCTTNAACTCTGGCTGAAGTGGANAGGCTGAANGGGTTGCT	420
Sbjct	361	CAAGAATGCCATAGCAAATGCTTNAACTCTGGCTGAAGTGGANAGGCTGAANGGGTTGCT	420
Query	421	GCAGTCTGGTC	431
Sbjct	421	GCAGTCTGGTC	431

Sequence 497 matched with Sequence 140

Query= Sequence ID 497
Length=606

SEQ ID NO: 140

ALIGNMENTS

Identities = 606/606 (100%), Gaps = 0/606 (0%)

Query	1	GAAGACCTCACATCTGAGAGCTCATCTGCGTTGGCATTCTGGAGAACGCCCTTTTGT	60
Sbjct	1	GAAGACCTCACATCTGAGAGCTCATCTGCGTTGGCATTCTGGAGAACGCCCTTTTGT	60
Query	61	TAACTGGATGTACTGTGGTAAAAGATTTACTCGAAGTGATGAATTACAGAGGCACAGAAG	120
Sbjct	61	TAACTGGATGTACTGTGGTAAAAGATTTACTCGAAGTGATGAATTACAGAGGCACAGAAG	120
Query	121	AACACATACAGGTGAGAAGAAATTTGTTTGTCCAGAATGTTCAAAACGCTTTATGANAAG	180
Sbjct	121	AACACATACAGGTGAGAAGAAATTTGTTTGTCCAGAATGTTCAAAACGCTTTATGANAAG	180
Query	181	TGACCACCTTGCCAAACATATTAACACACCAGAATAAAAAAGGTATTCACTCTANCAG	240
Sbjct	181	TGACCACCTTGCCAAACATATTAACACACCAGAATAAAAAAGGTATTCACTCTANCAG	240
Query	241	TACAGTGCTGGCATCTGTGGAAGCTGCGCGAGATGATACTTTGATTACTGCAGGAGGAAC	300
Sbjct	241	TACAGTGCTGGCATCTGTGGAAGCTGCGCGAGATGATACTTTGATTACTGCAGGAGGAAC	300
Query	301	AACGCTTATCCTTGCAAATATTCAACAAGGTTCTGTTTCAGGGATAGGAACTGTTAATAC	360
Sbjct	301	AACGCTTATCCTTGCAAATATTCAACAAGGTTCTGTTTCAGGGATAGGAACTGTTAATAC	360
Query	361	TTCCGCCACCAGCAATCAAGATATCCTTACCAACACTGAAATACCTTTACAGCTTGTAC	420
Sbjct	361	TTCCGCCACCAGCAATCAAGATATCCTTACCAACACTGAAATACCTTTACAGCTTGTAC	420
Query	421	AGTTTCTGGAAATGAGACAATGGGAGTAAATATTACACAAATACTTATTCATTGNGGT	480
Sbjct	421	AGTTTCTGGAAATGAGACAATGGGAGTAAATATTACACAAATACTTATTCATTGNGGT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTTTATACAGTAGTGAGAAGAATATTGTTCTAAGTTCTTAGATATCtttttttGGATG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTTTATACAGTAGTGAGAAGAATATTGTTCTAAGTTCTTAGATATCTTTTTTTGGATG  540

Query  541  TGCAAAAATTTTGGATTGACAGTAACTTGGGTATACATGACACTGAAATGCCTTACTTT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TGCAAAAATTTTGGATTGACAGTAACTTGGGTATACATGACACTGAAATGCCTTACTTT  600

Query  601  GGATGA  606
          |||||
Sbjct   601  GGATGA  606
```


Sequence 499 matched with Sequence 141

Query= Sequence ID 499
Length=564

SEQ ID NO: 141

ALIGNMENTS

Identities = 564/564 (100%), Gaps = 0/564 (0%)

Query	1	TGCCTGCGGGCCAGGACCTCGCCCAGCCCATGTTTCATCCAGTCAGCCAACCAGCCCTCCG	60
Sbjct	1	TGCCTGCGGGCCAGGACCTCGCCCAGCCCATGTTTCATCCAGTCAGCCAACCAGCCCTCCG	60
Query	61	ANGGGCAGGCCCCCAGGTGACCGGCGACTGAGGGCCTGAGCTGGCAAGGCCAAGGACAC	120
Sbjct	61	ANGGGCAGGCCCCCAGGTGACCGGCGACTGAGGGCCTGAGCTGGCAAGGCCAAGGACAC	120
Query	121	CCAACACAATTTTGGCATAACAGCCCCAGGCAATGGGCACAGCCTTCCTCCCCANAGGAC	180
Sbjct	121	CCAACACAATTTTGGCATAACAGCCCCAGGCAATGGGCACAGCCTTCCTCCCCANAGGAC	180
Query	181	CCGGCCGACCTCAGCGCCTCCTGCAGGCTAGGACACTGGTGCACTACACCCCATGCCTGG	240
Sbjct	181	CCGGCCGACCTCAGCGCCTCCTGCAGGCTAGGACACTGGTGCACTACACCCCATGCCTGG	240
Query	241	GGGCCGAGATTCTCCAGCAGAAAGATGCAATATtttttgtttccttttttccatttttt	300
Sbjct	241	GGGCCGAGATTCTCCAGCAGAAAGATGCAATATTTTTTGTTCCTTTTTTCCATTTTTT	300
Query	301	tCTCTAAGGAATCAATATTTCAATATGTTGAGTGTGTGTCCAATGCTATGAAATTAATAA	360
Sbjct	301	TCTCTAAGGAATCAATATTTCAATATGTTGAGTGTGTGTCCAATGCTATGAAATTAATAA	360
Query	361	ATTAAATAACATATTTATGGCATTCTTGAAGAGTGTGGTTGAAGAAATATTTCTCctt	420
Sbjct	361	ATTAAATAACATATTTATGGCATTCTTGAAGAGTGTGGTTGAAGAAATATTTCTCCTT	420
Query	421	ttgtttttcttttttttttGNTTGNTACTGCCACTTCTTTTTAGGAGCAAATCTCCCCAG	480
Sbjct	421	TTGTTTTTCTTTTTTTTTTNTTGNTACTGCCACTTCTTTTTAGGAGCAAATCTCCCCAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGTGTACGGNATTTCTTGACTCTGGGAACAGCTGCTACCCCCAAGACTTGCCACGTTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGGTGTACGGNATTTCTTGACTCTGGGAACAGCTGCTACCCCCAAGACTTGCCACGTTGT  540

Query  541  TCTGCCCTCAAATGGAATTAAGTG  564
          ||||||||||||||||
Sbjct   541  TCTGCCCTCAAATGGAATTAAGTG  564
```

Sequence 500 matched with Sequence 142

Query= Sequence ID - 500 nt: 390
Length=390

SEQ ID NO: 142 nt: 390

ALIGNMENTS

Identities = 390/390 (100%), Gaps = 0/390 (0%)

```
Query 1   GGAATATGGTCAGGATCTTCTCCATACTGTCTTCAAGAATGGCAAGGTGACAAAAAGCTA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   GGAATATGGTCAGGATCTTCTCCATACTGTCTTCAAGAATGGCAAGGTGACAAAAAGCTA 60

Query 61  TTCATTTGATGAAATAAGAAAAAATGCACAGCTGAATATTGAACTGGAAGCAGCACATCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TTCATTTGATGAAATAAGAAAAAATGCACAGCTGAATATTGAACTGGAAGCAGCACATCA 120

Query 121 TTAGGCTTTATGACTGGgtgtgtgtgtgtgtatgtaatacataatgtttattgtacana 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TTAGGCTTTATGACTGGGTGTGTGTGTGTGTATGTAATACATAATGTTTATTGTACANA 180

Query 181 tgtgtgggggtttgtgttttATGATACATTACAGCCAAATTATTTGTTGGTTNATGGACAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 TGTGTGGGGTTTGTGTTTTATGATACATTACAGCCAAATTATTTGTTGGTTNATGGACAT 240

Query 241 ACTGCCCTTTCAttttttCTTTCCAGTGTTTAGGTGATCTCAAATTAAGAAATGCATT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 ACTGCCCTTTCATTTTTTTCTTTCCAGTGTTTAGGTGATCTCAAATTAAGAAATGCATT 300

Query 301 TAACCATGTAAANATGANTGCTAAAGTCAGCTTTTTAGGGCCCTTTGCCAATAGGTANT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 TAACCATGTAAANATGANTGCTAAAGTCAGCTTTTTAGGGCCCTTTGCCAATAGGTANT 360

Query 361 CATTCAATCTGGTATTGATCTTTTCACAAA 390
          ||||||||||||||||||||||||
Sbjct 361 CATTCAATCTGGTATTGATCTTTTCACAAA 390
```

Sequence 502 matched with Sequence 143

Query= Sequence ID 502
Length=546

SEQ ID NO: 143

ALIGNMENTS

Identities = 546/546 (100%), Gaps = 0/546 (0%)

Query	1	ACCCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCAC	60
Sbjct	1	ACCCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCAC	60
Query	61	CCGATATATGTTCTCTAGGCCTTTTANAAAACATGGAGTTGTTTCCTTTGGCCACATATAT	120
Sbjct	61	CCGATATATGTTCTCTAGGCCTTTTANAAAACATGGAGTTGTTTCCTTTGGCCACATATAT	120
Query	121	GCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGG	180
Sbjct	121	GCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGG	180
Query	181	AATGCCCCACAAGTGTACCATGGCAAACTGGAAGAGTCTACAATGTTACCCAGCATGC	240
Sbjct	181	AATGCCCCACAAGTGTACCATGGCAAACTGGAAGAGTCTACAATGTTACCCAGCATGC	240
Query	241	TGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGT	300
Sbjct	241	TGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGT	300
Query	301	GCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGA	360
Sbjct	301	GCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGA	360
Query	361	AAATGATCAGAAAAAGAAAGGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCA	420
Sbjct	361	AAATGATCAGAAAAAGAAAGGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCA	420
Query	421	GCCTGCTCCACCCAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCT	480
Sbjct	421	GCCTGCTCCACCCAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGAACCTATTCCTATGAATTCATGGCATAATAGGTGTTaaaaaaaaaaaaTAAAGGACC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGAACCTATTCCTATGAATTCATGGCATAATAGGTGTTAAAAAAAAAAAAAATAAGGACC  540

Query  541  TCTGGG  546
          |||||
Sbjct   541  TCTGGG  546
```

Sequence 503 matched with Sequence 144

Query= Sequence ID - 503 nt: 109
Length=109

SEQ ID NO: 144 nt: 109

ALIGNMENTS

Identities = 109/109 (100%), Gaps = 0/109 (0%)

Query	1	ACATTTTCCGGNCCTTTTGCCATACACAGTTACAGAGATCAGTCAAATCCATACCACCAC	60
Sbjct	1	ACATTTTCCGGNCCTTTTGCCATACACAGTTACAGAGATCAGTCAAATCCATACCACCAC	60
Query	61	TGAGATCTCATTTATTGCCACAGATGCACAAAATAAATAACCCAAAATC	109
Sbjct	61	TGAGATCTCATTTATTGCCACAGATGCACAAAATAAATAACCCAAAATC	109

Sequence 504 matched with Sequence 145

Query= Sequence ID - 504 nt: 374
Length=374

SEQ ID NO: 145 nt: 374

ALIGNMENTS

Identities = 374/374 (100%), Gaps = 0/374 (0%)

```
Query 1  CCAGCAACGACCCATACCTCAGACCCGACGGCCCGGAGCGGAGCGCGCCCTGCCCTGGCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  CCAGCAACGACCCATACCTCAGACCCGACGGCCCGGAGCGGAGCGCGCCCTGCCCTGGCG 60

Query 61 CAGCCAGAGCCGCCGGGTGCCCGCTGCAGTTTCTTGGGACATAGGAGCGCAAAGAAGCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 CAGCCAGAGCCGCCGGGTGCCCGCTGCAGTTTCTTGGGACATAGGAGCGCAAAGAAGCTA 120

Query 121 CAGCCTGGACTTACCACCACTAAACTGCGAGAGAAGCTAAACGTGTTTATTTCCCTTAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 CAGCCTGGACTTACCACCACTAAACTGCGAGAGAAGCTAAACGTGTTTATTTCCCTTAA 180

Query 181 ATTATTTTGTAAATGGTAGCTTTTCTACATCTTACTCCTGTTGATGCAGCTAAGGTACA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 ATTATTTTGTAAATGGTAGCTTTTCTACATCTTACTCCTGTTGATGCAGCTAAGGTACA 240

Query 241 TTTGTaaaaagaaaaaaaaaCCAGACTTTTCANACAAACCCTTTGTATTGTANATAAGAGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TTTGTAAAAAGAAAAAAACCAGACTTTTCANACAAACCCTTTGTATTGTANATAAGAGG 300

Query 301 AAAAGACTGAGCATGCTCACTTTTTTATATTAATTTTACAGTATTTGTAAGAATAAAGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 AAAAGACTGAGCATGCTCACTTTTTTATATTAATTTTACAGTATTTGTAAGAATAAAGC 360

Query 361 ANCATTGAAATCG 374
          |||||||||
Sbjct 361 ANCATTGAAATCG 374
```

Sequence 505 matched with Sequence 146

Query= Sequence ID 505
Length=357

SEQ ID NO: 146

ALIGNMENTS

Identities = 357/357 (100%), Gaps = 0/357 (0%)

Query	1	GTACAGGAGGTAAATTGGATACCCCATCTAAGGGGATCTGTGAGACCAGGTAGTTATTTG	60
Sbjct	1	GTACAGGAGGTAAATTGGATACCCCATCTAAGGGGATCTGTGAGACCAGGTAGTTATTTG	60
Query	61	GAATGAAAGAGTAAGATATTTAAACCAGCCAGCATGTCAACAGGTGGGTGATAGTCTTGTT	120
Sbjct	61	GAATGAAAGAGTAAGATATTTAAACCAGCCAGCATGTCAACAGGTGGGTGATAGTCTTGTT	120
Query	121	CTCACAGACAACAGATGGCCATCATCTTAAACAACATTTATGTTAACCAGCAGATAAGG	180
Sbjct	121	CTCACAGACAACAGATGGCCATCATCTTAAACAACATTTATGTTAACCAGCAGATAAGG	180
Query	181	GACTCCTGCATTGTCAGTGGACTTTGAGCCTGAGTTTTTCTACTTGCATAGGTGAAAGTG	240
Sbjct	181	GACTCCTGCATTGTCAGTGGACTTTGAGCCTGAGTTTTTCTACTTGCATAGGTGAAAGTG	240
Query	241	GACTGCAATGCTAGTATAAATGCCGTATGATGACTAGTACCCCTTAGGGAGCTCCAGTTT	300
Sbjct	241	GACTGCAATGCTAGTATAAATGCCGTATGATGACTAGTACCCCTTAGGGAGCTCCAGTTT	300
Query	301	GCCTTCCTGGGGAACCACAGACCCCAAGTGTAATTTCTGAGGACAGCCCGACTTCT	357
Sbjct	301	GCCTTCCTGGGGAACCACAGACCCCAAGTGTAATTTCTGAGGACAGCCCGACTTCT	357

Sequence 506 matched with Sequence 147

Query= Sequence ID 506
Length=293

SEQ ID NO: 147

ALIGNMENTS

Identities = 293/293 (100%), Gaps = 0/293 (0%)

Query	1	GTTACTGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGCTGAGG	60
Sbjct	1	GTTACTGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGCTGAGG	60
Query	61	TGNGACACCTGCTGCACTCATCTGATGTAAAACCATCCCANAGCTGGCGAGAGGATGGAG	120
Sbjct	61	TGNGACACCTGCTGCACTCATCTGATGTAAAACCATCCCANAGCTGGCGAGAGGATGGAG	120
Query	121	CTGGGTGGAACTGCTTTGCACTATCGTTTGCTTGGTGTGTTGTTTTAACGCACAACTTG	180
Sbjct	121	CTGGGTGGAACTGCTTTGCACTATCGTTTGCTTGGTGTGTTGTTTTAACGCACAACTTG	180
Query	181	CTTGTACAGTAACTGTCTTCTGTACTATTTAACTGTAAAATGGAATTTTGACTGATTTG	240
Sbjct	181	CTTGTACAGTAACTGTCTTCTGTACTATTTAACTGTAAAATGGAATTTTGACTGATTTG	240
Query	241	TTACAATAATATAACTCTGAGATGTGTGaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	293
Sbjct	241	TTACAATAATATAACTCTGAGATGTGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	293

Sequence 507 matched with Sequence 148

Query= Sequence ID - 507 nt: 521
Length=521

SEQ ID NO: 148 nt: 521

ALIGNMENTS

Identities = 521/521 (100%), Gaps = 0/521 (0%)

Query	1	CTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGAAGACCAT	60
Sbjct	1	CTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGAAGACCAT	60
Query	61	CACCCTCGAGGTTGAACCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAA	120
Sbjct	61	CACCCTCGAGGTTGAACCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAA	120
Query	121	GGAAGGAATTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGG	180
Sbjct	121	GGAAGGAATTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGG	180
Query	181	ACGTACTTTGTCTGACTACAATATTCAAAAGGAGTCTACTCTTCATCTTGTGTTGAGACT	240
Sbjct	181	ACGTACTTTGTCTGACTACAATATTCAAAAGGAGTCTACTCTTCATCTTGTGTTGAGACT	240
Query	241	TCGTGGTGGTGCTaagaaaaggaagaagaagtcttacaccactcccaagaagaataagca	300
Sbjct	241	TCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTCCCAAGAAGAATAAGCA	300
Query	301	caagagaaagaagGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGAATGGCAA	360
Sbjct	301	CAAGAGAAAGAAGGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGAATGGCAA	360
Query	361	AATTAGTCGCCTTCGTCGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGC	420
Sbjct	361	AATTAGTCGCCTTCGTCGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGC	420
Query	421	AAGTCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACC	480
Sbjct	421	AAGTCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGAAGACAAGTAACTGTATGAGTTAATAAAAGACATGAACT	521
Sbjct	481	AGAAGACAAGTAACTGTATGAGTTAATAAAAGACATGAACT	521

Sequence 508 matched with Sequence 149

Query= Sequence ID 508
Length=470

SEQ ID NO: 149

ALIGNMENTS

Identities = 470/470 (100%), Gaps = 0/470 (0%)

Query	1	AAGCTCATGATTTTAAATGTATTTTCTAATAAACTATACTCCCATTAAAAATCACCAA	60
Sbjct	1	AAGCTCATGATTTTAAATGTATTTTCTAATAAACTATACTCCCATTAAAAATCACCAA	60
Query	61	TACCTTAATGTTTCAATTATATAAGCTAATTAATAAAAGGCTGGGCGTGGTGGCTCAC	120
Sbjct	61	TACCTTAATGTTTCAATTATATAAGCTAATTAATAAAAGGCTGGGCGTGGTGGCTCAC	120
Query	121	TTTGGAAGACCGAGGCAGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGCCCAA	180
Sbjct	121	TTTGGAAGACCGAGGCAGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGCCCAA	180
Query	181	CATGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCACATGCC	240
Sbjct	181	CATGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCACATGCC	240
Query	241	CGTAATCCCAGCTACTGGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGGG	300
Sbjct	241	CGTAATCCCAGCTACTGGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGGG	300
Query	301	GCTGCAGTGAGCCGAGATCATGCCATTGCACTCCAGTCTGGGCAACAATAGTGGAATCC	360
Sbjct	301	GCTGCAGTGAGCCGAGATCATGCCATTGCACTCCAGTCTGGGCAACAATAGTGGAATCC	360
Query	361	ATCTCaaaaataataaaaaaaaaataaaataaaaaataaaattcaaacctaaaataGATGCTC	420
Sbjct	361	ATCTCAAAAATAATAAAAAAAAAATAAAATAAAAATAAAATTCAAACCTAAATAGATGCTC	420
Query	421	TACTTCAGGAGTGGGCAAATTAATCACCTGCATCCTTTTTTTGGGCTTTC	470
Sbjct	421	TACTTCAGGAGTGGGCAAATTAATCACCTGCATCCTTTTTTTGGGCTTTC	470

Sequence 509 matched with Sequence 150

Query= Sequence ID - 509 nt: 575
Length=575

SEQ ID NO: 150 nt: 575

ALIGNMENTS

Identities = 575/575 (100%), Gaps = 0/575 (0%)

Query	1	tttttttCTAAATGGNGATTACTAATATATGTGGAGACTATTAATCTCTTTTCTGTTGCC	60
Sbjct	1	TTTTTTTCTAAATGGNGATTACTAATATATGTGGAGACTATTAATCTCTTTTCTGTTGCC	60
Query	61	ATTAGTTCATTTTTCCCCAAAAGCCAATACATGTTTCATTACaaaaatgaattataaaata	120
Sbjct	61	ATTAGTTCATTTTTCCCCAAAAGCCAATACATGTTTCATTACAAAAATGAATTATAAAATA	120
Query	121	taagttaaaaagaaaaacataaaaCCCTACAATCTTACCCACCCAGACAACTACTATTAAT	180
Sbjct	121	TAAGTTAAAAGAAAAACATAAAACCCTACAATCTTACCCACCCAGACAACTACTATTAAT	180
Query	181	ACCTTAGTATTAACATATACACATCATGTATATGTATAAATTTATCTTAAACAAAAATAA	240
Sbjct	181	ACCTTAGTATTAACATATACACATCATGTATATGTATAAATTTATCTTAAACAAAAATAA	240
Query	241	AATTATTCTTTACATATTGTTTTAAACCTATTTATCTGGCCAGGTGCCGTGGCTCACGC	300
Sbjct	241	AATTATTCTTTACATATTGTTTTAAACCTATTTATCTGGCCAGGTGCCGTGGCTCACGC	300
Query	301	TTGTAATCCCAGCACTTTGGGAGGCTGAGGCACGTGGATCACCTGAGGTCAGGAATTCGA	360
Sbjct	301	TTGTAATCCCAGCACTTTGGGAGGCTGAGGCACGTGGATCACCTGAGGTCAGGAATTCGA	360
Query	361	GACCAGCCCAGCCAACATGGTGAAACCCTGTCTCTAATGGTTTAAATACCAAAAAATTAG	420
Sbjct	361	GACCAGCCCAGCCAACATGGTGAAACCCTGTCTCTAATGGTTTAAATACCAAAAAATTAG	420
Query	421	CTGGGCATGGTGGCACATGCCTGTAATATCAGCTAACATGGGAGGCTGAGGCAGGAGAAT	480
Sbjct	421	CTGGGCATGGTGGCACATGCCTGTAATATCAGCTAACATGGGAGGCTGAGGCAGGAGAAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CACTTGAACCANGGAGGGGGAGGTTGCAGTGAGCCGAAATCACACCACTTCACTGCAGCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CACTTGAACCANGGAGGGGGAGGTTGCAGTGAGCCGAAATCACACCACTTCACTGCAGCC  540

Query  541  TGGGCAACAAAGCAAGACTGTCTCAAAAAGAAAAA  575
          ||||||||||||||||||||||||||||
Sbjct   541  TGGGCAACAAAGCAAGACTGTCTCAAAAAGAAAAA  575
```

Sequence 510 matched with Sequence 151

Query= Sequence ID 510
Length=430

SEQ ID NO: 151

ALIGNMENTS

Identities = 430/430 (100%), Gaps = 0/430 (0%)

Query	1	CACTGTCATTCCCAGGAGGCTTTGGAGTCAGAACTGGATTCAAATTCTGACTNTATGTTG	60
Sbjct	1	CACTGTCATTCCCAGGAGGCTTTGGAGTCAGAACTGGATTCAAATTCTGACTNTATGTTG	60
Query	61	TGTGACTTGGGCCAATAGCTTCTTTNTGTGCCTCAGTTTCTTTAGCTGTAAATANACGGG	120
Sbjct	61	TGTGACTTGGGCCAATAGCTTCTTTNTGTGCCTCAGTTTCTTTAGCTGTAAATANACGGG	120
Query	121	TAGGTCACCCCTTACCCCATAGGTTATGGGGAAAGTTACAGAAAATGGTCAGCTGGGCNC	180
Sbjct	121	TAGGTCACCCCTTACCCCATAGGTTATGGGGAAAGTTACAGAAAATGGTCAGCTGGGCNC	180
Query	181	AGTGGCTCAAGCCTGTGGTCCCAGCNCCTTGGGAGGCCAAGGTGAGCAGATTGCTTGAGC	240
Sbjct	181	AGTGGCTCAAGCCTGTGGTCCCAGCNCCTTGGGAGGCCAAGGTGAGCAGATTGCTTGAGC	240
Query	241	CCAGGAGTTTGACACCAGTNTGGCAACGTGACGAAACCCTATCNCTGTGAAAAATACAAA	300
Sbjct	241	CCAGGAGTTTGACACCAGTNTGGCAACGTGACGAAACCCTATCNCTGTGAAAAATACAAA	300
Query	301	AAATTAGCCAGGCATGGTGGTGTGTCTGTGGTTCCAGCTGCTTGAGAGTTTGAAGTGG	360
Sbjct	301	AAATTAGCCAGGCATGGTGGTGTGTCTGTGGTTCCAGCTGCTTGAGAGTTTGAAGTGG	360
Query	361	GAGGATCACCTGAGCCCAGAAGGTCGAGGCTGCAGTGAGCTGTGATCGCGTCACTGCACT	420
Sbjct	361	GAGGATCACCTGAGCCCAGAAGGTCGAGGCTGCAGTGAGCTGTGATCGCGTCACTGCACT	420
Query	421	CCAGCCTGGC	430
Sbjct	421	CCAGCCTGGC	430

Sequence 512 matched with Sequence 152

Query= Sequence ID 512
Length=631

SEQ ID NO: 152

ALIGNMENTS

Identities = 631/631 (100%), Gaps = 0/631 (0%)

Query	1	GTGAGCGGTGGTGGTTTATTCTTCCGTGGAGTTAAGGGCTCCGTGGACATCTCAGGTCTT	60
Sbjct	1	GTGAGCGGTGGTGGTTTATTCTTCCGTGGAGTTAAGGGCTCCGTGGACATCTCAGGTCTT	60
Query	61	CAGGGTCTTCCATCTGGAACATATAAAGTTTCAGAAAACATGTCTCGAAGATATGACTCC	120
Sbjct	61	CAGGGTCTTCCATCTGGAACATATAAAGTTTCAGAAAACATGTCTCGAAGATATGACTCC	120
Query	121	AGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATATGCCATGGAAGCT	180
Sbjct	121	AGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATATGCCATGGAAGCT	180
Query	181	ATTGGACATGCAGGCACCTGTTTGGGAATTTTAGCAAATGATGGTGTGTTTGCTTGCAGCA	240
Sbjct	181	ATTGGACATGCAGGCACCTGTTTGGGAATTTTAGCAAATGATGGTGTGTTTGCTTGCAGCA	240
Query	241	GAGAGACNCAACATCCACAAGCTTCTTGATGAAGTCtttttttCTGAAAAAATTTATAAA	300
Sbjct	241	GAGAGACNCAACATCCACAAGCTTCTTGATGAAGCTTTTTTTTCTGAAAAAATTTATAAA	300
Query	301	CTCAATGAGGACATGGCTTGCAGTGTGGCAGGCATAACTTCTGATGCTAATGTTCTGACT	360
Sbjct	301	CTCAATGAGGACATGGCTTGCAGTGTGGCAGGCATAACTTCTGATGCTAATGTTCTGACT	360
Query	361	AATGAACTAAGGCTCATTGCTCAAAGGTATTTATTACAGTATCAGGAGCCAATACCTTGT	420
Sbjct	361	AATGAACTAAGGCTCATTGCTCAAAGGTATTTATTACAGTATCAGGAGCCAATACCTTGT	420
Query	421	GAGCAGTTGGTTACAGCGCTGTGTGATATCAAACAAGCTTATACACAATTTGGAGGAAAA	480
Sbjct	421	GAGCAGTTGGTTACAGCGCTGTGTGATATCAAACAAGCTTATACACAATTTGGAGGAAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CGTCCCTTTGGTGTTTCATTGCTGTACATTGGCTGGGATAAGCACTATGGCTTTCAGCTC  540
          |||
Sbjct  481  CGTCCCTTTGGTGTTTCATTGCTGTACATTGGCTGGGATAAGCACTATGGCTTTCAGCTC  540

Query  541  TATCAGAGTGACCCTAGTGGAAATTCGGGGGATGGGAAGGCCACATGCATTGGAAATAAT  600
          |||
Sbjct  541  TATCAGAGTGACCCTAGTGGAAATTCGGGGGATGGGAAGGCCACATGCATTGGAAATAAT  600

Query  601  ANCGCTGCAGCTGTGTCAATGTTGAAACAAG  631
          |||
Sbjct  601  ANCGCTGCAGCTGTGTCAATGTTGAAACAAG  631
```

Sequence 513 matched with Sequence 153

Query= Sequence ID 513
Length=646

SEQ ID NO: 153

ALIGNMENTS

Identities = 646/646 (100%), Gaps = 0/646 (0%)

Query	1	tttttttttttATAAACTCCAATCATTTCCAGAGCTACTTAGCTCAGCATCtttttttttCC	60
Sbjct	1	TTTTTTTTTTTATAAACTCCAATCATTTCCAGAGCTACTTAGCTCAGCATCTTTTTTTTCC	60
Query	61	ACGCTCTTAAGTTGTGTTTATACATTTTTGATACAGTTAGATTGTTTTGTCACATTCTT	120
Sbjct	61	ACGCTCTTAAGTTGTGTTTATACATTTTTGATACAGTTAGATTGTTTTGTCACATTCTT	120
Query	121	CATTCTATCCTGGGATCCCCCAACCACCTAAGTGGATTTTTTGATAATTGCGATGCTTTA	180
Sbjct	121	CATTCTATCCTGGGATCCCCCAACCACCTAAGTGGATTTTTTGATAATTGCGATGCTTTA	180
Query	181	AGGATAACTCTTCATTCTGNAAAGGGCTATGGGTTTTGGCAAATGCAGAGTCATGTATCC	240
Sbjct	181	AGGATAACTCTTCATTCTGNAAAGGGCTATGGGTTTTGGCAAATGCAGAGTCATGTATCC	240
Query	241	AAGATTACAATATCGCACAGAAGAGTTTCATCACTATATAAACTCACCAGTCTTCCTCC	300
Sbjct	241	AAGATTACAATATCGCACAGAAGAGTTTCATCACTATATAAACTCACCAGTCTTCCTCC	300
Query	301	TATTCAACCATCTCCATGCCTTCTTCCCAGCCCTAACTCCTTAAACCACTCATATCTTT	360
Sbjct	301	TATTCAACCATCTCCATGCCTTCTTCCCAGCCCTAACTCCTTAAACCACTCATATCTTT	360
Query	361	ACTATTGCTATAGTATTGCCTCTTCCACCATGTGCATATAAATGGAAACATACAGTATTAG	420
Sbjct	361	ACTATTGCTATAGTATTGCCTCTTCCACCATGTGCATATAAATGGAAACATACAGTATTAG	420
Query	421	TCTTCTCAAACCTAGTTTCTTTTACCTAACAACATGCATTTAAGATTCATAGTGTCTTTTA	480
Sbjct	421	TCTTCTCAAACCTAGTTTCTTTTACCTAACAACATGCATTTAAGATTCATAGTGTCTTTTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATGACTTGATAGATTATTTCTTTGTAGCTGAATAATATTGCATCTTATAGATGTAACCGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATGACTTGATAGATTATTTCTTTGTAGCTGAATAATATTGCATCTTATAGATGTAACCGT  540

Query  541  TTGTATATCCATATTTTCTCACAGCCTATGACTTGNCCTTTTGATTCTCTGAACAGGCCAT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TTGTATATCCATATTTTCTCACAGCCTATGACTTGNCCTTTTGATTCTCTGAACAGGCCAT  600

Query  601  TCACAAAGCAGAAGTTTTAATTTTATAAAGCTAATGNATCAACTT  646
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TCACAAAGCAGAAGTTTTAATTTTATAAAGCTAATGNATCAACTT  646
```

Sequence 515 matched with Sequence 154

Query= Sequence ID 515
Length=69

SEQ ID NO: 154

ALIGNMENTS

Identities = 69/69 (100%), Gaps = 0/69 (0%)

```
Query  1  CCTGGATGACAGCATATCTGTTTATAGCTCAGTTTACTGAATACTTTAAGCCCACTGTTG  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1  CCTGGATGACAGCATATCTGTTTATAGCTCAGTTTACTGAATACTTTAAGCCCACTGTTG  60

Query  61  AAACCTGCT  69
          ||||||||
Sbjct  61  AAACCTGCT  69
```

Sequence 518 matched with Sequence 155

Query= Sequence ID - 518 nt: 502
Length=502

SEQ ID NO: 155 nt: 502

ALIGNMENTS

Identities = 502/502 (100%), Gaps = 0/502 (0%)

Query	1	GATGCATGTCCAGCATAGGCAGGATTGCTCGGTGGTGAGAAGGTTAGGTCCGGCTCAGAC	60
Sbjct	1	GATGCATGTCCAGCATAGGCAGGATTGCTCGGTGGTGAGAAGGTTAGGTCCGGCTCAGAC	60
Query	61	TGAATAAGAAGAGATAAAATTTGCCTTAAAACTTACCTGGCAGTGGCTTTGCTGCACGGT	120
Sbjct	61	TGAATAAGAAGAGATAAAATTTGCCTTAAAACTTACCTGGCAGTGGCTTTGCTGCACGGT	120
Query	121	CTGAAACCACCTGTTCCACCCCTCTTGACCGAAATTTCTTGTGACACAGAGAAGGGCAA	180
Sbjct	121	CTGAAACCACCTGTTCCACCCCTCTTGACCGAAATTTCTTGTGACACAGAGAAGGGCAA	180
Query	181	AGGTCTGAGCCCAGAGTTGACGGAGGGAGTATTTAGGGTTCACTTCAGGGGCTCCCAAA	240
Sbjct	181	AGGTCTGAGCCCAGAGTTGACGGAGGGAGTATTTAGGGTTCACTTCAGGGGCTCCCAAA	240
Query	241	GCGACAAGATCGTTAGGGAGAGAGGCCAGGGTGGGGACTGGGAATTTAAGGAGAGCTGG	300
Sbjct	241	GCGACAAGATCGTTAGGGAGAGAGGCCAGGGTGGGGACTGGGAATTTAAGGAGAGCTGG	300
Query	301	GAACGGATCCCTTAGGTTACAGGAAGCTTCTGTGCAAGCTGCGAGGATGGCTTGGGCCGAA	360
Sbjct	301	GAACGGATCCCTTAGGTTACAGGAAGCTTCTGTGCAAGCTGCGAGGATGGCTTGGGCCGAA	360
Query	361	GGGTTGCTCTGCCC GCCGCTAGCTGTGAGCTGAGCAAAGCCCTGGGCTCACAGCACCC	420
Sbjct	361	GGGTTGCTCTGCCC GCCGCTAGCTGTGAGCTGAGCAAAGCCCTGGGCTCACAGCACCC	420
Query	421	CAAAAGCCTGTGGCTTCAGTCCTGCGTCTGCACCACACATTCAAAAGGATCGTTTTGTTT	480
Sbjct	421	CAAAAGCCTGTGGCTTCAGTCCTGCGTCTGCACCACACATTCAAAAGGATCGTTTTGTTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TGT TTTTAAAGAAAGGTGANAT  502
          ||||||||||||||||
Sbjct  481  TGT TTTTAAAGAAAGGTGANAT  502
```

Blast comparison trimmed “NAT” from the 3’ end of both sequences and reported 499 identities. The report has been manually corrected for this. “NAT” has been appended to both sequences and identity count has been increased to 502.

Sequence 519 matched with Sequence 156

Query= Sequence ID 519
Length=373

SEQ ID NO: 156

ALIGNMENTS

Identities = 373/373 (100%), Gaps = 0/373 (0%)

Query	1	CTGCGATNGAGTTTTGAGAGGAAGGANTAAAGTNCTCATCTCNGACGGTGAGAAAGATCA	60
Sbjct	1	CTGCGATNGAGTTTTGAGAGGAAGGANTAAAGTNCTCATCTCNGACGGTGAGAAAGATCA	60
Query	61	TNACTAAGGAAACGCAGGGTTGGAAGCAGTGCTGANTGTCCAGTTGAGTTTCATGANCAA	120
Sbjct	61	TNACTAAGGAAACGCAGGGTTGGAAGCAGTGCTGANTGTCCAGTTGAGTTTCATGANCAA	120
Query	121	ACATTTGCTGTGGGACCAGTTTTCATGGNGGTTTGTCAATTTGTCCAGCTGCCTGGAGCT	180
Sbjct	121	ACATTTGCTGTGGGACCAGTTTTCATGGNGGTTTGTCAATTTGTCCAGCTGCCTGGAGCT	180
Query	181	GCTTGTTGAAGGCACAGAATAATCAGGATTAATTGTTNAACTTGTATGAATTTCTTTAT	240
Sbjct	181	GCTTGTTGAAGGCACAGAATAATCAGGATTAATTGTTNAACTTGTATGAATTTCTTTAT	240
Query	241	TTTAAATAGGAATAATATCTGCCTTGGGAGCAAGTTGTAAGAGTTAACTGAAAGCTTNA	300
Sbjct	241	TTTAAATAGGAATAATATCTGCCTTGGGAGCAAGTTGTAAGAGTTAACTGAAAGCTTNA	300
Query	301	GGAAAACTTTCCTTGCTATTTAAGTAGGGCTTTACAAGTTACAATTCTATCACAGTTT	360
Sbjct	301	GGAAAACTTTCCTTGCTATTTAAGTAGGGCTTTACAAGTTACAATTCTATCACAGTTT	360
Query	361	TAAGATTATAAAC	373
Sbjct	361	TAAGATTATAAAC	373

Sequence 521 matched with Sequence 157

Query= Sequence ID 521
Length=155

SEQ ID NO: 157

ALIGNMENTS

Identities = 155/155 (100%), Gaps = 0/155 (0%)

Query	1	GCGGCGCANCTGCGGATCCANAAGGNCATAAACGANCNGAACCTGCCCAANNCGTGTGAT	60
Sbjct	1	GCGGCGCANCTGCGGATCCANAAGGNCATAAACGANCNGAACCTGCCCAANNCGTGTGAT	60
Query	61	ATCACCTTCTNAGATCCAGACNACCTCCTCAACTTCAAGCTGGTCATCTGTCCTGATGAG	120
Sbjct	61	ATCACCTTCTNAGATCCAGACNACCTCCTCAACTTCAAGCTGGTCATCTGTCCTGATGAG	120
Query	121	GGCTTCNACAAGAGTGGGAAGTTTGTCTCAAAAAA	155
Sbjct	121	GGCTTCNACAAGAGTGGGAAGTTTGTCTCAAAAAA	155

Sequence 523 matched with Sequence 158

Query= Sequence ID - 523 nt: 585
Length=585

SEQ ID NO: 158 nt: 585

ALIGNMENTS

Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query	1	GATTTACTGTGGGAATTTGCTCATGCAATTATGGAAACCTAGAAGTCCCATAATATGCCA	60
Sbjct	1	GATTTACTGTGGGAATTTGCTCATGCAATTATGGAAACCTAGAAGTCCCATAATATGCCA	60
Query	61	TCTTCAAGCTGGAATCCCAGGAAAGCAGGTGGTGTAACTCTGAGATTGAAGTCTTGAGAA	120
Sbjct	61	TCTTCAAGCTGGAATCCCAGGAAAGCAGGTGGTGTAACTCTGAGATTGAAGTCTTGAGAA	120
Query	121	CCGGGGGAGTCAATGGTGTAACTCCCAATCTAGGGCTTAAGGCCCAAGGACCAGGGCTGC	180
Sbjct	121	CCGGGGGAGTCAATGGTGTAACTCCCAATCTAGGGCTTAAGGCCCAAGGACCAGGGCTGC	180
Query	181	TGGTGTGCAGATGCAAATCCTGGAGTTCAAAGGATTGAGAACCAGGAGCTCTGGTGTCTG	240
Sbjct	181	TGGTGTGCAGATGCAAATCCTGGAGTTCAAAGGATTGAGAACCAGGAGCTCTGGTGTCTG	240
Query	241	AGGGCAGTAGAAGATGGATGTTCCAGCTCAAGAAGGGAAAGTAAGAATCCGTCCTTCCTC	300
Sbjct	241	AGGGCAGTAGAAGATGGATGTTCCAGCTCAAGAAGGGAAAGTAAGAATCCGTCCTTCCTC	300
Query	301	CACTTTTTTGTTCATTTCAGATGAGCCCTCAATGGACTGAACGATGCTCACCACACTGT	360
Sbjct	301	CACTTTTTTGTTCATTTCAGATGAGCCCTCAATGGACTGAACGATGCTCACCACACTGT	360
Query	361	GAGGGCTGGTCTTCTTTATTCAATCCACTGACTTAAGTGCTGATCTCTTCTGGAAACACC	420
Sbjct	361	GAGGGCTGGTCTTCTTTATTCAATCCACTGACTTAAGTGCTGATCTCTTCTGGAAACACC	420
Query	421	TTCACAGACACACCCAGAAATAATGTTCTACCAGCCATGGGCCTGTTACTTAGCCCAGTC	480
Sbjct	421	TTCACAGACACACCCAGAAATAATGTTCTACCAGCCATGGGCCTGTTACTTAGCCCAGTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAGTTGACACAGAAAATTAGCTATCACAACATCtgtgtgtgtatatatacatatgtatttgc  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AAGTTGACACAGAAAATTAGCTATCACAACATCTGTGTGTGTATATACATATGTATTTGC  540

Query  541  atgtgtgtgtatatatggngtatatatattcatgtgtgtgtatat  585
          ||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATGTGTGTGTATATATGGNGTATATATATTCATGTGTGTGTATAT  585
```

Sequence 524 matched with Sequence 159

Query= Sequence ID 524
Length=454

SEQ ID NO: 159

ALIGNMENTS

Identities = 454/454 (100%), Gaps = 0/454 (0%)

Query	1	CTTTTGCCAGTAGGCCCCCTGAGTAGGTTCTCTATCTTTTGGCATGACCCCAAGTCT	60
Sbjct	1	CTTTTGCCAGTAGGCCCCCTGAGTAGGTTCTCTATCTTTTGGCATGACCCCAAGTCT	60
Query	61	TTGATAACTTCCTTGCTTTCTGATGTGACAAGACATCCAGGGCCAGATTGTCCATATCCT	120
Sbjct	61	TTGATAACTTCCTTGCTTTCTGATGTGACAAGACATCCAGGGCCAGATTGTCCATATCCT	120
Query	121	GCCCCGGATGCACGATGCACTGTTTCTCCAAGAATCCCTGTGTCCTTTGCTGATGATGCC	180
Sbjct	121	GCCCCGGATGCACGATGCACTGTTTCTCCAAGAATCCCTGTGTCCTTTGCTGATGATGCC	180
Query	181	ATGATTTTAAGTTCTCTAATATAGTTTTATCTCTTTGTTTCAGATAATGCTTTTGTGTTC	240
Sbjct	181	ATGATTTTAAGTTCTCTAATATAGTTTTATCTCTTTGTTTCAGATAATGCTTTTGTGTTC	240
Query	241	TCACATGTCCTGctctctctctctctctcATTTTGGTGTTGATCAGTCTTCCATAAGAT	300
Sbjct	241	TCACATGTCCTGCTCTCTCTCTCTCTCATTTTGGTGTTGATCAGTCTTCCATAAGAT	300
Query	301	TGTTTATTTCACTAGTCCTTCATTCTTCTTTTTTCTAAATTTACTCTTCTTGACTAGTAT	360
Sbjct	301	TGTTTATTTCACTAGTCCTTCATTCTTCTTTTTTCTAAATTTACTCTTCTTGACTAGTAT	360
Query	361	CCTGTCACTTCTGAGGACTCATATTTTGGCAACTTGAAAATTATTCTTATTTATTTAAGT	420
Sbjct	361	CCTGTCACTTCTGAGGACTCATATTTTGGCAACTTGAAAATTATTCTTATTTATTTAAGT	420
Query	421	ATATGTTNCTGAAACTCTCATTAGACACATTTTG	454
Sbjct	421	ATATGTTNCTGAAACTCTCATTAGACACATTTTG	454

Sequence 525 matched with Sequence 160

Query= Sequence ID 525
Length=346

SEQ ID NO: 160

ALIGNMENTS

Identities = 346/346 (100%), Gaps = 0/346 (0%)

```
Query 1   GTTaaaaaaaGTAAAAGGAACTCGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCAC  60
          |||
Sbjct 1   GTTAAAAAAGTAAAAGGAACTCGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCAC  60

Query 61  CTGGTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATGTTTAACGGCCGC  120
          |||
Sbjct 61  CTGGTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATGTTTAACGGCCGC  120

Query 121 GGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCTTAAATAGGGACCTGTATGA  180
          |||
Sbjct 121 GGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCTTAAATAGGGACCTGTATGA  180

Query 181 ATGGCTCCACNAGGGTTCANCTGTCTCTTACTTTTAACCAGTGAAATTGACCTGCCCCGTG  240
          |||
Sbjct 181 ATGGCTCCACNAGGGTTCANCTGTCTCTTACTTTTAACCAGTGAAATTGACCTGCCCCGTG  240

Query 241 AAGAGGCGGGCATAACACAGCTGaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  300
          |||
Sbjct 241 AAGAGGCGGGCATAACACAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  300

Query 301 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaTTTT  346
          |||
Sbjct 301 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTT  346
```

Sequence 526 matched with Sequence 161

Query= Sequence ID - 526 nt: 516
Length=516

SEQ ID NO: 161 nt: 516

ALIGNMENTS

Identities = 516/516 (100%), Gaps = 0/516 (0%)

Query	1	CTTTTCATGGTCTCTTGTTCAATTAATCATCTAAAATCCAAGCNCAGAGAATTCAATTTTA	60
Sbjct	1	CTTTTCATGGTCTCTTGTTCAATTAATCATCTAAAATCCAAGCNCAGAGAATTCAATTTTA	60
Query	61	GATGGTCTCCAGAGCAGAATTTGATGTATAATCTTAATTACAAATCATAGATAATTAATA	120
Sbjct	61	GATGGTCTCCAGAGCAGAATTTGATGTATAATCTTAATTACAAATCATAGATAATTAATA	120
Query	121	TTGNTTACAAAATCANAATACGATTAGAGGTAGGGATCCTGCACACACCCTATTTTCCTC	180
Sbjct	121	TTGNTTACAAAATCANAATACGATTAGAGGTAGGGATCCTGCACACACCCTATTTTCCTC	180
Query	181	CCCAGTGTCTGACCGAGAGACTAATTAATAATTCAAGGAACTTACAGTGAATGANAACC	240
Sbjct	181	CCCAGTGTCTGACCGAGAGACTAATTAATAATTCAAGGAACTTACAGTGAATGANAACC	240
Query	241	CATGGTTTTGCTTAATTATCAGAACAGCTAGATCTGAGAACAGCTGTCTCCACATGGAT	300
Sbjct	241	CATGGTTTTGCTTAATTATCAGAACAGCTAGATCTGAGAACAGCTGTCTCCACATGGAT	300
Query	301	AGACACTTATTCCACCCATTTGCAGGTAGAATAGCTGGCAATAATAAGTCCTTCCCATTG	360
Sbjct	301	AGACACTTATTCCACCCATTTGCAGGTAGAATAGCTGGCAATAATAAGTCCTTCCCATTG	360
Query	361	GATATGTTGAAAGGTGCCTGCCATGGCATAGTTGCCACAAGAGAGGAAGAAATGGACACA	420
Sbjct	361	GATATGTTGAAAGGTGCCTGCCATGGCATAGTTGCCACAAGAGAGGAAGAAATGGACACA	420
Query	421	AATGTAGGCTGTTTTCAGGGCANAGGGAAGGTGGGAGGAAACCAANTTGCTGGTTTTTCAC	480
Sbjct	421	AATGTAGGCTGTTTTCAGGGCANAGGGAAGGTGGGAGGAAACCAANTTGCTGGTTTTTCAC	480

PATENT SEQUENCE ALIGNMENT

Query	481	ACACCCTCTGGGGAACACCCATGCACCTATGANATG	516
Sbjct	481	ACACCCTCTGGGGAACACCCATGCACCTATGANATG	516

Sequence 527 matched with Sequence 162

Query= Sequence ID 527
Length=385

SEQ ID NO: 162

ALIGNMENTS

Identities = 385/385 (100%), Gaps = 0/385 (0%)

Query	1	GACAAAAGCTGAGAGAAttttttCTTGAATATTTGCACTAAAAGATAGGTTAAAATTCT	60
Sbjct	1	GACAAAAGCTGAGAGAATTTTCTTGAATATTTGCACTAAAAGATAGGTTAAAATTCT	60
Query	61	TCAGGCTGAAGAGAGCATACCAGGTGGAGATTTGGATCTACAAAAGGAAGGAAGATTTG	120
Sbjct	61	TCAGGCTGAAGAGAGCATACCAGGTGGAGATTTGGATCTACAAAAGGAAGGAAGATTTG	120
Query	121	GAAATGGATTTGGCACCATTGACTCAATTTCCAGAACAAGAAAGCAGGGACAGTTTGGG	180
Sbjct	121	GAAATGGATTTGGCACCATTGACTCAATTTCCAGAACAAGAAAGCAGGGACAGTTTGGG	180
Query	181	AAGCTCAAGACACACTGCCCATGAGCAGCAATTTGGACCTCCTGCTGCATCCACTGTGCA	240
Sbjct	181	AAGCTCAAGACACACTGCCCATGAGCAGCAATTTGGACCTCCTGCTGCATCCACTGTGCA	240
Query	241	TCAAACACACACTGTACAGACAAAGACTCCCAGGAAAAGAAGTATAAACATGGACTAACA	300
Sbjct	241	TCAAACACACACTGTACAGACAAAGACTCCCAGGAAAAGAAGTATAAACATGGACTAACA	300
Query	301	CAGAGATGGGCAAACCTACAGCCTGTGACCCAGCCACCTGTTTATGTAGAATCCAAAGTAA	360
Sbjct	301	CAGAGATGGGCAAACCTACAGCCTGTGACCCAGCCACCTGTTTATGTAGAATCCAAAGTAA	360
Query	361	GAATCTTTAACTTACACATAAACTT	385
Sbjct	361	GAATCTTTAACTTACACATAAACTT	385

Sequence 530 matched with Sequence 165

Query= Sequence ID - 530 nt: 660
Length=660

SEQ ID NO: 165 nt: 660

ALIGNMENTS

Identities = 660/660 (100%), Gaps = 0/660 (0%)

Query	1	GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGAAGGAACCA	60
Sbjct	1	GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGAAGGAACCA	60
Query	61	TCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGCCTTCCTGA	120
Sbjct	61	TCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGCCTTCCTGA	120
Query	121	TTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAGAACTTAGATGTC	180
Sbjct	121	TTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAGAACTTAGATGTC	180
Query	181	AGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATCAAAGAACTGAGAGTGA	240
Sbjct	181	AGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATCAAAGAACTGAGAGTGA	240
Query	241	TTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGTAAAGCTTTCTGATGGAAGAN	300
Sbjct	241	TTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGTAAAGCTTTCTGATGGAAGAN	300
Query	301	AGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANAGGGTTGTGGANAAGTTTTTGAAGA	360
Sbjct	301	AGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANAGGGTTGTGGANAAGTTTTTGAAGA	360
Query	361	GGGCTGAGAATTCATaaaaaaTTCATTCTCTGTGGTATCCAAGAATCAGTGAAGATGCC	420
Sbjct	361	GGGCTGAGAATTCATAAAAAAATTCATTCTCTGTGGTATCCAAGAATCAGTGAAGATGCC	420
Query	421	AGTGAAACTTCAAGCAAATCTACTTCAACACTTCATGTATTGTGTGGGTCTGTTGTAGGG	480
Sbjct	421	AGTGAAACTTCAAGCAAATCTACTTCAACACTTCATGTATTGTGTGGGTCTGTTGTAGGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTGCCAGATGCAATACAAGATTCCTGGTTAAATTTGAATTCAGTAAACAATGAATAGTT	540
Sbjct	481	TTGCCAGATGCAATACAAGATTCCTGGTTAAATTTGAATTCAGTAAACAATGAATAGTT	540
Query	541	TTTCATTGTACCATGAAATATCCAGAACATACTTATATGTAAAGTATTATTTATTTGAAT	600
Sbjct	541	TTTCATTGTACCATGAAATATCCAGAACATACTTATATGTAAAGTATTATTTATTTGAAT	600
Query	601	CTACAAAAACAACAAATAATTTTGTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA	660
Sbjct	601	CTACAAAAACAACAAATAATTTTGTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA	660

Sequence 532 matched with Sequence 166

Query= Sequence ID 532
Length=542

SEQ ID NO: 166

ALIGNMENTS

Identities = 542/542 (100%), Gaps = 0/542 (0%)

Query	1	GAATTGTGATAGTTCAGCTTGAATGTCTCTTAGAGGGTGGGCTTTTGTGATGAGGGAGG	60
Sbjct	1	GAATTGTGATAGTTCAGCTTGAATGTCTCTTAGAGGGTGGGCTTTTGTGATGAGGGAGG	60
Query	61	GGAAACtttttttttttCTATAGACTTTTTTCANATAACATCTTCTGAGTCATAACCAGC	120
Sbjct	61	GGAAACTTTTTTTTTTTCTATAGACTTTTTTCANATAACATCTTCTGAGTCATAACCAGC	120
Query	121	CTGGCAGTATGATGGCCTANATGCAGAGAAAACAGCTCCTTGGTGAATTGATAAGTAAAG	180
Sbjct	121	CTGGCAGTATGATGGCCTANATGCAGAGAAAACAGCTCCTTGGTGAATTGATAAGTAAAG	180
Query	181	GCAGAAAAGATTATATGTCATACCTCCATTGGGGAATAAGCATAACCCTGAGATTCTTAC	240
Sbjct	181	GCAGAAAAGATTATATGTCATACCTCCATTGGGGAATAAGCATAACCCTGAGATTCTTAC	240
Query	241	TACTGATGAGAACATTATCTGCATATGCCAAAAAATTTTAAGCAAATGAAAGCTACCAAT	300
Sbjct	241	TACTGATGAGAACATTATCTGCATATGCCAAAAAATTTTAAGCAAATGAAAGCTACCAAT	300
Query	301	TTAAAGTTACGGAATCTACCATTTTAAAGTTAATTGCTTGTCAAGCTATAACCACAAAAA	360
Sbjct	301	TTAAAGTTACGGAATCTACCATTTTAAAGTTAATTGCTTGTCAAGCTATAACCACAAAAA	360
Query	361	TAATGAATTGATGAGAAATACAATGAAGAGGCAATGTCCATCTCAAAATACTGCTTTTAC	420
Sbjct	361	TAATGAATTGATGAGAAATACAATGAAGAGGCAATGTCCATCTCAAAATACTGCTTTTAC	420
Query	421	AAAAGCAGAATAAAAGCGAAAAGAAATGAAATGTTACACTACATTAATCCTGGAATAAA	480
Sbjct	421	AAAAGCAGAATAAAAGCGAAAAGAAATGAAATGTTACACTACATTAATCCTGGAATAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGAAGCCGAAATAAATGAGAGATGAGTTGGGATCAAGTGGGATTGANGANGCTGTGCTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGAAGCCGAAATAAATGAGAGATGAGTTGGGATCAAGTGGGATTGANGANGCTGTGCTGT  540

Query  541  GT   542
          ||
Sbjct  541  GT   542
```


Sequence 534 matched with Sequence 168

Query= Sequence ID 534
Length=472

SEQ ID NO: 168

ALIGNMENTS

Identities = 472/472 (100%), Gaps = 0/472 (0%)

Query	1	GGGAAGGGAGCTATGAggtgtgtgtgtgtgtATGGACTCACTCCCAGGTTACCTGGCCA	60
Sbjct	1	GGGAAGGGAGCTATGAGTGTGTGTGTGTGTATGGACTCACTCCCAGGTTACCTGGCCA	60
Query	61	CAGGTGCACCCTTCCCACACCCTTTACATTCCCCAGAGCCAAGGGAGTTAAGTTTGCAG	120
Sbjct	61	CAGGTGCACCCTTCCCACACCCTTTACATTCCCCAGAGCCAAGGGAGTTAAGTTTGCAG	120
Query	121	TTACAGGCCAGTTCTCCAGCTCTCCATCTTANAGAGACAGGTCACCTTGCAGGCCTGCTT	180
Sbjct	121	TTACAGGCCAGTTCTCCAGCTCTCCATCTTANAGAGACAGGTCACCTTGCAGGCCTGCTT	180
Query	181	GCAGGAAATGAATCCAGCAGCCAACTCGAATCCCCCTAGGGCTCAGGCACTGAGGGCCTG	240
Sbjct	181	GCAGGAAATGAATCCAGCAGCCAACTCGAATCCCCCTAGGGCTCAGGCACTGAGGGCCTG	240
Query	241	GGGACAGTGGAGCATATGGGTGGGAGACAGATGGAGGGTACCCTATTTACAACTGAGTCA	300
Sbjct	241	GGGACAGTGGAGCATATGGGTGGGAGACAGATGGAGGGTACCCTATTTACAACTGAGTCA	300
Query	301	GCCAAGCCACTGATGGGAATATACAGATTTAGGTGCTAAACCGTTTATTTTCCACGGATG	360
Sbjct	301	GCCAAGCCACTGATGGGAATATACAGATTTAGGTGCTAAACCGTTTATTTTCCACGGATG	360
Query	361	AGTCACAATCTGAAGAATCAAACCTCCATCCTGAAAATCTATATGTTTCAAAACCACTTG	420
Sbjct	361	AGTCACAATCTGAAGAATCAAACCTCCATCCTGAAAATCTATATGTTTCAAAACCACTTG	420
Query	421	CCATCCTGTTAGATTGCCAGTTCCTGGGACCAGGCCTCANACTGTGAAAGTA	472
Sbjct	421	CCATCCTGTTAGATTGCCAGTTCCTGGGACCAGGCCTCANACTGTGAAAGTA	472

Sequence 560 matched with Sequence 169

Query= Sequence ID 560
Length=638

SEQ ID NO: 169

ALIGNMENTS

Identities = 638/638 (100%), Gaps = 0/638 (0%)

Query	1	GGCGGAGGTTGCAGTGAGCTGAGATGGCGCCATTGCTCTCCCAGCCTGGGTGACAAGAGC	60
Sbjct	1	GGCGGAGGTTGCAGTGAGCTGAGATGGCGCCATTGCTCTCCCAGCCTGGGTGACAAGAGC	60
Query	61	AAAACCTCCGTCTCaaaaaaaaaaaaaaaaaaaaaGCAATTTACTTAAAAACATACAAAC	120
Sbjct	61	AAAACCTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAGCAATTTACTTAAAAACATACAAAC	120
Query	121	ACAGAGACAAGTATTTTTGAGAAACAAATACCTtttttcattttttATACCAATGTAACAA	180
Sbjct	121	ACAGAGACAAGTATTTTTGAGAAACAAATACCTTTTTTCATTTTTTATACCAATGTAACAA	180
Query	181	TAATCCATTAAACACACCTTTACTAACTGTTTTCTAGGAGTCTGATATGATGAGGAAATA	240
Sbjct	181	TAATCCATTAAACACACCTTTACTAACTGTTTTCTAGGAGTCTGATATGATGAGGAAATA	240
Query	241	GGTAAACCTTTAATAGCCAGTACTAAATTAGAGTGGCACAACCTTTCACTGGGAAAAAAGA	300
Sbjct	241	GGTAAACCTTTAATAGCCAGTACTAAATTAGAGTGGCACAACCTTTCACTGGGAAAAAAGA	300
Query	301	TGGGTATTTTACTTTTCTGTTTTAGAAAAGTGGCTTGACAACAGTATGCTTATGTCTTAG	360
Sbjct	301	TGGGTATTTTACTTTTCTGTTTTAGAAAAGTGGCTTGACAACAGTATGCTTATGTCTTAG	360
Query	361	AGTTTGAAATTCAAGTTCTTGAACATTATTAATGGCTACAATCATTACATCCACATTGG	420
Sbjct	361	AGTTTGAAATTCAAGTTCTTGAACATTATTAATGGCTACAATCATTACATCCACATTGG	420
Query	421	GCTGTATTCTTGATGAATCCAAAGTGATTTTCACCTCAACTCTGAATTTCACTCTCCTCT	480
Sbjct	421	GCTGTATTCTTGATGAATCCAAAGTGATTTTCACCTCAACTCTGAATTTCACTCTCCTCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTTGAATATAATACAACCATCTCACTAGAGGAAGCATTTCAGTCTTTTCTGATTGGAGAT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTTGAATATAATACAACCATCTCACTAGAGGAAGCATTTCAGTCTTTTCTGATTGGAGAT  540

Query  541  TCATTATTGTTTTAGATAATGTTTTCATTTGCTTATGGGTATATAAAAAATTTTATCTTA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TCATTATTGTTTTAGATAATGTTTTCATTTGCTTATGGGTATATAAAAAATTTTATCTTA  600

Query  601  AAAATATTTCTCTCATTTAGCTAGCAACATTGTTTTC  638
          |||||||||||||||||||||||||||||||
Sbjct   601  AAAATATTTCTCTCATTTAGCTAGCAACATTGTTTTC  638
```

Sequence 561 matched with Sequence 170

Query= Sequence ID 561
Length=512

SEQ ID NO: 170

ALIGNMENTS

Identities = 512/512 (100%), Gaps = 0/512 (0%)

Query	1	CTCAGGGTGATCTCTGAACCCAAACTTGCCCCAAAGAAGGTTGCTCTGTCCTCTCCACAT	60
Sbjct	1	CTCAGGGTGATCTCTGAACCCAAACTTGCCCCAAAGAAGGTTGCTCTGTCCTCTCCACAT	60
Query	61	CCCCATCTCCTCCCTAGGGCCTTGTTGGGGAGAGGCTCCTCCATCTTTCCCAAGTCACAC	120
Sbjct	61	CCCCATCTCCTCCCTAGGGCCTTGTTGGGGAGAGGCTCCTCCATCTTTCCCAAGTCACAC	120
Query	121	CATCGTTTCCTACGTGGTCTGGACAAGAGCAAGAGCACACCTTGTCCTCCACCTTCTCCAG	180
Sbjct	121	CATCGTTTCCTACGTGGTCTGGACAAGAGCAAGAGCACACCTTGTCCTCCACCTTCTCCAG	180
Query	181	AGCAGCCAGAACCCACCTCAGGTGCCTTCCCCATCCGGTGCAGTTAAGGCACTTCTGCCA	240
Sbjct	181	AGCAGCCAGAACCCACCTCAGGTGCCTTCCCCATCCGGTGCAGTTAAGGCACTTCTGCCA	240
Query	241	GCACCATGGTATGAGCACTAGACTTGGAGTTAAGATTTGAGAGCCCCCTCTGTCACTGTG	300
Sbjct	241	GCACCATGGTATGAGCACTAGACTTGGAGTTAAGATTTGAGAGCCCCCTCTGTCACTGTG	300
Query	301	GAAGCTTGAGCATGTTGCTTGATCTCTCTGAACCTTGTTGTTTCTCATCTGTGAAAGGTGA	360
Sbjct	301	GAAGCTTGAGCATGTTGCTTGATCTCTCTGAACCTTGTTGTTTCTCATCTGTGAAAGGTGA	360
Query	361	TAATGTGGGGCTGCTGTGAGATTTAAAGGACATAATGCACCTACGGTCCAAGCACTGCCT	420
Sbjct	361	TAATGTGGGGCTGCTGTGAGATTTAAAGGACATAATGCACCTACGGTCCAAGCACTGCCT	420
Query	421	GGAATACAGCANAAGCTCAACAGATACTGGACAACCCATCCCCTTAGTAGAGGCACTAAC	480
Sbjct	421	GGAATACAGCANAAGCTCAACAGATACTGGACAACCCATCCCCTTAGTAGAGGCACTAAC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CATGTGACCCAAGGCAAAAGTGCTTaaaaaaa	512
Sbjct	481	CATGTGACCCAAGGCAAAAGTGCTTAAAAAAA	512

Sequence 562 matched with Sequence 171

Query= Sequence ID - 562 nt: 580
Length=580

SEQ ID NO: 171 nt: 580

ALIGNMENTS

Identities = 580/580 (100%), Gaps = 0/580 (0%)

Query	1	ATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTG	60
Sbjct	1	ATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTG	60
Query	61	GAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGC	120
Sbjct	61	GAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGC	120
Query	121	AAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCGT	180
Sbjct	121	AAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCGT	180
Query	181	GATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCACTGGACAAGAAGGCTGCTGGA	240
Sbjct	181	GATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCACTGGACAAGAAGGCTGCTGGA	240
Query	241	GCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTA	300
Sbjct	241	GCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTA	300
Query	301	ATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTC	360
Sbjct	301	ATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTC	360
Query	361	ATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTTAATGATAACAATGCATCGTAAAACC	420
Sbjct	361	ATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTTAATGATAACAATGCATCGTAAAACC	420
Query	421	TTCAGAAGGAAAGGAGAATgttttgtggaccactttggttttctttttgCGTgtggcag	480
Sbjct	421	TTCAGAAGGAAAGGAGAATGTTTTGTGGACCACTTTGGTTTTCTTTTTGCGTGTGGCAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ttttaagttattagttttttaaatacagtactttttaATGGAAACAACTTGACCAAAAATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTTTAAGTTATTAGTTTTTAAATCAGTACTTTTAAATGGAAACAACTTGACCAAAAATT  540

Query  541  TGTCACAGAATTTTGAGACCCATTAAAAAAGTTAAATGAG  580
          ||||||||||||||||||||||||||||||||
Sbjct   541  TGTCACAGAATTTTGAGACCCATTAAAAAAGTTAAATGAG  580
```


Sequence 563 matched with Sequence 172

Query= Sequence ID 563
Length=541

SEQ ID NO: 172

ALIGNMENTS

Identities = 541/541 (100%), Gaps = 0/541 (0%)

Query	1	GCAACCTGCACAACCCCGCCCTGTTTCGAGGGCCGGAGCCCTGCCGTGTGGGAGCTGGCCG	60
Sbjct	1	GCAACCTGCACAACCCCGCCCTGTTTCGAGGGCCGGAGCCCTGCCGTGTGGGAGCTGGCCG	60
Query	61	AGGAGTATCTGGACATCGTGCGGGAGCACCCCTGCCCCCTGTCCTACGTCCGGGCCCCACC	120
Sbjct	61	AGGAGTATCTGGACATCGTGCGGGAGCACCCCTGCCCCCTGTCCTACGTCCGGGCCCCACC	120
Query	121	TCTTCAAGCTGTGGCACCACACGCTGCAGGTGCACCAGGAGCTGCGAGAGGAGCTGGCCA	180
Sbjct	121	TCTTCAAGCTGTGGCACCACACGCTGCAGGTGCACCAGGAGCTGCGAGAGGAGCTGGCCA	180
Query	181	AGGTGAANACCCTGGAGGGCATCGCTGCTGTGAGCCAGGAGCTGAAGCTGCGGTGTCAGG	240
Sbjct	181	AGGTGAANACCCTGGAGGGCATCGCTGCTGTGAGCCAGGAGCTGAAGCTGCGGTGTCAGG	240
Query	241	AGGAGATATCCAGGCAGGAGGGAGCGAAGCCCACCGGCGACTTGCCCTTCCACTGGATCT	300
Sbjct	241	AGGAGATATCCAGGCAGGAGGGAGCGAAGCCCACCGGCGACTTGCCCTTCCACTGGATCT	300
Query	301	GCCAGCCCTACATCCGGCCGGGGCCCCAGGGAGGGGAGCAAGGAGAAGGCAGGTGCGCGCA	360
Sbjct	301	GCCAGCCCTACATCCGGCCGGGGCCCCAGGGAGGGGAGCAAGGAGAAGGCAGGTGCGCGCA	360
Query	361	GCAAGCGGGCCCTGGAGGAAGAGGAGGGTGGCACGGAGGTCCTGTCCAAGAACAAGCAAA	420
Sbjct	361	GCAAGCGGGCCCTGGAGGAAGAGGAGGGTGGCACGGAGGTCCTGTCCAAGAACAAGCAAA	420
Query	421	AGAAGCAGCTGAGGAACCCCCACAAGACCTTCGACCCCTCTCTGAACCAAAAATATGCAAA	480
Sbjct	421	AGAAGCAGCTGAGGAACCCCCACAAGACCTTCGACCCCTCTCTGAACCAAAAATATGCAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTGTGACCAGTGTGGAAACCCAAAGGGCAACAGATGTGTGTTTCAGCCTGTGCCGCGGNTT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTGTGACCAGTGTGGAAACCCAAAGGGCAACAGATGTGTGTTTCAGCCTGTGCCGCGGNTT  540

Query  541  G   541
          |
Sbjct   541  G   541
```

Sequence 564 matched with Sequence 173

Query= Sequence ID - 564 nt: 671
Length=671

SEQ ID NO: 173 nt: 671

ALIGNMENTS

Identities = 671/671 (100%), Gaps = 0/671 (0%)

```
Query 1   GGAATAGAATTTTAAATAGTAATAACTGCTTGtttttttGTGCAAGTACTTTTATACAT 60
          |||
Sbjct 1   GGAATAGAATTTTAAATAGTAATAACTGCTTGTTTTTTTGTGCAAGTACTTTTATACAT 60

Query 61  AAGATAAACAAAAACCTTACCACCAAACATACCAAATGCACCTCTTTCATAAGTGAGTT 120
          |||
Sbjct 61  AAGATAAACAAAAACCTTACCACCAAACATACCAAATGCACCTCTTTCATAAGTGAGTT 120

Query 121 ACTAAGATTTCTATACCTGGAATATCATGTATGTTTCATTTACTGGATGTTTACATTTTA 180
          |||
Sbjct 121 ACTAAGATTTCTATACCTGGAATATCATGTATGTTTCATTTACTGGATGTTTACATTTTA 180

Query 181 GGAAGGAAAATAGTTTTGTTTATTTAAACAACCTGAATACTTATAAACTGTTGTTCTGGA 240
          |||
Sbjct 181 GGAAGGAAAATAGTTTTGTTTATTTAAACAACCTGAATACTTATAAACTGTTGTTCTGGA 240

Query 241 AGTTATTTATTCCATAAAAAATTTGTTCTTTTGTGCATGAATTTATAATTCCTAAATGAAG 300
          |||
Sbjct 241 AGTTATTTATTCCATAAAAAATTTGTTCTTTTGTGCATGAATTTATAATTCCTAAATGAAG 300

Query 301 ACCAGAAAGTACAAATTGCTGGGAGGAAGAATAGGCTTTATTAATCAACTGATGTCTTGA 360
          |||
Sbjct 301 ACCAGAAAGTACAAATTGCTGGGAGGAAGAATAGGCTTTATTAATCAACTGATGTCTTGA 360

Query 361 TTTTCTAAATGGGAAGATTGCTTTATTTTAACTAATTATGGGAGCAGATTCTTAGC 420
          |||
Sbjct 361 TTTTCTAAATGGGAAGATTGCTTTATTTTAACTAATTATGGGAGCAGATTCTTAGC 420

Query 421 AAACCTCTTTGGAAAAGTTAATGTTATGATGTGCATTAGGCTGCCCCATCGTGTATATAA 480
          |||
Sbjct 421 AAACCTCTTTGGAAAAGTTAATGTTATGATGTGCATTAGGCTGCCCCATCGTGTATATAA 480
```

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATGAAGCAGATTTGATTTTGTATTCTTACGTTTCTCTGCTTTGTAGTTGTGGCTGTACT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATGAAGCAGATTTGATTTTGTATTCTTACGTTTCTCTGCTTTGTAGTTGTGGCTGTACT  540

Query  541  TAAAGAAATACAGAATTCATATATTTAAAAATGTTTAAAATGTGACCCACAGACATTGT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TAAAGAAATACAGAATTCATATATTTAAAAATGTTTAAAATGTGACCCACAGACATTGT  600

Query  601  AAATGGATTNAAAAC TAACATGAAAAATATTCAACCTAAAAGAATTCTTAAC TTCACAAG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  AAATGGATTNAAAAC TAACATGAAAAATATTCAACCTAAAAGAATTCTTAAC TTCACAAG  660

Query  661  TGTTTTACTTC   671
          |||||||||
Sbjct   661  TGTTTTACTTC   671
```

Sequence 565 matched with Sequence 174

Query= Sequence ID 565
Length=607

SEQ ID NO: 174

ALIGNMENTS

Identities = 607/607 (100%), Gaps = 0/607 (0%)

Query	1	CTTGGTTCCGCGTTCCCTGCACAAAATGCCCGGCGAAGCCACAGAAACCGTCCCTGCTAC	60
Sbjct	1	CTTGGTTCCGCGTTCCCTGCACAAAATGCCCGGCGAAGCCACAGAAACCGTCCCTGCTAC	60
Query	61	AGAGCAGGAGTTGCCGCAGCCCCAGGCTGAGACAGGGTCTGGAACAGAATCTGACAGTGA	120
Sbjct	61	AGAGCAGGAGTTGCCGCAGCCCCAGGCTGAGACAGGGTCTGGAACAGAATCTGACAGTGA	120
Query	121	TGAATCAGTACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCACACAACAAGCCCA	180
Sbjct	121	TGAATCAGTACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCACACAACAAGCCCA	180
Query	181	GCTGGCGGCAGCAGCTGAAATCGATGAAGAACCAGTCAGTAAAGCAAAACAGAGTCGGAG	240
Sbjct	181	GCTGGCGGCAGCAGCTGAAATCGATGAAGAACCAGTCAGTAAAGCAAAACAGAGTCGGAG	240
Query	241	TGAAAAGAAGGCACGGAAGGCTATGTCCAAACTGGGTCTTCGGCAGGTTACAGGAGTTAC	300
Sbjct	241	TGAAAAGAAGGCACGGAAGGCTATGTCCAAACTGGGTCTTCGGCAGGTTACAGGAGTTAC	300
Query	301	TAGAGTCACTATCCGGAATCTAAGAATATCCTCTTTGTCATCACAAAACCAGATGTCTA	360
Sbjct	301	TAGAGTCACTATCCGGAATCTAAGAATATCCTCTTTGTCATCACAAAACCAGATGTCTA	360
Query	361	CAAGAGCCCTGCTTCAGATACTTACATAGTTTTTGGGGAAGCCAAGATCGAAGATTTATC	420
Sbjct	361	CAAGAGCCCTGCTTCAGATACTTACATAGTTTTTGGGGAAGCCAAGATCGAAGATTTATC	420
Query	421	CCAGCAAGCACAACTAGCAGCTGCTGAGAAATTCAAAGTTCAAGGTGAAGCTGTCTCAAA	480
Sbjct	421	CCAGCAAGCACAACTAGCAGCTGCTGAGAAATTCAAAGTTCAAGGTGAAGCTGTCTCAAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CATTCAAGAAAACACACAGACTCCA	ACTGTACAAGAGGAGAGTGAAGAGGAAGAGGTCGA	540
Sbjct	481	CATTCAAGAAAACACACAGACTCCA	ACTGTACAAGAGGAGAGTGAAGAGGAAGAGGTCGA	540
Query	541	TGAAACAGGTGTAGAAAGTTAAGGACATAGAATTTGGTCATTGTCACAAAAGCAAATGTGTC	600	
Sbjct	541	TGAAACAGGTGTAGAAAGTTAAGGACATAGAATTTGGTCATTGTCACAAAAGCAAATGTGTC	600	
Query	601	GAGAGCA	607	
Sbjct	601	GAGAGCA	607	

Sequence 566 matched with Sequence 175

Query= Sequence ID 566
Length=583

SEQ ID NO: 175

ALIGNMENTS

Identities = 583/583 (100%), Gaps = 0/583 (0%)

Query	1	GTCACCAAGAGCTTGTGTGTCAGGTTTTCACTTGCTATTCGCAGAGAttttttttAAAGGC	60
Sbjct	1	GTCACCAAGAGCTTGTGTGTCAGGTTTTCACTTGCTATTCGCAGAGATTTTTTTTAAAGGC	60
Query	61	ACTATTTGTAGTGTTAAAAGGGTGAATTTATCANAAGGCATAATAATCATAAATGTGTAT	120
Sbjct	61	ACTATTTGTAGTGTTAAAAGGGTGAATTTATCANAAGGCATAATAATCATAAATGTGTAT	120
Query	121	ATGCCTAATAATAGAACTTTAAAAGGCATGAAGCAACACTCAAAAGGATTAAAGGGAGAT	180
Sbjct	121	ATGCCTAATAATAGAACTTTAAAAGGCATGAAGCAACACTCAAAAGGATTAAAGGGAGAT	180
Query	181	CATCTCACCCCCTTCTTACCAATTGATAGAATGATCTGATGAAAACAGTAAAAATAACAAC	240
Sbjct	181	CATCTCACCCCCTTCTTACCAATTGATAGAATGATCTGATGAAAACAGTAAAAATAACAAC	240
Query	241	AGATCTGAACACTGTCAACCATCTTGACAAATACTTATGCCTAGTGTTCATTATTGGAA	300
Sbjct	241	AGATCTGAACACTGTCAACCATCTTGACAAATACTTATGCCTAGTGTTCATTATTGGAA	300
Query	301	CACTAAACATGTGGAATGATTTATATCCTACTGCTCAAGGTCATCACCAAGGTCTAATTG	360
Sbjct	301	CACTAAACATGTGGAATGATTTATATCCTACTGCTCAAGGTCATCACCAAGGTCTAATTG	360
Query	361	TAAAATTTCAAAAAATTGCAACCTCAGGCATAAATGGGTTAATCGACATTTATAGCACAC	420
Sbjct	361	TAAAATTTCAAAAAATTGCAACCTCAGGCATAAATGGGTTAATCGACATTTATAGCACAC	420
Query	421	ACATGCAACATGTACCAGAGATTCCTTCTTTTCTATGAACATGGTACTTCCACCAAGATA	480
Sbjct	421	ACATGCAACATGTACCAGAGATTCCTTCTTTTCTATGAACATGGTACTTCCACCAAGATA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GACCACATTGTGAAC TATAAAACAAATCTAAAAACATTTGAAATGAAGGAAATTATATAA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GACCACATTGTGAAC TATAAAACAAATCTAAAAACATTTGAAATGAAGGAAATTATATAA  540

Query  541  AATATGTTCTCTTGATCTCAATGAAATTAAATTAATACTATAT  583
          |||||||||||||||||||||||||||||||||||||||
Sbjct   541  AATATGTTCTCTTGATCTCAATGAAATTAAATTAATACTATAT  583
```


Sequence 567 matched with Sequence 176

Query= Sequence ID 567
Length=549

SEQ ID NO: 176

ALIGNMENTS

Identities = 549/549 (100%), Gaps = 0/549 (0%)

Query	1	CTCATGGCGGCCAATGTAGGCCCAAACTTCCTCAAGTCAAACCTCCAGGCCACCTTC	60
Sbjct	1	CTCATGGCGGCCAATGTAGGCCCAAACTTCCTCAAGTCAAACCTCCAGGCCACCTTC	60
Query	61	TGCTTCCCGGTGGCATCAACAGGCCAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTG	120
Sbjct	61	TGCTTCCCGGTGGCATCAACAGGCCAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTG	120
Query	121	CTCTTGCCTCCCAGGGGCTTTTCCAGGCCAGCTCTTGCCTCATGGCAGCTGCCCCAGG	180
Sbjct	121	CTCTTGCCTCCCAGGGGCTTTTCCAGGCCAGCTCTTGCCTCATGGCAGCTGCCCCAGG	180
Query	181	CCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCCTCCCTCACAGTGGCC	240
Sbjct	181	CCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCCTCCCTCACAGTGGCC	240
Query	241	CATTTAGGCCCAACTCATGACTGTGAGGCCATTTCCAGGCCTAGTGCCTGCCTCGTGGCT	300
Sbjct	241	CATTTAGGCCCAACTCATGACTGTGAGGCCATTTCCAGGCCTAGTGCCTGCCTCGTGGCT	300
Query	301	GACTCTTGAAGCCCAAACTTCCTCAAATCAGCCTTTTGCCCAACTTCTGTCTACTGTCTG	360
Sbjct	301	GACTCTTGAAGCCCAAACTTCCTCAAATCAGCCTTTTGCCCAACTTCTGTCTACTGTCTG	360
Query	361	GACTCTACAGGTCAGCCTCTGCCTCACAGTGGACCCTCCAGACCCAGATGGTGTCTNCTG	420
Sbjct	361	GACTCTACAGGTCAGCCTCTGCCTCACAGTGGACCCTCCAGACCCAGATGGTGTCTNCTG	420
Query	421	TGGCATCCTCAGGCGAAGCTCCTGCCTTTTCGGCAGCCTCTCCAGGCCAGCTCCTCCTGC	480
Sbjct	421	TGGCATCCTCAGGCGAAGCTCCTGCCTTTTCGGCAGCCTCTCCAGGCCAGCTCCTCCTGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TCCAGCCTTCTCTCCAGGCTCTGAACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TCCAGCCTTCTCTCCAGGCTCTGAACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGA  540

Query  541  GTGTAGTAG  549
          |||||||
Sbjct   541  GTGTAGTAG  549
```

Sequence 568 matched with Sequence 177

Query= Sequence ID 568
Length=662

SEQ ID NO: 177

ALIGNMENTS

Identities = 662/662 (100%), Gaps = 0/662 (0%)

Query	1	TATATATGTAATGCCCTTAACCTAGTGTGTTGGCATGATCGTTGCTGAAAGGGAAGCTTGT	60
Sbjct	1	TATATATGTAATGCCCTTAACCTAGTGTGTTGGCATGATCGTTGCTGAAAGGGAAGCTTGT	60
Query	61	GGGTACAGTGTCCCCTCAGAAGCCAAAGCCCAGGGAAGGTCGCCTGCCCAGGTCAGGCTC	120
Sbjct	61	GGGTACAGTGTCCCCTCAGAAGCCAAAGCCCAGGGAAGGTCGCCTGCCCAGGTCAGGCTC	120
Query	121	CCAGCGAGTTTGTCTGGGGAGGGGCCATTACATCCTCCAGGTCAGGACAGAGGCTCGGGC	180
Sbjct	121	CCAGCGAGTTTGTCTGGGGAGGGGCCATTACATCCTCCAGGTCAGGACAGAGGCTCGGGC	180
Query	181	TGAGGGAACCCTACACAGGTCCTGGAAGCAGATCCTTCCTGCCTAAGCCAGCAGGACAGC	240
Sbjct	181	TGAGGGAACCCTACACAGGTCCTGGAAGCAGATCCTTCCTGCCTAAGCCAGCAGGACAGC	240
Query	241	TCAACAGGAAGCATCTTCCAGCCACGGGAGGAGAGGCAGCACCTTTTTTGAACCATACA	300
Sbjct	241	TCAACAGGAAGCATCTTCCAGCCACGGGAGGAGAGGCAGCACCTTTTTTGAACCATACA	300
Query	301	GAGCTAAGAATGGTGGTACAAGTAATAGATTCTGTACTGGCAACCCCACTTGGTGGAGCA	360
Sbjct	301	GAGCTAAGAATGGTGGTACAAGTAATAGATTCTGTACTGGCAACCCCACTTGGTGGAGCA	360
Query	361	AGTTCTAGGAAAAGGGGGCTGTCCTTGAGTCAGCCATGGGGTCAGCCACACAGTCACCGC	420
Sbjct	361	AGTTCTAGGAAAAGGGGGCTGTCCTTGAGTCAGCCATGGGGTCAGCCACACAGTCACCGC	420
Query	421	AGCTGCTCTTTGGCACCGGGCGCTGGAAAGACCTAGGATGACACAGCCTGGAAAGAGCTT	480
Sbjct	421	AGCTGCTCTTTGGCACCGGGCGCTGGAAAGACCTAGGATGACACAGCCTGGAAAGAGCTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGAAAAGCTCATCTTCCACAGAACTACCTGCTATACCAGCCAGGGCAGGTGCTTATTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGGAAAAGCTCATCTTCCACAGAACTACCTGCTATACCAGCCAGGGCAGGTGCTTATTCC  540

Query  541  CACAACAGCCCTCTGTTGTAGGCGGCAGTGCCATCCTGAANGTGCCGTGGTACCTTCTGA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CACAACAGCCCTCTGTTGTAGGCGGCAGTGCCATCCTGAANGTGCCGTGGTACCTTCTGA  600

Query  601  ANACCCAGCTGAGGGCCTGTAATGGCACTTGCATGCCACATGGNACACCCTTTCCCGGTT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  ANACCCAGCTGAGGGCCTGTAATGGCACTTGCATGCCACATGGNACACCCTTTCCCGGTT  660

Query  661  AA  662
          ||
Sbjct   661  AA  662
```

Sequence 570 matched with Sequence 178

Query= Sequence ID 570
Length=339

SEQ ID NO: 178

ALIGNMENTS

Identities = 339/339 (100%), Gaps = 0/339 (0%)

```
Query 1  ACCGCGGCCGCGTnaaaaaaaaaaaaaaaaaGAATTCCACTTGATCAACTTAATTCCTTNT 60
          |||
Sbjct 1  ACCGCGGCCGCGTNAANAAAAAAAAAAAAAAAAAGAATTCCACTTGATCAACTTAATTCCTTNT 60

Query 61 CTTTATCTTCCCTCCCTCACTTCCCTTTTCTCCACCCTCTTTTCCAAGCTGTTTCGCTT 120
          |||
Sbjct 61 CTTTATCTTCCCTCCCTCACTTCCCTTTTCTCCACCCTCTTTTCCAAGCTGTTTCGCTT 120

Query 121 TGCAATATATTACTGGTAATGAGTTGCAGGATAATGCAGTCATAACTTGTTTTCTCCTAA 180
          |||
Sbjct 121 TGCAATATATTACTGGTAATGAGTTGCAGGATAATGCAGTCATAACTTGTTTTCTCCTAA 180

Query 181 GTATTTGAGTTCAAAACCTCCTGTATCTAAAGAAATACGGTTGGGGTCATTAATAAAGAAA 240
          |||
Sbjct 181 GTATTTGAGTTCAAAACCTCCTGTATCTAAAGAAATACGGTTGGGGTCATTAATAAAGAAA 240

Query 241 ATCTTTCTATCTTaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 300
          |||
Sbjct 241 ATCTTTCTATCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 300

Query 301 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 339
          |||
Sbjct 301 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 339
```

Sequence 571 matched with Sequence 179

Query= Sequence ID - 571 nt: 457
Length=457

SEQ ID NO: 179 nt: 457

ALIGNMENTS

Identities = 457/457 (100%), Gaps = 0/457 (0%)

Query	1	TTAGAGAGGTGAGGATCTGGTATTTCTGGACTAAATCCCCTTGGGGAAGACGAAGGGA	60
Sbjct	1	TTAGAGAGGTGAGGATCTGGTATTTCTGGACTAAATCCCCTTGGGGAAGACGAAGGGA	60
Query	61	TGCTGCAGTTCCAAAAGAGAAGGACTCTTCCAGAGTCATCTACCTGAGTCCCAAAGCTCC	120
Sbjct	61	TGCTGCAGTTCCAAAAGAGAAGGACTCTTCCAGAGTCATCTACCTGAGTCCCAAAGCTCC	120
Query	121	CTGTCCTGAAAGCCACAGACAATATGGTCCCAAATGACTGACTGCACCTTCTGTGCCTCA	180
Sbjct	121	CTGTCCTGAAAGCCACAGACAATATGGTCCCAAATGACTGACTGCACCTTCTGTGCCTCA	180
Query	181	GCCGTTCTTGACATCAAGAATCTTCTGTTCCACATCCACACAGCCAATACAATTAGTCAA	240
Sbjct	181	GCCGTTCTTGACATCAAGAATCTTCTGTTCCACATCCACACAGCCAATACAATTAGTCAA	240
Query	241	ACCACTGTTATTAACAGATGTAGCAACATGAGAAACGCTTATGTTACAGGTTACATGAGA	300
Sbjct	241	ACCACTGTTATTAACAGATGTAGCAACATGAGAAACGCTTATGTTACAGGTTACATGAGA	300
Query	301	GCAATCATGTAAGTCTATATGACTTCAGAAATGTTAAAATAGACTAACCTCTAACAACAA	360
Sbjct	301	GCAATCATGTAAGTCTATATGACTTCAGAAATGTTAAAATAGACTAACCTCTAACAACAA	360
Query	361	ATTAAAAGTGATTGTTTCAAGGTGATGCAATTATTGATGACCTATTTTATTTTCTATAA	420
Sbjct	361	ATTAAAAGTGATTGTTTCAAGGTGATGCAATTATTGATGACCTATTTTATTTTCTATAA	420
Query	421	TGATCATATATTACCTTTGTAATAAAACATTTTCCC	457
Sbjct	421	TGATCATATATTACCTTTGTAATAAAACATTTTCCC	457

Sequence 572 matched with Sequence 180

Query= Sequence ID 572
Length=658

SEQ ID NO: 180

ALIGNMENTS

Identities = 658/658 (100%), Gaps = 0/658 (0%)

Query	1	CGTCTATTTGNGTTTCTTCTCACAATTGGTAAGTTCTCTGTATTGATTGATGGCTAAGTT	60
Sbjct	1	CGTCTATTTGNGTTTCTTCTCACAATTGGTAAGTTCTCTGTATTGATTGATGGCTAAGTT	60
Query	61	TGATTAGTGTTTTCTCTAGTTGGTAATTATATTCTAGTATTTTATCATCTTATTGTTTA	120
Sbjct	61	TGATTAGTGTTTTCTCTAGTTGGTAATTATATTCTAGTATTTTATCATCTTATTGTTTA	120
Query	121	CTCAACTNAAAGTGNACAGAAGAGTTGCCAGGTTTCTCTTGATATGAGATCTCTNNTT	180
Sbjct	121	CTCAACTNAAAGTGNACAGAAGAGTTGCCAGGTTTCTCTTGATATGAGATCTCTNNTT	180
Query	181	GATTTGGAATGCAAATCANAAGTGTCATGTTTTGAATAAAGGGACCAGATGACTTATAGG	240
Sbjct	181	GATTTGGAATGCAAATCANAAGTGTCATGTTTTGAATAAAGGGACCAGATGACTTATAGG	240
Query	241	TATTCTTTCTCTAAATATAACTAAGGTAAGATTTTGTGTTTGAGGTACTTAATCTATATA	300
Sbjct	241	TATTCTTTCTCTAAATATAACTAAGGTAAGATTTTGTGTTTGAGGTACTTAATCTATATA	300
Query	301	AGTGGTAAAGAATTTACTTGAATTTCTCCAAATTCTCATGTCTAAAGTCTGATTGATTAA	360
Sbjct	301	AGTGGTAAAGAATTTACTTGAATTTCTCCAAATTCTCATGTCTAAAGTCTGATTGATTAA	360
Query	361	ATTCATTCTTGGTATTTCAATTTGAAAAGAATGTAGCTTTAGCAAACCTCTTGTATAAA	420
Sbjct	361	ATTCATTCTTGGTATTTCAATTTGAAAAGAATGTAGCTTTAGCAAACCTCTTGTATAAA	420
Query	421	TGCAGTGGGATTAAGGTCatttaaaaaattggttatatcattgtatttttaaaatttacca	480
Sbjct	421	TGCAGTGGGATTAAGGTCATTTAAAAAATTGTTATATCATTGTATTTTAAAAATTACCA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  gttttatttttctttttaccctttaGCCCAGCCTCAGAAAGTGTGTTTGTGTCCATTTCT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTTTTATTTTCTTTTACCCTTTAGCCCAGCCTCAGAAAGTGTGTTTGTGTCCATTTCT  540

Query  541  CCCAGCGCACCTCTGCATATCTCTACCCACTTGTGCATAATTCAGCATCCAGCAGAGGAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CCCAGCGCACCTCTGCATATCTCTACCCACTTGTGCATAATTCAGCATCCAGCAGAGGAA  600

Query  601  AACAAAGTGTTGCGTACAGTTCCTCTACTAGCAGCATGCCTCCCCCAGGACAAGTGTA  658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  AACAAAGTGTTGCGTACAGTTCCTCTACTAGCAGCATGCCTCCCCCAGGACAAGTGTA  658
```

Sequence 574 matched with Sequence 181

Query= Sequence ID 574
Length=452

SEQ ID NO: 181

ALIGNMENTS

Identities = 452/452 (100%), Gaps = 0/452 (0%)

Query	1	TTATTGCTGACATAAAAAATGGTGCACATCGGCCAGGGCCCAGGATGAATCAGCCAATCTG	60
Sbjct	1	TTATTGCTGACATAAAAAATGGTGCACATCGGCCAGGGCCCAGGATGAATCAGCCAATCTG	60
Query	61	CACCATTTATACATGGAAGTGGAGAACATTGTGCCAATAATCATTTAATATATGCCAAAT	120
Sbjct	61	CACCATTTATACATGGAAGTGGAGAACATTGTGCCAATAATCATTTAATATATGCCAAAT	120
Query	121	CTTACACGTCTACTCTAAAGTCTCTAATGAAGTTTCAGTGACCTTGAGGGCTAAAGATT	180
Sbjct	121	CTTACACGTCTACTCTAAAGTCTCTAATGAAGTTTCAGTGACCTTGAGGGCTAAAGATT	180
Query	181	GTTCTTCTGGGTAAGAGCTCTTGGGCTGGTTTTTTCANAGCAGAGTTCTTGTGTGGGTAG	240
Sbjct	181	GTTCTTCTGGGTAAGAGCTCTTGGGCTGGTTTTTTCANAGCAGAGTTCTTGTGTGGGTAG	240
Query	241	ACTGTGACTAGGTTTACAGCCTTTGTGGAACATTCCGTATAACGGCATTGTGGAAGCAAT	300
Sbjct	241	ACTGTGACTAGGTTTACAGCCTTTGTGGAACATTCCGTATAACGGCATTGTGGAAGCAAT	300
Query	301	AACTAGTTCCTATGAAAGAACCAGAGCTGGGAAGATGGCTGGGAAGCCAGGCCAAAGTGG	360
Sbjct	301	AACTAGTTCCTATGAAAGAACCAGAGCTGGGAAGATGGCTGGGAAGCCAGGCCAAAGTGG	360
Query	361	GGGCAACAGCTTGCTTCTCTTTCTCTTCTCACCCTCAGTTTGTATGGGAAAATGGAGATG	420
Sbjct	361	GGGCAACAGCTTGCTTCTCTTTCTCTTCTCACCCTCAGTTTGTATGGGAAAATGGAGATG	420
Query	421	TCCTCTCCACTTTATCCACGATATCTAAATG	452
Sbjct	421	TCCTCTCCACTTTATCCACGATATCTAAATG	452

Sequence 575 matched with Sequence 182

Query= Sequence ID - 575 nt: 209
Length=188

SEQ ID NO: 182 nt: 209

ALIGNMENTS

Identities = 188/188 (100%), Gaps = 0/188 (0%)

Query	1	CAGGATATCGAGACCATCCCAGACAGCATGGTGAAACTCCGTCTCTACTGGAATACAAAA	60
Sbjct	1	CAGGATATCGAGACCATCCCAGACAGCATGGTGAAACTCCGTCTCTACTGGAATACAAAA	60
Query	61	AGTTAGCCGTGTGTGGTGGCACGCGCCTCTAATCCCAGCTATTCGGGAGGCTTAGGCAGG	120
Sbjct	61	AGTTAGCCGTGTGTGGTGGCACGCGCCTCTAATCCCAGCTATTCGGGAGGCTTAGGCAGG	120
Query	121	AGAATTACTTGAACCCGGGAGGCGAAGGTTGCAGTGAGCTGAGATCGCACCATTGCACTC	180
Sbjct	121	AGAATTACTTGAACCCGGGAGGCGAAGGTTGCAGTGAGCTGAGATCGCACCATTGCACTC	180
Query	181	CACCCTGG	188
Sbjct	181	CACCCTGG	188

Sequence 576 matched with Sequence 183

Query= Sequence ID - 576 nt: 541
Length=541

SEQ ID NO: 183 nt: 541

ALIGNMENTS

Identities = 541/541 (100%), Gaps = 0/541 (0%)

Query	1	CAGCCAACCCAGAAGGAGCCAGTCTACAACTATGCCTGATCCTCCTCATGGCAGGCCACG	60
Sbjct	1	CAGCCAACCCAGAAGGAGCCAGTCTACAACTATGCCTGATCCTCCTCATGGCAGGCCACG	60
Query	61	AAGCATTGCTGCCATGTGTTGAATTATAAAACCCACATTGCTTTTTGAACCCTGTTGCGG	120
Sbjct	61	AAGCATTGCTGCCATGTGTTGAATTATAAAACCCACATTGCTTTTTGAACCCTGTTGCGG	120
Query	121	GTAAAAATAACCAAATTATCAGTCCTTGAAACCCAGGCAATCAAGTGAGTACAAGGTAA	180
Sbjct	121	GTAAAAATAACCAAATTATCAGTCCTTGAAACCCAGGCAATCAAGTGAGTACAAGGTAA	180
Query	181	AGATAAGTATGGTTTAGAGGAGAAAATTATGTTCTGAACTGGTGTCTTTGATGGCAGCG	240
Sbjct	181	AGATAAGTATGGTTTAGAGGAGAAAATTATGTTCTGAACTGGTGTCTTTGATGGCAGCG	240
Query	241	TCAGCCTTGCTAAGTCAGAGTAGAGGGAGCAGTGACCTTAATAAGCTTTGGTGAGCATCA	300
Sbjct	241	TCAGCCTTGCTAAGTCAGAGTAGAGGGAGCAGTGACCTTAATAAGCTTTGGTGAGCATCA	300
Query	301	TGTGCACGCGTGGGTGGGAGTCCCTTTCACTGATGCTTTTAAAAGTGCTTTTGCAGACCC	360
Sbjct	301	TGTGCACGCGTGGGTGGGAGTCCCTTTCACTGATGCTTTTAAAAGTGCTTTTGCAGACCC	360
Query	361	TGGAAGGGATCCTCCACACATATGAGGTGTGGGACAGGTAGGCCAGAGAGGATTAGCCCT	420
Sbjct	361	TGGAAGGGATCCTCCACACATATGAGGTGTGGGACAGGTAGGCCAGAGAGGATTAGCCCT	420
Query	421	GCTTTTCGAGACTAGAAATCTACAGTCCTGAAGGAGCAGTAATTAATTGGTACACCTGTCA	480
Sbjct	421	GCTTTTCGAGACTAGAAATCTACAGTCCTGAAGGAGCAGTAATTAATTGGTACACCTGTCA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGCCAGCCCCCAGGTCTCCTGGCTTTTTCCAGGTTTCTGTCTCACATGATTTTGCTTT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGGCCAGCCCCCAGGTCTCCTGGCTTTTTCCAGGTTTCTGTCTCACATGATTTTGCTTT  540

Query  541  T   541
          |
Sbjct   541  T   541
```

Sequence 577 matched with Sequence 184

Query= Sequence ID 577
Length=640

SEQ ID NO: 184

ALIGNMENTS

Identities = 640/640 (100%), Gaps = 0/640 (0%)

Query	1	CTTTAATTTTCAAGTGTTTAAAAACAATTTTATACTTAAGCCAGCCTTGAAGATAAGC	60
Sbjct	1	CTTTAATTTTCAAGTGTTTAAAAACAATTTTATACTTAAGCCAGCCTTGAAGATAAGC	60
Query	61	ACAAAATTTACCAGTTTACATTTaaaaaacaacaaaaaCGACAACAACTCAAGCACCC	120
Sbjct	61	ACAAAATTTACCAGTTTACATTTAAAAACAACAAAAACGACAACAACTCAAGCACCC	120
Query	121	GCTCTGTGCATAGCACTATTCTAGGTGCAATAAAAGGGAATCTTAACCTTAGAAATATGA	180
Sbjct	121	GCTCTGTGCATAGCACTATTCTAGGTGCAATAAAAGGGAATCTTAACCTTAGAAATATGA	180
Query	181	GTTCACTTTCTGGAATTGTATTATCTCCTTTTCCAGAGAGTAAAAATAAAATCACC	240
Sbjct	181	GTTCACTTTCTGGAATTGTATTATCTCCTTTTCCAGAGAGTAAAAATAAAATCACC	240
Query	241	ATTGTTTACTACAGATCTGCCCCAAACCACATCTGGTTCACAGAAAGGCTAATTTCTGCC	300
Sbjct	241	ATTGTTTACTACAGATCTGCCCCAAACCACATCTGGTTCACAGAAAGGCTAATTTCTGCC	300
Query	301	AAATTAAAGATGTAATGAACTCAGTTCCTGCTTTCCAAAAACACGAAAGCAGAATTCCT	360
Sbjct	301	AAATTAAAGATGTAATGAACTCAGTTCCTGCTTTCCAAAAACACGAAAGCAGAATTCCT	360
Query	361	TTTCACTGaaaaaaaTAAACAGTTTCCATGCAAGGGCAGTTTGCTTCTAATAAGTAttt	420
Sbjct	361	TTTCACTGAAAAAATAAACAGTTTCCATGCAAGGGCAGTTTGCTTCTAATAAGTATTT	420
Query	421	tttaaaaaatttttttCCTCTAGCTTTTCTTTAAATTTTCTCCTCTAATATTGCCTT	480
Sbjct	421	TTTAAAAAATTTTTTTTCTCCTAGCTTTTCTTTAAATTTTCTCCTCTAATATTGCCTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTCTTGTAACAAGGCAGACCAGGTATCTTTTTATGCTGTTTTTCCTTTACTAAGAAAAGTA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTCTTGTAACAAGGCAGACCAGGTATCTTTTTATGCTGTTTTTCCTTTACTAAGAAAAGTA  540

Query  541  TTGCATCTTGAAGACAAACCATTTCAGAGTAGTGATAAAAAATAACACTaaaaaaaCT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TTGCATCTTGAAGACAAACCATTTCAGAGTAGTGATAAAAAATAACACTAAAAAAACT  600

Query  601  TTAAAGGTGAGTCACTTCATCACCTTGATGAAGTAAAAAA  640
          ||||||||||||||||||||||||||||||||||||
Sbjct   601  TTAAAGGTGAGTCACTTCATCACCTTGATGAAGTAAAAAA  640
```


Sequence 578 matched with Sequence 185

Query= Sequence ID 578
Length=633

SEQ ID NO: 185

ALIGNMENTS

Identities = 633/633 (100%), Gaps = 0/633 (0%)

Query	1	GGAAAAAATATTTCCACTTAGATATTTTACATGGTTTTGTTTAAAATTACCATTACTTGT	60
Sbjct	1	GGAAAAAATATTTCCACTTAGATATTTTACATGGTTTTGTTTAAAATTACCATTACTTGT	60
Query	61	TTTTTAAAAACACATGACCACATATGTATATGTATATCTACCTAAACATTGTATCATGGT	120
Sbjct	61	TTTTTAAAAACACATGACCACATATGTATATGTATATCTACCTAAACATTGTATCATGGT	120
Query	121	TTCAGTATGTTATTCATGTATTACTGGGAGATGCTACCAAGAAACCAACCCAAAGAAAAT	180
Sbjct	121	TTCAGTATGTTATTCATGTATTACTGGGAGATGCTACCAAGAAACCAACCCAAAGAAAAT	180
Query	181	TCTGGAAAATACATTTCTATTTATAGAATAAATGTTTCATTTATATAAAAAGCAAAAGAAC	240
Sbjct	181	TCTGGAAAATACATTTCTATTTATAGAATAAATGTTTCATTTATATAAAAAGCAAAAGAAC	240
Query	241	TTAGAGTTCTAATAAATGGGATGTCTAATAAATTATGAAGTTACTGATTGAATATATTA	300
Sbjct	241	TTAGAGTTCTAATAAATGGGATGTCTAATAAATTATGAAGTTACTGATTGAATATATTA	300
Query	301	TATTTTTATAACTTCCTTGCCAAAGTCCTGATTTAGTACATTAGAGAACCTGTGTTTCCT	360
Sbjct	301	TATTTTTATAACTTCCTTGCCAAAGTCCTGATTTAGTACATTAGAGAACCTGTGTTTCCT	360
Query	361	CTCTCCTCTACCATTTCATCTCTCTTCCATACAGTCATTGGGCTTTTTACTCAAAGAGAA	420
Sbjct	361	CTCTCCTCTACCATTTCATCTCTCTTCCATACAGTCATTGGGCTTTTTACTCAAAGAGAA	420
Query	421	TCAAGAAATAATAAGGTATAACAAGCTTGGCAAAGTGTTGGCTTTTTTaaaaaaaatttt	480
Sbjct	421	TCAAGAAATAATAAGGTATAACAAGCTTGGCAAAGTGTTGGCTTTTTTAAAAAAAAATTTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  tttAATCTCTAGCAGTTTGGTAATTTAGCAGCATCATTTATTTGGGATTCTTTTATCTGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTTAATCTCTAGCAGTTTGGTAATTTAGCAGCATCATTTATTTGGGATTCTTTTATCTGA  540

Query  541  TTTCAACAGTGAAAAACATCCCTATGATAAAGCCTAATGACCCATTTCCTAAAAGATGGAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TTTCAACAGTGAAAAACATCCCTATGATAAAGCCTAATGACCCATTTCCTAAAAGATGGAA  600

Query  601  TTGCCCTTCCTAGAAAATATGACGGAGAAAAGT  633
          ||||||||||||||||||||||||
Sbjct   601  TTGCCCTTCCTAGAAAATATGACGGAGAAAAGT  633
```

Sequence 579 matched with Sequence 186

Query= Sequence ID - 579 nt: 502
Length=502

SEQ ID NO: 186 nt: 502

ALIGNMENTS

Identities = 502/502 (100%), Gaps = 0/502 (0%)

Query	1	CGAATAGCCAAGTGGTCTGACAAGATCGAGAGTAATGAGGCCCATACTTTAGTACAGTCT	60
Sbjct	1	CGAATAGCCAAGTGGTCTGACAAGATCGAGAGTAATGAGGCCCATACTTTAGTACAGTCT	60
Query	61	TGAATGGCCAGATGGTGCTGGGCATACCCCAACCAGAGATATGTAAGTCTTTATGTTGTC	120
Sbjct	61	TGAATGGCCAGATGGTGCTGGGCATACCCCAACCAGAGATATGTAAGTCTTTATGTTGTC	120
Query	121	AAAATTTCCAGAAACATGAATTTCCCACTAAGATTCATTAAGGAAAAC TAGAATGAAAA	180
Sbjct	121	AAAATTTCCAGAAACATGAATTTCCCACTAAGATTCATTAAGGAAAAC TAGAATGAAAA	180
Query	181	CAAAAACGTTTCCTTG TATAATATTCATTANAAAGAAATGAAGAAGGCCGGGCATGGTGGC	240
Sbjct	181	CAAAAACGTTTCCTTG TATAATATTCATTANAAAGAAATGAAGAAGGCCGGGCATGGTGGC	240
Query	241	TCACGCCTGTAATCCCAGCACTTTGAGAGGCCAAGGTAGGCAGATCATGAGGTCAGGAGT	300
Sbjct	241	TCACGCCTGTAATCCCAGCACTTTGAGAGGCCAAGGTAGGCAGATCATGAGGTCAGGAGT	300
Query	301	TTGAGACCAGCCTGGCCAACATAGTGAAATCCCGTCTCTACCAAAAAATACaaaaaaTTA	360
Sbjct	301	TTGAGACCAGCCTGGCCAACATAGTGAAATCCCGTCTCTACCAAAAAATACAAAAAAATTA	360
Query	361	GCCGGGCATGGTGGCACACACCTGTCATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAT	420
Sbjct	361	GCCGGGCATGGTGGCACACACCTGTCATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAT	420
Query	421	TGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGTACTACAGCC	480
Sbjct	421	TGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGTACTACAGCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAGGTGACAGTGCAAGACTCTG	502
Sbjct	481	TAGGTGACAGTGCAAGACTCTG	502

Sequence 580 matched with Sequence 187

Query= Sequence ID - 580 nt: 316
Length=316

SEQ ID NO: 187 nt: 316

ALIGNMENTS

Identities = 316/316 (100%), Gaps = 0/316 (0%)

```
Query 1 CCTATGCCAAACTAAAGAAAGCTTGCCTGGCCTACAGGCCTAAAGGTTCAAATGNGGATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 CCTATGCCAAACTAAAGAAAGCTTGCCTGGCCTACAGGCCTAAAGGTTCAAATGNGGATT 60

Query 61 aaaaaaaCACAGTAGTCACATAAAATGTCTGCTGGCTGGCTGGAATTCCATCACCTACAA 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AAAAAAACACAGTAGTCACATAAAATGTCTGCTGGCTGGCTGGAATTCCATCACCTACAA 120

Query 121 TTTACCTGCTTTCAAAAACCTGTGTTCAACATTGAGAAAACAGAAAACCACTTATCTTGAG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TTTACCTGCTTTCAAAAACCTGTGTTCAACATTGAGAAAACAGAAAACCACTTATCTTGAG 180

Query 181 CTTAATATGGGCTTCTTTTTCCTTAACTGTAGAACACTTACTGAAATATCAAATCAATGG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 CTTAATATGGGCTTCTTTTTCCTTAACTGTAGAACACTTACTGAAATATCAAATCAATGG 240

Query 241 TTAGGATATGTATCCTAGGCAGGCCTAAACCATTAACACTTGGTTTAAGCAACTTTGTAT 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TTAGGATATGTATCCTAGGCAGGCCTAAACCATTAACACTTGGTTTAAGCAACTTTGTAT 300

Query 301 AATTNACCTCCTAAAT 316
      ||||||||||||||||
Sbjct 301 AATTNACCTCCTAAAT 316
```

Sequence 581 matched with Sequence 188

Query= Sequence ID 581
Length=94

SEQ ID NO: 188

ALIGNMENTS

Identities = 94/94 (100%), Gaps = 0/94 (0%)

```
Query 1  CTTCATGAGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCACACA  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  CTTCATGAGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCACACA  60

Query 61  TCCAGTCAGTCACTCATCAACTCTATTGATTCTG  94
          ||||||||||||||||||||||||||||
Sbjct 61  TCCAGTCAGTCACTCATCAACTCTATTGATTCTG  94
```

Sequence 582 matched with Sequence 189

Query= Sequence ID 582
Length=644

SEQ ID NO: 189

ALIGNMENTS

Identities = 644/644 (100%), Gaps = 0/644 (0%)

Query	1	TAGAATTCTCGCCTGCCTTGGCTTCTCCCTCTAGTTGTTTCCTTCTCTGTCTTCTGTGGGC	60
Sbjct	1	TAGAATTCTCGCCTGCCTTGGCTTCTCCCTCTAGTTGTTTCCTTCTCTGTCTTCTGTGGGC	60
Query	61	TTCTTATTGTCTGCTCACTCCTTCTTCAGTGTCTCTCATGGGCTTCCTTCCCTTCTCAG	120
Sbjct	61	TTCTTATTGTCTGCTCACTCCTTCTTCAGTGTCTCTCATGGGCTTCCTTCCCTTCTCAG	120
Query	121	CTGATGCCATCACCTGGGGAATCACAGTTACTCAGCAGCACTGGGGCCTCTCTATCTCTA	180
Sbjct	121	CTGATGCCATCACCTGGGGAATCACAGTTACTCAGCAGCACTGGGGCCTCTCTATCTCTA	180
Query	181	TGCTGGTCATGCCTATGTGTGAGCTGCAGACCCAGTGAATTTCCATTTGTGCATCCCAT	240
Sbjct	181	TGCTGGTCATGCCTATGTGTGAGCTGCAGACCCAGTGAATTTCCATTTGTGCATCCCAT	240
Query	241	GCCCAGCCCACCCTCCACCAGCCTCGAATGCAGCTGTTTCCAGCCCTACCCAGTCCCTCAGA	300
Sbjct	241	GCCCAGCCCACCCTCCACCAGCCTCGAATGCAGCTGTTTCCAGCCCTACCCAGTCCCTCAGA	300
Query	301	AAAGTTCCTCTCCCTGGATCCTCTTTTTCTTCATGAGTGCCCGGTTGCCCAAGTCAAAA	360
Sbjct	301	AAAGTTCCTCTCCCTGGATCCTCTTTTTCTTCATGAGTGCCCGGTTGCCCAAGTCAAAA	360
Query	361	ACCTGGGAGTGATATAAACTCCCCACACATCCAGTCAGTCACTCATCAACTCTATTGATT	420
Sbjct	361	ACCTGGGAGTGATATAAACTCCCCACACATCCAGTCAGTCACTCATCAACTCTATTGATT	420
Query	421	CTGTCTGCTAAATATATCTCAATTGTATTAACCTAAACATATGCATAATACATCTTCTTC	480
Sbjct	421	CTGTCTGCTAAATATATCTCAATTGTATTAACCTAAACATATGCATAATACATCTTCTTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTCACTGCATTTTTGTGGGCTGCACTTACCTTTCAGGTAACAACAACACTGGCCCCTCTT	540
Sbjct	481	TTCACTGCATTTTTGTGGGCTGCACTTACCTTTCAGGTAACAACAACACTGGCCCCTCTT	540
Query	541	GCCCTTCTAGTCAGAAGTGCCAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAAC	600
Sbjct	541	GCCCTTCTAGTCAGAAGTGCCAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAAC	600
Query	601	ATTAACTGAATGTGCAAACTGGAAGGGCATCCAAACAGAGGA	644
Sbjct	601	ATTAACTGAATGTGCAAACTGGAAGGGCATCCAAACAGAGGA	644

Sequence 583 matched with Sequence 190

Query= Sequence ID - 583 nt: 631
Length=631

SEQ ID NO: 190 nt: 631

ALIGNMENTS

Identities = 631/631 (100%), Gaps = 0/631 (0%)

Query	1	CTGAGGTGGGAGGATTCCACTCTCACCCATTTCTTCTTTCAATTTTCAGTTTCTCCAGTTA	60
Sbjct	1	CTGAGGTGGGAGGATTCCACTCTCACCCATTTCTTCTTTCAATTTTCAGTTTCTCCAGTTA	60
Query	61	GTAAGTGAAGATGTTCTTTGAGTAATTAAGTGAGTGAGAAAATTTTAAAGTGAGAAATCT	120
Sbjct	61	GTAAGTGAAGATGTTCTTTGAGTAATTAAGTGAGTGAGAAAATTTTAAAGTGAGAAATCT	120
Query	121	ATAAAAAGAACCATGTAAACATAAATATTTTCAGTCCTTACAAGTTGGTATTGACTTTTCT	180
Sbjct	121	ATAAAAAGAACCATGTAAACATAAATATTTTCAGTCCTTACAAGTTGGTATTGACTTTTCT	180
Query	181	CATTGGTAATCTGACTGATTAAATACTGCTCATTCCAATATCTGGTGATGTAATTCTGGT	240
Sbjct	181	CATTGGTAATCTGACTGATTAAATACTGCTCATTCCAATATCTGGTGATGTAATTCTGGT	240
Query	241	TATGAATCCTTGTATTAATAACACCTCCTGGGAGGttttttttCCCCAACATTACATTCA	300
Sbjct	241	TATGAATCCTTGTATTAATAACACCTCCTGGGAGGTTTTTTTTCCCCAACATTACATTCA	300
Query	301	GAATATTAGAGCTGAAAATACCTTTTTTAAGGTTATCAGGAGGAGGGAGCTTATGTTTAA	360
Sbjct	301	GAATATTAGAGCTGAAAATACCTTTTTTAAGGTTATCAGGAGGAGGGAGCTTATGTTTAA	360
Query	361	TGTGGTGGATAAACTTAACTGCTGGTTAATACAATTGTTATTCAGGTGAAATTCCTTAA	420
Sbjct	361	TGTGGTGGATAAACTTAACTGCTGGTTAATACAATTGTTATTCAGGTGAAATTCCTTAA	420
Query	421	ACTTTTCACGTGCAAAGTTTTGTATGTATACAGACATTTGGGGAAAAGTTTATCATCCC	480
Sbjct	421	ACTTTTCACGTGCAAAGTTTTGTATGTATACAGACATTTGGGGAAAAGTTTATCATCCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TAAAACCGGTTACTGTCCAGAAAATGATAAGAATCCCTGGGTTCCAAATCCTTCATAAGG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TAAAACCGGTTACTGTCCAGAAAATGATAAGAATCCCTGGGTTCCAAATCCTTCATAAGG  540

Query  541  TATTTATTCATTTATTTATTCAACACATTTACTCAATGCCTCCGCTCTGCTGCAACTACA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TATTTATTCATTTATTTATTCAACACATTTACTCAATGCCTCCGCTCTGCTGCAACTACA  600

Query  601  CTGACATTCTGCTTCTAATCTAACCGAAAAT  631
          |||||||||||||||||||||||||||
Sbjct   601  CTGACATTCTGCTTCTAATCTAACCGAAAAT  631
```

Sequence 585 matched with Sequence 191

Query= Sequence ID 585
Length=638

SEQ ID NO: 191

ALIGNMENTS

Identities = 638/638 (100%), Gaps = 0/638 (0%)

Query	1	TTTCAAATTGTACAATAACACAAACAAC	60
Sbjct	1	TTTCAAATTGTACAATAACACAAACAAC	60
Query	61	TGGACAAAAGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGCTCATAAAA	120
Sbjct	61	TGGACAAAAGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGCTCATAAAA	120
Query	121	ATCATGAAAAGTTGGAAAGACTGTAAATCACTGAACTTCAAATATATCTTACACAATC	180
Sbjct	121	ATCATGAAAAGTTGGAAAGACTGTAAATCACTGAACTTCAAATATATCTTACACAATC	180
Query	181	TTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATCATGGTAATTTTATGCA	240
Sbjct	181	TTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATCATGGTAATTTTATGCA	240
Query	241	AATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTCTCAGTTCTGTTATTTGTGAA	300
Sbjct	241	AATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTCTCAGTTCTGTTATTTGTGAA	300
Query	301	AAGATCAATACCAGATTGAATGACTACCTATTGGCAAAGGGCCCTAAAAAGCTTACTTTA	360
Sbjct	301	AAGATCAATACCAGATTGAATGACTACCTATTGGCAAAGGGCCCTAAAAAGCTTACTTTA	360
Query	361	GCACTCATCTTTTACATGGTTAAATGCATTTCCCTAATTTGAGATCACCTAAACACTGGAA	420
Sbjct	361	GCACTCATCTTTTACATGGTTAAATGCATTTCCCTAATTTGAGATCACCTAAACACTGGAA	420
Query	421	AAGaaaaaaaTGAAAGGGCAGTATGTCCATAAACCAACAAATAATTTGGCTGTAATGTA	480
Sbjct	421	AAGAAAAAAATGAAAGGGCAGTATGTCCATAAACCAACAAATAATTTGGCTGTAATGTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCATaaaacacaaacccccacacatctgtacaataaacattatgtattacatacacacaac	540
Sbjct	481	TCATAAAACACAAACCCACACATCTGTACAATAAACATTATGTATTACATACACACAAC	540
Query	541	acacacCCAGTCATAAAGCCTAATGATGTGCTGCTTCCAGTTCAATATTCAGCTGTGCAT	600
Sbjct	541	ACACACCCAGTCATAAAGCCTAATGATGTGCTGCTTCCAGTTCAATATTCAGCTGTGCAT	600
Query	601	TTTTTCTTATTTTCATCAAATGAATAGCTTTTTGTCACC	638
Sbjct	601	TTTTTCTTATTTTCATCAAATGAATAGCTTTTTGTCACC	638

Sequence 586 matched with Sequence 192

Query= Sequence ID 586
Length=283

SEQ ID NO: 192

ALIGNMENTS

Identities = 283/283 (100%), Gaps = 0/283 (0%)

Query	1	GTAAACTGTTCTCTCCGAGGGAAAAAATGGAAGTTATCCTCACAGTTCACTGCCGTGGTA	60
Sbjct	1	GTAAACTGTTCTCTCCGAGGGAAAAAATGGAAGTTATCCTCACAGTTCACTGCCGTGGTA	60
Query	61	TTTCTTCTGTCCCATGCTTTGCATGACTGCCATGGTACAGCCTTGTTTCAAACGTTCAC	120
Sbjct	61	TTTCTTCTGTCCCATGCTTTGCATGACTGCCATGGTACAGCCTTGTTTCAAACGTTCAC	120
Query	121	TGTGATCTGTGGGTCTTTGAGTTTCAGTGAGTTTGCTGAAATGTCGAAGAAGTAGTTCCA	180
Sbjct	121	TGTGATCTGTGGGTCTTTGAGTTTCAGTGAGTTTGCTGAAATGTCGAAGAAGTAGTTCCA	180
Query	181	AACTTCAATGTTCAATGAAATTTTTGTTCAAGTTTGAAATGGAGAGAGCAGCTTTAAAAG	240
Sbjct	181	AACTTCAATGTTCAATGAAATTTTTGTTCAAGTTTGAAATGGAGAGAGCAGCTTTAAAAG	240
Query	241	GTACTAAGCCTTTTACAAATTGGTGAGTACTGGCACATGAGAT	283
Sbjct	241	GTACTAAGCCTTTTACAAATTGGTGAGTACTGGCACATGAGAT	283

Sequence 587 matched with Sequence 193

Query= Sequence ID 587
Length=613

SEQ ID NO: 193

ALIGNMENTS

Identities = 613/613 (100%), Gaps = 0/613 (0%)

Query	1	tttttttttttCCTTAAAAGGTAACCCCTAAACACAGCTAAACTATGCCATCAGCTGAC	60
Sbjct	1	TTTTTTTTTTTCCTTAAAAGGTAACCCCTAAACACAGCTAAACTATGCCATCAGCTGAC	60
Query	61	TCCAAGGNACACACAGTCCTGTATCTGGAAGTACTGAGTGGCAGGCATCTTCTCTGCCT	120
Sbjct	61	TCCAAGGNACACACAGTCCTGTATCTGGAAGTACTGAGTGGCAGGCATCTTCTCTGCCT	120
Query	121	CTGACAGTGGAGTCCCCATCACTGCAGAGCATAGCCAAAGGAGTCAAAGGTCTCAGCGGG	180
Sbjct	121	CTGACAGTGGAGTCCCCATCACTGCAGAGCATAGCCAAAGGAGTCAAAGGTCTCAGCGGG	180
Query	181	TCACTGCCTTATCAACCCTCACCAGTCCCTTATGTTTTTTAATATTTTATAATCTTGACA	240
Sbjct	181	TCACTGCCTTATCAACCCTCACCAGTCCCTTATGTTTTTTAATATTTTATAATCTTGACA	240
Query	241	TGACACCAAGATGCTTTAATAAAAAAGCACCTCTAACTCGGTCTTGTATTCACTTACCTT	300
Sbjct	241	TGACACCAAGATGCTTTAATAAAAAAGCACCTCTAACTCGGTCTTGTATTCACTTACCTT	300
Query	301	GAGCCTGGGACTTCTCTAGGCTCCTGAGGCAAAAACAGGTAGAGGGGAGATGGTGGAACA	360
Sbjct	301	GAGCCTGGGACTTCTCTAGGCTCCTGAGGCAAAAACAGGTAGAGGGGAGATGGTGGAACA	360
Query	361	TAAACACAATTTTGCTTGGCACCCACCTTGGCGTCTGTCCCATGACCAGGTCTTTCAA	420
Sbjct	361	TAAACACAATTTTGCTTGGCACCCACCTTGGCGTCTGTCCCATGACCAGGTCTTTCAA	420
Query	421	TTCGATGATTTTGTCAATTGATGGAGGAGCGATATCGTTTCTCAATGATATTATGGGTTGT	480
Sbjct	421	TTCGATGATTTTGTCAATTGATGGAGGAGCGATATCGTTTCTCAATGATATTATGGGTTGT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCGCCTTTCTCCTTCTTTGGGGGGCTCAAGCTGCTTGACTCCCCCAGGTACCTGCTTAAT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CCGCCTTTCTCCTTCTTTGGGGGGCTCAAGCTGCTTGACTCCCCCAGGTACCTGCTTAAT  540

Query  541  GGGGCACTTTCTCTTGCCCCATCATTACAGGCATTGTGGTCAGAATGGTCCCACTGCTGC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GGGGCACTTTCTCTTGCCCCATCATTACAGGCATTGTGGTCAGAATGGTCCCACTGCTGC  600

Query  601  CCACCAGGGTCTA  613
          |||||||||||
Sbjct   601  CCACCAGGGTCTA  613
```

Sequence 588 matched with Sequence 194

Query= Sequence ID 588
Length=350

SEQ ID NO: 194

ALIGNMENTS

Identities = 350/350 (100%), Gaps = 0/350 (0%)

Query	1	CTAGTCTTTTCATAGTCTGCATAGAGTCTGGCCATTACCATCAGTTTTTAAGATGTCCAT	60
Sbjct	1	CTAGTCTTTTCATAGTCTGCATAGAGTCTGGCCATTACCATCAGTTTTTAAGATGTCCAT	60
Query	61	ATTGTGGCCGGGCGCGGTGGCTCACGCCTGGTAGTCCCAGCACTTTGGGAGGCTGAGGCA	120
Sbjct	61	ATTGTGGCCGGGCGCGGTGGCTCACGCCTGGTAGTCCCAGCACTTTGGGAGGCTGAGGCA	120
Query	121	GGTGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCGTCTCT	180
Sbjct	121	GGTGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCGTCTCT	180
Query	181	ACTaaaaaaaatattaaaaaaTTGGCCAGGCCTGGTGGTGGGCGCCTGTGGTCCCGGCTG	240
Sbjct	181	ACTAAAAAAATATTAAAAAATTGGCCAGGCCTGGTGGTGGGCGCCTGTGGTCCCGGCTG	240
Query	241	CTTGGGAGGCTGAGGCAGGANAATGGTGTGAACCCGGAAGTCGGAGGTTGCAGTGAGCCA	300
Sbjct	241	CTTGGGAGGCTGAGGCAGGANAATGGTGTGAACCCGGAAGTCGGAGGTTGCAGTGAGCCA	300
Query	301	AGATTGCACCTGGGCAACACAGCGAGACTCCGTCTCaaaaaaaaaaaaaaaaa	350
Sbjct	301	AGATTGCACCTGGGCAACACAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAA	350

Sequence 589 matched with Sequence 195

Query= Sequence ID 589
Length=541

SEQ ID NO: 195

ALIGNMENTS

Identities = 541/541 (100%), Gaps = 0/541 (0%)

Query	1	CAATTATTTATTACCTTTCCATTTGTTGCGCTGATGATGTGACAATGCATGGTCTTTGTG	60
Sbjct	1	CAATTATTTATTACCTTTCCATTTGTTGCGCTGATGATGTGACAATGCATGGTCTTTGTG	60
Query	61	CATGCTGCTAGACACTTTTCTTTCCCAGCCGAAAAGTCTATTATGTAATTTTACATTCA	120
Sbjct	61	CATGCTGCTAGACACTTTTCTTTCCCAGCCGAAAAGTCTATTATGTAATTTTACATTCA	120
Query	121	TAATTTTAATGTGGATGATCAGGATTAAATCAAGATATATATCTGGAACCTCTTATAAAT	180
Sbjct	121	TAATTTTAATGTGGATGATCAGGATTAAATCAAGATATATATCTGGAACCTCTTATAAAT	180
Query	181	GGAGCACTTAGAAATTTGTTGTTCTGCACTTAACCTAGAGAGAGAAAAAATGCTTTTCTT	240
Sbjct	181	GGAGCACTTAGAAATTTGTTGTTCTGCACTTAACCTAGAGAGAGAAAAAATGCTTTTCTT	240
Query	241	TGTGAAAAATCTGAATTCCTGTCCTGACCTTCTGTGATGTGGAAACCCTAGGCTCTGAGA	300
Sbjct	241	TGTGAAAAATCTGAATTCCTGTCCTGACCTTCTGTGATGTGGAAACCCTAGGCTCTGAGA	300
Query	301	CACACTCTCTGGTGTCTGAGACAGAACCAAAGCAATAACGTTGTGATGCCCACAGGCCTG	360
Sbjct	301	CACACTCTCTGGTGTCTGAGACAGAACCAAAGCAATAACGTTGTGATGCCCACAGGCCTG	360
Query	361	GAGCCAGCTAGCGACCTTGTGCCGCCAGCTGTCCATGGCCCGTGCAGAGCAGAGGACAG	420
Sbjct	361	GAGCCAGCTAGCGACCTTGTGCCGCCAGCTGTCCATGGCCCGTGCAGAGCAGAGGACAG	420
Query	421	TGAGTGTCTGCACTGAGAACCCTTAAACCACAGTTGAACATACCCACACCTGTTTGTCTTA	480
Sbjct	421	TGAGTGTCTGCACTGAGAACCCTTAAACCACAGTTGAACATACCCACACCTGTTTGTCTTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGCTATAGTGTA AAAACAAAGTTTGGGCTCTGAAAATTAACTGAAAAAGATTCCTTGT  540
          |||
Sbjct   481  AGCTATAGTGTA AAAACAAAGTTTGGGCTCTGAAAATTAACTGAAAAAGATTCCTTGT  540

Query  541  T   541
          |
Sbjct   541  T   541
```

Sequence 590 matched with Sequence 196

Query= Sequence ID 590
Length=336

SEQ ID NO: 196

ALIGNMENTS

Identities = 336/336 (100%), Gaps = 0/336 (0%)

```
Query 1   GTGGCAGCAGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   GTGGCAGCAGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCT  60

Query 61  GTACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATC  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  GTACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATC  120

Query 121 CATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAA  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 CATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAA  180

Query 181 AACTTATGCTATCTGCGGGGCCATTTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AACTTATGCTATCTGCGGGGCCATTTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCG  240

Query 241 ATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAGAATCACAGATGT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 ATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAGAATCACAGATGT  300

Query 301 GGAATATTTGTCATAAATAAATAATGAAAACCTAAA  336
          ||||||||||||||||||||||||||||
Sbjct 301 GGAATATTTGTCATAAATAAATAATGAAAACCTAAA  336
```

Sequence 591 matched with Sequence 197

Query= Sequence ID 591
Length=377

SEQ ID NO: 197

ALIGNMENTS

Identities = 377/377 (100%), Gaps = 0/377 (0%)

Query	1	CAGCAGCAGAAATGTTTGCAAGATAGGCCAAAATGAGTACAAAAGGTCTGTCTTCCATCA	60
Sbjct	1	CAGCAGCAGAAATGTTTGCAAGATAGGCCAAAATGAGTACAAAAGGTCTGTCTTCCATCA	60
Query	61	GACCCAGTGATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGTAGGGAGGT	120
Sbjct	61	GACCCAGTGATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGTAGGGAGGT	120
Query	121	TTATTCANATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGATCACTGTGCAGTG	180
Sbjct	121	TTATTCANATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGATCACTGTGCAGTG	180
Query	181	GGACCACCCTCACTGGCCTTCTGCAGCAGGGTTCTGGGATGTTTTCACTGGTCAAAAATAC	240
Sbjct	181	GGACCACCCTCACTGGCCTTCTGCAGCAGGGTTCTGGGATGTTTTCACTGGTCAAAAATAC	240
Query	241	TCTGTTTAGAGCAAGGGCTCAGAAAACAGAAATACTGTCATGGAGGTGCTGAACACAGGG	300
Sbjct	241	TCTGTTTAGAGCAAGGGCTCAGAAAACAGAAATACTGTCATGGAGGTGCTGAACACAGGG	300
Query	301	AAGGTCTGGTACATATTGGAAATTATGAGCAGAACAAATACTCAACTAAATGCACAAAGT	360
Sbjct	301	AAGGTCTGGTACATATTGGAAATTATGAGCAGAACAAATACTCAACTAAATGCACAAAGT	360
Query	361	ATAAAGTGTAGCCATGT	377
Sbjct	361	ATAAAGTGTAGCCATGT	377

Sequence 592 matched with Sequence 198

Query= Sequence ID 592
Length=63

SEQ ID NO: 198

ALIGNMENTS

Identities = 63/63 (100%), Gaps = 0/63 (0%)

Query	1	TACTCAATGAAAAACCATGATAATTCTTTGTATATAAAATAAACATTTGaaaaaaaaa	60
Sbjct	1	TACTCAATGAAAAACCATGATAATTCTTTGTATATAAAATAAACATTTGAAAAAAAAA	60
Query	61	aaa 63	
Sbjct	61	AAA 63	

Sequence 593 matched with Sequence 199

Query= Sequence ID - 593 nt: 565
Length=565

SEQ ID NO: 199 nt: 565

ALIGNMENTS

Identities = 565/565 (100%), Gaps = 0/565 (0%)

Query	1	CAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAATTTCGCATCCGCAAACCTCTGTCTC	60
Sbjct	1	CAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAATTTCGCATCCGCAAACCTCTGTCTC	60
Query	61	AACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAG	120
Sbjct	61	AACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAG	120
Query	121	CTCACAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATC	180
Sbjct	121	CTCACAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATC	180
Query	181	CGGAGAAATGAAAAGATTGCTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATC	240
Sbjct	181	CGGAGAAATGAAAAGATTGCTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATC	240
Query	241	TTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGTTAAGAAAAACAACCTTCTCAGATACT	300
Sbjct	241	TTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGTTAAGAAAAACAACCTTCTCAGATACT	300
Query	301	GGAAACTTTGGTTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAATATGACCCAAGC	360
Sbjct	301	GGAAACTTTGGTTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAATATGACCCAAGC	360
Query	361	ATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCA	420
Sbjct	361	ATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCA	420
Query	421	GACAAGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCC	480
Sbjct	421	GACAAGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATGCGCTGGTTCAGCAGAAGTATGATGGGATCATCCTTCCTGGCAAATAAATTCCCGTT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGCGCTGGTTCAGCAGAAGTATGATGGGATCATCCTTCCTGGCAAATAAATTCCCGTT  540

Query  541  TCTATCCAAAAGAGCAATAAAAAAGT  565
          ||||||||||||||||||||
Sbjct  541  TCTATCCAAAAGAGCAATAAAAAAGT  565
```

Sequence 594 matched with Sequence 200

Query= Sequence ID 594
Length=629

SEQ ID NO: 200

ALIGNMENTS

Identities = 629/629 (100%), Gaps = 0/629 (0%)

Query	1	CAGAAGAGTAAGCAAATCTCaaagcagcgaaggggaagaaactaaaaaaggtagagcaga	60
Sbjct	1	CAGAAGAGTAAGCAAATCTCAAAGCAGCGAAAGGGAAGAACTAAAAAAGGTAGAGCAGA	60
Query	61	aataagagaaaatagagaagagaacaattgagaaaaataattgaaacaaaaGGTGGTTC	120
Sbjct	61	AATAAGAGAAAATAGAGAAGAGACAATTGAGAAAAATAATTGAAACCAAAGGTGGTTC	120
Query	121	TTTGAAGAGCCTAACAAAATGGACACATCTTTAGTTAGAGTGACCAAGAAAAAAGGGCAG	180
Sbjct	121	TTTGAAGAGCCTAACAAAATGGACACATCTTTAGTTAGAGTGACCAAGAAAAAAGGGCAG	180
Query	181	TGACTCAGATTACTTCATTCAAGAGTGAAAGAGGGGCACATCACTACCAATTTACAGAAAT	240
Sbjct	181	TGACTCAGATTACTTCATTCAAGAGTGAAAGAGGGGCACATCACTACCAATTTACAGAAAT	240
Query	241	AAAAAGGATTATGAGGAAATACTACAGATAATTGATGACATTAAGTATAGAGAATATATT	300
Sbjct	241	AAAAAGGATTATGAGGAAATACTACAGATAATTGATGACATTAAGTATAGAGAATATATT	300
Query	301	TCAAGAAAGACACAACTACTGAAACCGACTCAAGAAGAAACAGAAAATCTGAACAGACC	360
Sbjct	301	TCAAGAAAGACACAACTACTGAAACCGACTCAAGAAGAAACAGAAAATCTGAACAGACC	360
Query	361	TATAAAAAATAGAGATTTAATTGATATTCAGAAAGTTTCCCAAAAAGAAAAGCACTGGCC	420
Sbjct	361	TATAAAAAATAGAGATTTAATTGATATTCAGAAAGTTTCCCAAAAAGAAAAGCACTGGCC	420
Query	421	AAGATGACTTCACTGGTGAATTCTATCAAGTGTCAAAGATGAATTACTGACATTCATTCA	480
Sbjct	421	AAGATGACTTCACTGGTGAATTCTATCAAGTGTCAAAGATGAATTACTGACATTCATTCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CACTCCTTTAAGAAATAGAAGAGGGGACATCACTTTTCAAAGCATCGACATTCTAATCAT	540
Sbjct	481	CACTCCTTTAAGAAATAGAAGAGGGGACATCACTTTTCAAAGCATCGACATTCTAATCAT	540
Query	541	TAGTCCCTTGTTTCCTGCTCCCAAAGCCAGGTGATGTATCACaaaaaaCCCCTACAGA	600
Sbjct	541	TAGTCCCTTGTTTCCTGCTCCCAAAGCCAGGTGATGTATCACAAAAAACCCCTACAGA	600
Query	601	CCCACTGGGCACAATGGCTTTATGCCTAT	629
Sbjct	601	CCCACTGGGCACAATGGCTTTATGCCTAT	629

Sequence 595 matched with Sequence 201

Query= Sequence ID - 595 nt: 98
Length=98

SEQ ID NO: 201 nt: 98

ALIGNMENTS

Identities = 98/98 (100%), Gaps = 0/98 (0%)

```
Query 1  CTTTGCTCGAATNGTCAGATAAGGATTCTGTGAANGGAGATGAGATTCCATCCATGCTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  CTTTGCTCGAATNGTCAGATAAGGATTCTGTGAANGGAGATGAGATTCCATCCATGCTG 60

Query 61 ACTTTGANAATACATGTTCCCGAATTGGGGNCCCCAAA 98
          ||||||||||||||||||||||||||||
Sbjct 61 ACTTTGANAATACATGTTCCCGAATTGGGGNCCCCAAA 98
```

Sequence 596 matched with Sequence 202

Query= Sequence ID 596
Length=224

SEQ ID NO: 202

ALIGNMENTS

Identities = 224/224 (100%), Gaps = 0/224 (0%)

Query	1	CTCAAGTGTTCCCTCAGCTTAGGCTTTGTTTAAATGATCCCACCCAGGGGCGATGGTAGG	60
Sbjct	1	CTCAAGTGTTCCCTCAGCTTAGGCTTTGTTTAAATGATCCCACCCAGGGGCGATGGTAGG	60
Query	61	GAACAACAGGGTCACTAAACTATTTGGCTGGCTACAACCTCTGGGAAATGGTAAGACAGGG	120
Sbjct	61	GAACAACAGGGTCACTAAACTATTTGGCTGGCTACAACCTCTGGGAAATGGTAAGACAGGG	120
Query	121	AAAGGCCATGTTGTTTCATTCCCTTGTGCAGATCTAGGGAGAACCGCAGAGAGAACAGTTA	180
Sbjct	121	AAAGGCCATGTTGTTTCATTCCCTTGTGCAGATCTAGGGAGAACCGCAGAGAGAACAGTTA	180
Query	181	GCATTTCTTGTTCAATGAATTATCCTATTAAGAACACTGGATGT	224
Sbjct	181	GCATTTCTTGTTCAATGAATTATCCTATTAAGAACACTGGATGT	224

Sequence 597 matched with Sequence 203

Query= Sequence ID 597
Length=81

SEQ ID NO: 203

ALIGNMENTS

Identities = 81/81 (100%), Gaps = 0/81 (0%)

```
Query 1  CGGNCGCGGTCGACGCTACTCCTACCTATCTCCCCTTTTATACTAATAATCTTATAaaaa 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  CGGNCGCGGTCGACGCTACTCCTACCTATCTCCCCTTTTATACTAATAATCTTATAAAAA 60

Query 61  aaaaaaaaaaaaaaaaaaaaaa 81
          ||||||||||||||||
Sbjct 61  AAAAAAAAAANAAAAAAAAAAAA 81
```

Sequence 598 matched with Sequence 204

Query= Sequence ID - 598 nt: 362
Length=362

SEQ ID NO: 204 nt: 362

ALIGNMENTS

Identities = 362/362 (100%), Gaps = 0/362 (0%)

```
Query 1  GGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAAGAGTTCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  GGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAAGAGTTCAA 60

Query 61 GGCTGCAACAAGCTTTGATTGCGCCACTGCACTCCANCCTTGGCGACAGACTAAAACGCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GGCTGCAACAAGCTTTGATTGCGCCACTGCACTCCANCCTTGGCGACAGACTAAAACGCT 120

Query 121 GTCTCaaaaaaaaaacaacgacnaaaaaaaaaaacaacagaaaaaaTTAACTTAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 GTCTCAAAAAAAAAAACAAAAACGACNAAAAAAAAAACAAACAGAAAAAATTAACCTTAGGC 180

Query 181 AATGACAGTCCCTGGCAAATGCTGGGAGGGAGGCAACANTGGTCAAGGAAGGTAACCCCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AATGACAGTCCCTGGCAAATGCTGGGAGGGAGGCAACANTGGTCAAGGAAGGTAACCCCTG 240

Query 241 AANCAGGACTTGTAAGCAAATAANATTGGGAGGCCAAGGTGGGTGGATCACNAGGTCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AANCAGGACTTGTAAGCAAATAANATTGGGAGGCCAAGGTGGGTGGATCACNAGGTCAG 300

Query 301 GAGTTCGAGACCAACCTGGCCAACATAGTGAAACCCCGTCTTTCTAAAAATACaaaaaaa 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 GAGTTCGAGACCAACCTGGCCAACATAGTGAAACCCCGTCTTTCTAAAAATACAAAAAAA 360

Query 361 TT 362
          ||
Sbjct 361 TT 362
```

Sequence 599 matched with Sequence 205

Query= Sequence ID 599
Length=581

SEQ ID NO: 205

ALIGNMENTS

Identities = 581/581 (100%), Gaps = 0/581 (0%)

Query	1	GACAAAAGAACCATTTGGATACATAGGTATGGTCTGAGCTATGATATCAATTGGCTTCCT	60
Sbjct	1	GACAAAAGAACCATTTGGATACATAGGTATGGTCTGAGCTATGATATCAATTGGCTTCCT	60
Query	61	AGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACGTAGACACACGAGC	120
Sbjct	61	AGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACGTAGACACACGAGC	120
Query	121	ATATTTACCTCCGCTACCATAATCATCGCTATCCCCACGGCGTCAAAGTATTTAGCTG	180
Sbjct	121	ATATTTACCTCCGCTACCATAATCATCGCTATCCCCACGGCGTCAAAGTATTTAGCTG	180
Query	181	ACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTCTGAGCCCTAGG	240
Sbjct	181	ACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTCTGAGCCCTAGG	240
Query	241	ATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCAAACATCACT	300
Sbjct	241	ATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCAAACATCACT	300
Query	301	AGACATCGTACTACACGACACGTACTACGTTGTAGCTCACTTCCACTATGTCCTATCAAT	360
Sbjct	301	AGACATCGTACTACACGACACGTACTACGTTGTAGCTCACTTCCACTATGTCCTATCAAT	360
Query	361	AGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTATTCTCAGGCTA	420
Sbjct	361	AGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTATTCTCAGGCTA	420
Query	421	CACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCT	480
Sbjct	421	CACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AACTTTCTTCCCACAACACTTTCTCGGCCTGTCCGGAATGCCCCGACGTTACTCGGACTA  540
          |||
Sbjct  481  AACTTTCTTCCCACAACACTTTCTCGGCCTGTCCGGAATGCCCCGACGTTACTCGGACTA  540

Query  541  CCCCgATGCATACACCACATGAAACATCCTATCATCTGGAG  581
          |||
Sbjct  541  CCCCgATGCATACACCACATGAAACATCCTATCATCTGGAG  581
```

Sequence 600 matched with Sequence 206

Query= Sequence ID - 600 nt: 595
Length=595

SEQ ID NO: 206 nt: 595

ALIGNMENTS

Identities = 595/595 (100%), Gaps = 0/595 (0%)

Query	1	TTCAAATTCCTTGNTAANAGTCTTTGTTCTGAATTTTACTTTGTCTGTTATTCCTATAGCC	60
Sbjct	1	TTCAAATTCCTTGNTAANAGTCTTTGTTCTGAATTTTACTTTGTCTGTTATTCCTATAGCC	60
Query	61	TTTCCAATTTTCTTTTCGCTTGGAAttttacgtgataagttttttcccccattttactttta	120
Sbjct	61	TTTCCAATTTTCTTTTCGCTTGGAATTTTACGTGATAAGTTTTTTCCCCATTTTACTTTTA	120
Query	121	ncaactctatatattttttaGTTGAGGTTGGGTTTCTTGTAACAGCATATAATTTGGGTTT	180
Sbjct	121	NCAACTCTATATTTTTTAGTTGAGGTTGGGTTTCTTGTAACAGCATATAATTTGGGTTT	180
Query	181	TTTAATCCAATCTGAAAATTAATGTCCTTAATTTTGTGTTTATACCATTACACATAATG	240
Sbjct	181	TTTAATCCAATCTGAAAATTAATGTCCTTAATTTTGTGTTTATACCATTACACATAATG	240
Query	241	TACTCATATATAAGGTTTAACTGAAACCTACTATCTTGCTAGTTGTGCTCTACTTGAAAt	300
Sbjct	241	TACTCATATATAAGGTTTAACTGAAACCTACTATCTTGCTAGTTGTGCTCTACTTGAAAT	300
Query	301	tttttttAGTATTCTGTTTTAATTGACCAACATTTGACTGTATCTCTTTGTGTAATTCTT	360
Sbjct	301	TTTTTTTAGTATTCTGTTTTAATTGACCAACATTTGACTGTATCTCTTTGTGTAATTCTT	360
Query	361	TTACAGGTTGCTGTAGGCATGACAATATATACACTTAACTTTTCTCAGTACACTGAGAGT	420
Sbjct	361	TTACAGGTTGCTGTAGGCATGACAATATATACACTTAACTTTTCTCAGTACACTGAGAGT	420
Query	421	TGAAATTGTAGTACTTCGAGGAAAAACATAGAAAACCTTGCAATGATATCGGTTACATTTTA	480
Sbjct	421	TGAAATTGTAGTACTTCGAGGAAAAACATAGAAAACCTTGCAATGATATCGGTTACATTTTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCACCTCCATATGTTGCAATTATTAAATGTATTAGATCTGCCTACCTCGAAAACCCATCA	540
Sbjct	481	CCACCTCCATATGTTGCAATTATTAAATGTATTAGATCTGCCTACCTCGAAAACCCATCA	540
Query	541	GTCTTTTAACTTTGCTCTCAATGGTGATTCATATTTTaaaaaaCTTGAGGCAA	595
Sbjct	541	GTCTTTTAACTTTGCTCTCAATGGTGATTCATATTTTAAAAAACTTGAGGCAA	595

Sequence 601 matched with Sequence 207

Query= Sequence ID - 601 nt: 522
Length=522

SEQ ID NO: 207 nt: 522

ALIGNMENTS

Identities = 522/522 (100%), Gaps = 0/522 (0%)

Query	1	TCGACCGGGTTTGGAGCAGTGCCTTGTTTGCTGTGCAGCGGATACTCTACAGGTACATTT	60
Sbjct	1	TCGACCGGGTTTGGAGCAGTGCCTTGTTTGCTGTGCAGCGGATACTCTACAGGTACATTT	60
Query	61	CCTTTTTGGAACCAAAAGGGAGGGATTTGACAATATTGATGGTAGATCTTTTTCTTTAG	120
Sbjct	61	CCTTTTTGGAACCAAAAGGGAGGGATTTGACAATATTGATGGTAGATCTTTTTCTTTAG	120
Query	121	CAAGAATTAAGGATTTTGGTGGGTGGGGGAGGCTTCTGTGGGGACCAAGACAATGTACT	180
Sbjct	121	CAAGAATTAAGGATTTTGGTGGGTGGGGGAGGCTTCTGTGGGGACCAAGACAATGTACT	180
Query	181	GTCAGTCAGGATTTAAGTCGAACTACCTCATCCCTTGCCCCAGAGAACAGTTGATCGTGT	240
Sbjct	181	GTCAGTCAGGATTTAAGTCGAACTACCTCATCCCTTGCCCCAGAGAACAGTTGATCGTGT	240
Query	241	TTTAAACCAAAAGGTGCGGAATGGAGAGAGGGAGGCGGTGCATTGCAGCTTCCGATAGAG	300
Sbjct	241	TTTAAACCAAAAGGTGCGGAATGGAGAGAGGGAGGCGGTGCATTGCAGCTTCCGATAGAG	300
Query	301	CTTTTTATTTTGGATATCAGGAACCAATTTTGAAGATTTCTTAAGAAAGTCATTTACAT	360
Sbjct	301	CTTTTTATTTTGGATATCAGGAACCAATTTTGAAGATTTCTTAAGAAAGTCATTTACAT	360
Query	361	CAGGGACATGAAGAGCAAAGTAGGTATTTTGGTCAGTACTTGAATTTGATAGGCTTTAT	420
Sbjct	361	CAGGGACATGAAGAGCAAAGTAGGTATTTTGGTCAGTACTTGAATTTGATAGGCTTTAT	420
Query	421	GCAAACAACCTCTCCCTCTGCTGGAGTCTGGCAAGTTTGCTTTTCACTGGACGCTAATTCA	480
Sbjct	421	GCAAACAACCTCTCCCTCTGCTGGAGTCTGGCAAGTTTGCTTTTCACTGGACGCTAATTCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGTGCCATACAAAACATAAATAANAGTTTTACTTATAACACA	522
Sbjct	481	AGTGCCATACAAAACATAAATAANAGTTTTACTTATAACACA	522

Sequence 602 matched with Sequence 208

Query= Sequence ID 602
Length=585

SEQ ID NO: 208

ALIGNMENTS

Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query	1	CAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAACTGACATTGATACTACCT	60
Sbjct	1	CAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAACTGACATTGATACTACCT	60
Query	61	TCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTCTTACAAGAGGGAGTGTA	120
Sbjct	61	TCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTCTTACAAGAGGGAGTGTA	120
Query	121	TAAACCTTGGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTG	180
Sbjct	121	TAAACCTTGGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTG	180
Query	181	TCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTTGACAGTGCCAAATCAA	240
Sbjct	181	TCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTTGACAGTGCCAAATCAA	240
Query	241	AGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGGGGACTTCCAGCTACACACTA	300
Sbjct	241	AGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGGGGACTTCCAGCTACACACTA	300
Query	301	ATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGAAGATCTTG	360
Sbjct	301	ATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGAAGATCTTG	360
Query	361	ACACTTCAGTAAACCTTGCTTGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAG	420
Sbjct	361	ACACTTCAGTAAACCTTGCTTGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAG	420
Query	421	CTAAATATCAGTTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACTCTAGCTTAA	480
Sbjct	421	CTAAATATCAGTTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACTCTAGCTTAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTGGAGTAGGCTATACTCAGACTCTGAGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTGGAGTAGGCTATACTCAGACTCTGAGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGG  540

Query  541  TAGATGGGAAGAGCATTAAATGCTGGAGGCCACAAGGTTGGGCTCG  585
          |||||||||||||||||||||||||||||||||||||||
Sbjct   541  TAGATGGGAAGAGCATTAAATGCTGGAGGCCACAAGGTTGGGCTCG  585
```

Sequence 603 matched with Sequence 209

Query= Sequence ID - 603 nt: 624
Length=624

SEQ ID NO: 209 nt: 624

ALIGNMENTS

Identities = 624/624 (100%), Gaps = 0/624 (0%)

Query	1	GACACACGAGCATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA	60
Sbjct	1	GACACACGAGCATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA	60
Query	61	GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC	120
Sbjct	61	GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC	120
Query	121	TGAGCCCTAGGATTCATCTTTCTTTTACCGTAGGTGGCCTGACTGGCATTGTATTAGCA	180
Sbjct	121	TGAGCCCTAGGATTCATCTTTCTTTTACCGTAGGTGGCCTGACTGGCATTGTATTAGCA	180
Query	181	AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT	240
Sbjct	181	AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT	240
Query	241	GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA	300
Sbjct	241	GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA	300
Query	301	TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC	360
Sbjct	301	TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC	360
Query	361	GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT	420
Sbjct	361	GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT	420
Query	421	TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC	480
Sbjct	421	TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540

Query  541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGA CTATATGGATGCCCC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGA CTATATGGATGCCCC  600

Query  601  CCACCCTACCACACATT CGAAGAA  624
          |||||||||||||||||||
Sbjct   601  CCACCCTACCACACATT CGAAGAA  624
```

Sequence 605 matched with Sequence 210

Query= Sequence ID - 605 nt: 338
Length=338

SEQ ID NO: 210 nt: 338

ALIGNMENTS

Identities = 338/338 (100%), Gaps = 0/338 (0%)

```
Query 1  ACCTGAGGCCTCGGTGGGGCCAGTGCGACGCTGGCTTAAGGAGCTGGAGGGGTTCTTAAT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  ACCTGAGGCCTCGGTGGGGCCAGTGCGACGCTGGCTTAAGGAGCTGGAGGGGTTCTTAAT 60

Query 61 ACACATTTAATTTCAGTTTCTCTTCCCTAAGAGGCTGCCGGAGTTGGGGCCTCCTCCAGCA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 ACACATTTAATTTCAGTTTCTCTTCCCTAAGAGGCTGCCGGAGTTGGGGCCTCCTCCAGCA 120

Query 121 GAGACCCTCGGACCCCTGCAGGGCCTGGACTTGGGGTGAACAGGGCTTCAGTCAGCGCAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 GAGACCCTCGGACCCCTGCAGGGCCTGGACTTGGGGTGAACAGGGCTTCAGTCAGCGCAA 180

Query 181 GTATTCCATTTGCATTTGGTAATTTTTCATGCCACCTATTTATGAATATATAAAATCTTTA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 GTATTCCATTTGCATTTGGTAATTTTTCATGCCACCTATTTATGAATATATAAAATCTTTA 240

Query 241 TACCAAATCTATTTTTTAAAAACATGGAAAAGTTGCCTTTATGGAACTTGGCAGAGCCAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TACCAAATCTATTTTTTAAAAACATGGAAAAGTTGCCTTTATGGAACTTGGCAGAGCCAG 300

Query 301 AGTGTACACATTCCTAAACCATTAACAGATTTCTATA 338
          |||||||||||||||||||||||||||||||||||
Sbjct 301 AGTGTACACATTCCTAAACCATTAACAGATTTCTATA 338
```


Sequence 606 matched with Sequence 211

Query= Sequence ID - 606 nt: 556
Length=556

SEQ ID NO: 211 nt: 556

ALIGNMENTS

Identities = 556/556 (100%), Gaps = 0/556 (0%)

Query	1	GGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACTTGAGTGTGCAGCTGCATG	60
Sbjct	1	GGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACTTGAGTGTGCAGCTGCATG	60
Query	61	AGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATACCAGTAGGACAAGGCAGGA	120
Sbjct	61	AGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATACCAGTAGGACAAGGCAGGA	120
Query	121	AAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTTGGAAACTGGATGTTTGCT	180
Sbjct	121	AAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTTGGAAACTGGATGTTTGCT	180
Query	181	AAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACTCCAGAAACCTGGAGAGA	240
Sbjct	181	AAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACTCCAGAAACCTGGAGAGA	240
Query	241	TTAATGGGGCCTATGGAGAAAGTGCTCTGAACTCAGTGTTGGGACTTGAATAAAATTAACC	300
Sbjct	241	TTAATGGGGCCTATGGAGAAAGTGCTCTGAACTCAGTGTTGGGACTTGAATAAAATTAACC	300
Query	301	ATTGTCATGTTTTCAGAACAACCTAAGCTGTTTTATATTTTCATGTGCATGAAAGCCCTAGA	360
Sbjct	301	ATTGTCATGTTTTCAGAACAACCTAAGCTGTTTTATATTTTCATGTGCATGAAAGCCCTAGA	360
Query	361	ACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCACAGTTAGATGATGTGGCCATTA	420
Sbjct	361	ACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCACAGTTAGATGATGTGGCCATTA	420
Query	421	GGAAGTACCAAATTTATAAAAAATCACTGGAGGTCTGTCTGAGCAGTACCTAATAAAATAT	480
Sbjct	421	GGAAGTACCAAATTTATAAAAAATCACTGGAGGTCTGTCTGAGCAGTACCTAATAAAATAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGTATACTGAAAGTGAACAGATCTTTGTCTCTTTCTTTGGCTGCTTGATACTTTATCTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGTATACTGAAAGTGAACAGATCTTTGTCTCTTTCTTTGGCTGCTTGATACTTTATCTGT  540

Query  541  GTCTGCCGGACAGTGC  556
          ||||||||||||
Sbjct   541  GTCTGCCGGACAGTGC  556
```

Sequence 607 matched with Sequence 212

Query= Sequence ID 607
Length=305

SEQ ID NO: 212

ALIGNMENTS

Identities = 305/305 (100%), Gaps = 0/305 (0%)

```
Query  1      CAATAAAAGCAGGTAAACCTCAATGATAGCAGTTAAATGTTCTATCTTATGTATTTCTT  60
          |||
Sbjct  1      CAATAAAAGCAGGTAAACCTCAATGATAGCAGTTAAATGTTCTATCTTATGTATTTCTT  60

Query  61     TTAAGTATTACCATTATGGTGCTACTGAGCGTTTTCTTTGGTAAAAAGAAAAATGCCAT  120
          |||
Sbjct  61     TTAAGTATTACCATTATGGTGCTACTGAGCGTTTTCTTTGGTAAAAAGAAAAATGCCAT  120

Query  121    GGGCTGCAGTCTTCTCCATCACTTTTCCCTACCAGGTCCATTAATATGCTTATAACACT  180
          |||
Sbjct  121    GGGCTGCAGTCTTCTCCATCACTTTTCCCTACCAGGTCCATTAATATGCTTATAACACT  180

Query  181    AGTGCCAGTTATTTTATTTGATAATGCTTATGGTATTTGTATATTTGTTGCATTCCAAT  240
          |||
Sbjct  181    AGTGCCAGTTATTTTATTTGATAATGCTTATGGTATTTGTATATTTGTTGCATTCCAAT  240

Query  241    TTTGTTTAATAATGAGTGTGTAAACTGCATACGTAAATAAATGTAAATACTAATGTACT  300
          |||
Sbjct  241    TTTGTTTAATAATGAGTGTGTAAACTGCATACGTAAATAAATGTAAATACTAATGTACT  300

Query  301    GCTGC  305
          ||||
Sbjct  301    GCTGC  305
```

Sequence 609 matched with Sequence 213

Query= Sequence ID 609
Length=495

SEQ ID NO: 213

ALIGNMENTS

Identities = 495/495 (100%), Gaps = 0/495 (0%)

Query	1	TTTTATTACCCAAGTTTTAACCTCTGTCTGGTGATttgttggttggttggttgtngttgt	60
Sbjct	1	TTTTATTACCCAAGTTTTAACCTCTGTCTGGTGATTTGTTGTTGTTGTTGTTGTNGTTGT	60
Query	61	tgttgAAGTTCAGGCTGCATGTGGGATAGGTTTGCTCAGGCATACTTCTTAGGAAGTAGT	120
Sbjct	61	TGTTGAAGTTCAGGCTGCATGTGGGATAGGTTTGCTCAGGCATACTTCTTAGGAAGTAGT	120
Query	121	CACTTGCATGACTGTTTTTGGGATAACTCTTTGAGTATTTGGAGAGGTCTATTGTAACCTT	180
Sbjct	121	CACTTGCATGACTGTTTTTGGGATAACTCTTTGAGTATTTGGAGAGGTCTATTGTAACCTT	180
Query	181	CTGAAAGGCATTGTTTTTACGTATGAATGTTCTAAAATTCATTCTAAATGGTCATGAAAA	240
Sbjct	181	CTGAAAGGCATTGTTTTTACGTATGAATGTTCTAAAATTCATTCTAAATGGTCATGAAAA	240
Query	241	GAAAAGGATTACATTTTAGAATGGCAATAGTCCCTGAGGACTATTATGTCTTTTAGATT	300
Sbjct	241	GAAAAGGATTACATTTTAGAATGGCAATAGTCCCTGAGGACTATTATGTCTTTTAGATT	300
Query	301	TCCTGTGGGTTTCTAGGAATGTTAGTGTAACCTTANATTTCCACCTACCTGATTTCTGGAT	360
Sbjct	301	TCCTGTGGGTTTCTAGGAATGTTAGTGTAACCTTANATTTCCACCTACCTGATTTCTGGAT	360
Query	361	GTGCCTATTGGAACCTTGCTGAGATCtttttttttCCTTAACATGTTGTCCCCTTGACCCG	420
Sbjct	361	GTGCCTATTGGAACCTTGCTGAGATCTTTTTTTTTCCTTAACATGTTGTCCCCTTGACCCG	420
Query	421	TACTTCGAAACTAAACATATTATTTTATTTGCTTACACTTCAGGAGGCAATTGGCAGACA	480
Sbjct	421	TACTTCGAAACTAAACATATTATTTTATTTGCTTACACTTCAGGAGGCAATTGGCAGACA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCAGGCCAACAGTCT	495
Sbjct	481	CCAGGCCAACAGTCT	495

Sequence 610 matched with Sequence 214

Query= Sequence ID 610
Length=507

SEQ ID NO: 214

ALIGNMENTS

Identities = 507/507 (100%), Gaps = 0/507 (0%)

Query	1	GCTCTGACCCCAGTTGGAAATGTATCTGTACTTTGTCCGGCTTCCACTCAAGGACCATTT	60
Sbjct	1	GCTCTGACCCCAGTTGGAAATGTATCTGTACTTTGTCCGGCTTCCACTCAAGGACCATTT	60
Query	61	ATGACATTGCTTGGTGTCTGAGCTGACAGGGGCTCTGGCCACAGCTTGTGGGGATGACGCGA	120
Sbjct	61	ATGACATTGCTTGGTGTCTGAGCTGACAGGGGCTCTGGCCACAGCTTGTGGGGATGACGCGA	120
Query	121	TCCGCGTGTTTCAGGAGGATCCCAACTCGGATCCACAGCAGCCACCTTCTCCCTGACAG	180
Sbjct	121	TCCGCGTGTTTCAGGAGGATCCCAACTCGGATCCACAGCAGCCACCTTCTCCCTGACAG	180
Query	181	CCCACTTGCATCAGGCCCATTCCCAGGATGTCAACTGTGTGGCCTGGAACCCCAAGGAGC	240
Sbjct	181	CCCACTTGCATCAGGCCCATTCCCAGGATGTCAACTGTGTGGCCTGGAACCCCAAGGAGC	240
Query	241	CAGGGCTACTGGCCTCCTGCAGTGATGATGGGGAGGTGGCCTTCTGGAAGTATCAGCGGC	300
Sbjct	241	CAGGGCTACTGGCCTCCTGCAGTGATGATGGGGAGGTGGCCTTCTGGAAGTATCAGCGGC	300
Query	301	CTGAAGGCCTCTGAGCTACCTCGACTTTGGACAGAGTAATGACTCCCCAGAAAACGTCAT	360
Sbjct	301	CTGAAGGCCTCTGAGCTACCTCGACTTTGGACAGAGTAATGACTCCCCAGAAAACGTCAT	360
Query	361	ATAAGACTTTACCAGCCCCTGAGAGGACCAGGAGGAGCATCCTTGACCTTCATTTAACTT	420
Sbjct	361	ATAAGACTTTACCAGCCCCTGAGAGGACCAGGAGGAGCATCCTTGACCTTCATTTAACTT	420
Query	421	GGCTCACTTCTCTTCANACTTGGGTAGAAAGTGCAGAGCCACAAAATTGCTTTCCTTCCCC	480
Sbjct	421	GGCTCACTTCTCTTCANACTTGGGTAGAAAGTGCAGAGCCACAAAATTGCTTTCCTTCCCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCCTTTGACATGAGGCCTTCAGTAAAG	507
Sbjct	481	GCCTTTGACATGAGGCCTTCAGTAAAG	507

Sequence 611 matched with Sequence 215

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 611
Length=17

SEQ ID NO: 215

34.2 1e-08

ALIGNMENTS

Identities = 17/17 (100%), Gaps = 0/17 (0%)

```
Query 1  TGCAGGATCCGTCGACT 17
          |||||
Sbjct 1  TGCAGGATCCGTCGACT 17
```


Sequence 612 matched with Sequence 216

Query= Sequence ID - 612 nt: 576
Length=576

SEQ ID NO: 216 nt: 576

ALIGNMENTS

Identities = 576/576 (100%), Gaps = 0/576 (0%)

Query	1	GAGAAATATAAGATTATGTATAGATCAAATCTACCTCTATTTGGTGTCTGAAAGAGATG	60
Sbjct	1	GAGAAATATAAGATTATGTATAGATCAAATCTACCTCTATTTGGTGTCTGAAAGAGATG	60
Query	61	AGGAGAATGGGACAACTTGGAAAGCTTATTTCAAGATAACATTCCTGAGAACTTCCCCA	120
Sbjct	61	AGGAGAATGGGACAACTTGGAAAGCTTATTTCAAGATAACATTCCTGAGAACTTCCCCA	120
Query	121	ATCTTGCTAGAGAGGCCAACATTAATAATTCAGTAAATGCTGAAAACCTCCAGTAAGATATT	180
Sbjct	121	ATCTTGCTAGAGAGGCCAACATTAATAATTCAGTAAATGCTGAAAACCTCCAGTAAGATATT	180
Query	181	TCTTAAGAAAATTATTCCCAAGATATATACTCATCAAATTATCTAAGGTCAAATGAAGGA	240
Sbjct	181	TCTTAAGAAAATTATTCCCAAGATATATACTCATCAAATTATCTAAGGTCAAATGAAGGA	240
Query	241	AAAAATTTTATAGGCAGCTAGAGAGAAATGTCAGGTCACCTACAAAGAGAATGGCATAAG	300
Sbjct	241	AAAAATTTTATAGGCAGCTAGAGAGAAATGTCAGGTCACCTACAAAGAGAATGGCATAAG	300
Query	301	ACAAAAAGTAGAACTCCAGCAGAACTCTAAAAGCCAGAAGAGATTAGGGGCCAATATT	360
Sbjct	301	ACAAAAAGTAGAACTCCAGCAGAACTCTAAAAGCCAGAAGAGATTAGGGGCCAATATT	360
Query	361	TAACATTCTGAAAGAAATTCCAACAAGGAATTTTCATATCCAGCCAACTAAGCTTCATAA	420
Sbjct	361	TAACATTCTGAAAGAAATTCCAACAAGGAATTTTCATATCCAGCCAACTAAGCTTCATAA	420
Query	421	TTGAAGGAGAAATAAGATATTTTCCAGACAAGCAAATGCTGATGAAATCCATCACCACCA	480
Sbjct	421	TTGAAGGAGAAATAAGATATTTTCCAGACAAGCAAATGCTGATGAAATCCATCACCACCA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GACCTGCCTTATAAGAGCTCCTGAGGGAAGCACTAAATATTGAAAGGGAAGAACTTTATG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GACCTGCCTTATAAGAGCTCCTGAGGGAAGCACTAAATATTGAAAGGGAAGAACTTTATG  540

Query  541  AACCATTTCAAAAACACATTTAAGTNCACAAAGCAG  576
          |||||||||||||||||||||||||||||
Sbjct   541  AACCATTTCAAAAACACATTTAAGTNCACAAAGCAG  576
```

Sequence 613 matched with Sequence 217

Query= Sequence ID - 613 nt: 341
Length=341

SEQ ID NO: 217 nt: 341

ALIGNMENTS

Identities = 341/341 (100%), Gaps = 0/341 (0%)

```
Query 1 CCTTATTTTACAGGTGAAAAACCAAGTATCAGATAGATTTTATTTGCCCAAGTCACATA 60
      |||
Sbjct 1 CCTTATTTTACAGGTGAAAAACCAAGTATCAGATAGATTTTATTTGCCCAAGTCACATA 60

Query 61 ATATTAAGAACAGGCCAAGTGTGGTGGCTCATGTCTGTAATCTGAGCACTTTGGGAGGCT 120
      |||
Sbjct 61 ATATTAAGAACAGGCCAAGTGTGGTGGCTCATGTCTGTAATCTGAGCACTTTGGGAGGCT 120

Query 121 AAGGCGGGTGGATTTCTGAGCCTAGGAGTTTGAGATCAGCCTGGGCAACATGGCGAAAC 180
      |||
Sbjct 121 AAGGCGGGTGGATTTCTGAGCCTAGGAGTTTGAGATCAGCCTGGGCAACATGGCGAAAC 180

Query 181 CTCATCTCTACAAAACATACAAAAATTAGTCAGTGTGGTGGTGAGAGCCTGTAGTCCTGG 240
      |||
Sbjct 181 CTCATCTCTACAAAACATACAAAAATTAGTCAGTGTGGTGGTGAGAGCCTGTAGTCCTGG 240

Query 241 CTACTCGTGAGGCTGAGGTGGGAGCATCACCTGAGCCTGGGAAGTCGAGGCTGCAGTGGC 300
      |||
Sbjct 241 CTACTCGTGAGGCTGAGGTGGGAGCATCACCTGAGCCTGGGAAGTCGAGGCTGCAGTGGC 300

Query 301 AACAGAATGGGTAACCTGGACATCAGAGTGAGACCCTGTCT 341
      |||
Sbjct 301 AACAGAATGGGTAACCTGGACATCAGAGTGAGACCCTGTCT 341
```

Sequence 614 matched with Sequence 218

Query= Sequence ID 614
Length=494

SEQ ID NO: 218

ALIGNMENTS

Identities = 494/494 (100%), Gaps = 0/494 (0%)

Query	1	CTCACACCTGTAATTCATTACTTTGGAAGGCTGAGAGAGGAGGATCAGTGGAGCCCAGG	60
Sbjct	1	CTCACACCTGTAATTCATTACTTTGGAAGGCTGAGAGAGGAGGATCAGTGGAGCCCAGG	60
Query	61	AGTTTGAGACCAGCCTGGGCAATATAGGGAGACCCTGTCTCTACAAAAATGAAATAGCCA	120
Sbjct	61	AGTTTGAGACCAGCCTGGGCAATATAGGGAGACCCTGTCTCTACAAAAATGAAATAGCCA	120
Query	121	GGCGAGGTGGCATGTGCCTGTGGTCCCAGCTACTTGGGAGACTGAGGTGGAAGGCTGCCT	180
Sbjct	121	GGCGAGGTGGCATGTGCCTGTGGTCCCAGCTACTTGGGAGACTGAGGTGGAAGGCTGCCT	180
Query	181	TGAGCCCAGGAGTTCCAGGCTGCAGTGAGCCATCATTATGCCACTGCACTCCAACCTGGG	240
Sbjct	181	TGAGCCCAGGAGTTCCAGGCTGCAGTGAGCCATCATTATGCCACTGCACTCCAACCTGGG	240
Query	241	AGACAGAGTGAGAGAGACCCTGTCTCAAACAAACAAACCCAAAATAGGCCAGGCACAGTG	300
Sbjct	241	AGACAGAGTGAGAGAGACCCTGTCTCAAACAAACAAACCCAAAATAGGCCAGGCACAGTG	300
Query	301	ACTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAAATAGGCGGATCATTTGAGGTCAG	360
Sbjct	301	ACTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAAATAGGCGGATCATTTGAGGTCAG	360
Query	361	GAGTTCAAATTCAAGACCAGCCCGGCCAACATGGCAAACACATCTCTACTACAAATAA	420
Sbjct	361	GAGTTCAAATTCAAGACCAGCCCGGCCAACATGGCAAACACATCTCTACTACAAATAA	420
Query	421	AAAATTAGTTGGGTGTGGNGGAGCATTCTGTAATCACAGCTATTTCAGGAGGCTGAGGCA	480
Sbjct	421	AAAATTAGTTGGGTGTGGNGGAGCATTCTGTAATCACAGCTATTTCAGGAGGCTGAGGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGANAACCGCTTCA	494
Sbjct	481	TGANAACCGCTTCA	494

Sequence 615 matched with Sequence 219

Query= Sequence ID - 615 nt: 379
Length=379

SEQ ID NO: 219 nt: 379

ALIGNMENTS

Identities = 379/379 (100%), Gaps = 0/379 (0%)

```
Query 1   TAAATTTAAAACATTTTAATTAGCTGGCATGATGGCATGCACCTGTAGTCCTACCTACTT 60
          |||
Sbjct 1   TAAATTTAAAACATTTTAATTAGCTGGCATGATGGCATGCACCTGTAGTCCTACCTACTT 60

Query 61  GGGAGGCCAAGGCAGGAAGATTGCTTGAGCCCAGGAGTTTGAGCTTACTGTGAGCTGTGA 120
          |||
Sbjct 61  GGGAGGCCAAGGCAGGAAGATTGCTTGAGCCCAGGAGTTTGAGCTTACTGTGAGCTGTGA 120

Query 121 TCACACCACTGCACTCCAGCCTGGGTGACAAAGGAAGACCGTATTTCTaaaaataaaaa 180
          |||
Sbjct 121 TCACACCACTGCACTCCAGCCTGGGTGACAAAGGAAGACCGTATTTCTAAAAAATAAAAA 180

Query 181 aTACAAATACAAC TACAACTAGCACTAGACCAACAGTGACTATGTACCATGAACTGAGG 240
          |||
Sbjct 181 ATACAAATACAAC TACAACTAGCACTAGACCAACAGTGACTATGTACCATGAACTGAGG 240

Query 241 AATATTATTAATTCCACCATTTCATCTGAGGTTAACAATATGTCAATGACTTAAATAAC 300
          |||
Sbjct 241 AATATTATTAATTCCACCATTTCATCTGAGGTTAACAATATGTCAATGACTTAAATAAC 300

Query 301 ATCATATCTCTGAGAGTAATTTCTCCTATATTTCCATGACAAATGTTAGATAATTTTCCA 360
          |||
Sbjct 301 ATCATATCTCTGAGAGTAATTTCTCCTATATTTCCATGACAAATGTTAGATAATTTTCCA 360

Query 361 TTTTTTCCATTCAACAAAA 379
          |||
Sbjct 361 TTTTTTCCATTCAACAAAA 379
```

Sequence 617 matched with Sequence 220

Query= Sequence ID 617
Length=421

SEQ ID NO: 220

ALIGNMENTS

Identities = 421/421 (100%), Gaps = 0/421 (0%)

Query	1	TTTTCAGGCATGTCAGAGAAGGGAGGACTCACTAGAATTAGCAAACAAAACACCCTGAC	60
Sbjct	1	TTTTCAGGCATGTCAGAGAAGGGAGGACTCACTAGAATTAGCAAACAAAACACCCTGAC	60
Query	61	ATCCTCCTTCAGGAACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCGCATACCCG	120
Sbjct	61	ATCCTCCTTCAGGAACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCGCATACCCG	120
Query	121	AGACGATTGTATGAAGAAAATATGGAGGAACTGTTACATGTTTCGGTACTAAGTCATTTTC	180
Sbjct	121	AGACGATTGTATGAAGAAAATATGGAGGAACTGTTACATGTTTCGGTACTAAGTCATTTTC	180
Query	181	AGGGGATTGAAAGACTATTGCTGGATTTTCATGATGCTGACTGGCGTTAGCTGATTAACCC	240
Sbjct	181	AGGGGATTGAAAGACTATTGCTGGATTTTCATGATGCTGACTGGCGTTAGCTGATTAACCC	240
Query	241	ATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACAAAGACTGGCTTCTGGACTTC	300
Sbjct	241	ATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACAAAGACTGGCTTCTGGACTTC	300
Query	301	CTCCCTGATCCCCACTCTTACTCATCACCTGCAGTGGCCAGAATTAGGGACTCAGAATCA	360
Sbjct	301	CTCCCTGATCCCCACTCTTACTCATCACCTGCAGTGGCCAGAATTAGGGACTCAGAATCA	360
Query	361	AACCAGTGTAAGGCAGTGCTGGCTGCCATTGCCTGGTCACATTGAAATTGGTGGCTTCAT	420
Sbjct	361	AACCAGTGTAAGGCAGTGCTGGCTGCCATTGCCTGGTCACATTGAAATTGGTGGCTTCAT	420
Query	421	T	421
Sbjct	421	T	421

Sequence 618 matched with Sequence 221

Query= Sequence ID - 618 nt: 598
Length=598

SEQ ID NO: 221 nt: 598

ALIGNMENTS

Identities = 598/598 (100%), Gaps = 0/598 (0%)

Query	1	GATTAACTTTCATTTTAAGCTCTTCTCTACTAATTCTGTTCGTATGTTTATTCATTTTGC	60
Sbjct	1	GATTAACTTTCATTTTAAGCTCTTCTCTACTAATTCTGTTCGTATGTTTATTCATTTTGC	60
Query	61	GTTGATCATATTTTGTACACCAGGCACTCTTCTCAGTTTTATATGTGTGTTAATTTACTC	120
Sbjct	61	GTTGATCATATTTTGTACACCAGGCACTCTTCTCAGTTTTATATGTGTGTTAATTTACTC	120
Query	121	CTTTCAGAGCCCTATGATACATGAATTTATCTCCATTTTATAGATGAGGAAATTAAGAC	180
Sbjct	121	CTTTCAGAGCCCTATGATACATGAATTTATCTCCATTTTATAGATGAGGAAATTAAGAC	180
Query	181	CTAGAGTTACTGAACTTGCCCAAGGTTATACAGCTGATGGGTAGGGCCAGAACTTTGCCT	240
Sbjct	181	CTAGAGTTACTGAACTTGCCCAAGGTTATACAGCTGATGGGTAGGGCCAGAACTTTGCCT	240
Query	241	CAGAGAATCTGAATTTCCAAAAATAACCTAAAAGAGAAATTTAAGTACTAATTAGTAAG	300
Sbjct	241	CAGAGAATCTGAATTTCCAAAAATAACCTAAAAGAGAAATTTAAGTACTAATTAGTAAG	300
Query	301	CAAAGAAATGCACATTTAAGGAAGACAGTGCACATTTAAGGAAGACAGTAACCTTTTATC	360
Sbjct	301	CAAAGAAATGCACATTTAAGGAAGACAGTGCACATTTAAGGAAGACAGTAACCTTTTATC	360
Query	361	TATTAGAGAAAAACACACATTCTGTCTTTAACACACACATAAATCTTATATTGGCAGGGA	420
Sbjct	361	TATTAGAGAAAAACACACATTCTGTCTTTAACACACACATAAATCTTATATTGGCAGGGA	420
Query	421	TTTTCTTTATTCAGCAATTATTTATTGGTTGTCTGCTTTGTGGTACACATAAATGCTGGG	480
Sbjct	421	TTTTCTTTATTCAGCAATTATTTATTGGTTGTCTGCTTTGTGGTACACATAAATGCTGGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GATAAACTTAATAAAATATACTTCCTTCTCTTGAATATCTTGCACTTTAAGTGGGAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GATAAACTTAATAAAATATACTTCCTTCTCTTGAATATCTTGCACTTTAAGTGGGAAG  540

Query  541  GTAAGTCAACAGAGTAGAGGTGATATATCCAAGTGATAGACTGTTTCATTGCCAGTAG  598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTAAGTCAACAGAGTAGAGGTGATATATCCAAGTGATAGACTGTTTCATTGCCAGTAG  598
```

Sequence 619 matched with Sequence 222

Query= Sequence ID 619
Length=473

SEQ ID NO: 222

ALIGNMENTS

Identities = 473/473 (100%), Gaps = 0/473 (0%)

Query	1	GTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGGATCA	60
Sbjct	1	GTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGGATCA	60
Query	61	GAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCATGTGGGTTG	120
Sbjct	61	GAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCATGTGGGTTG	120
Query	121	TATTGTTAGAAGATGGAATTGAATTCTATAAGAAGAAAAGTGACAACAGCCCCAAAGGAA	180
Sbjct	121	TATTGTTAGAAGATGGAATTGAATTCTATAAGAAGAAAAGTGACAACAGCCCCAAAGGAA	180
Query	181	TGATCCCGCTGAAAGGGAGCACTCTGACTAGCCCTTGTCAAGACTTTGGCAAAAGGATGT	240
Sbjct	181	TGATCCCGCTGAAAGGGAGCACTCTGACTAGCCCTTGTCAAGACTTTGGCAAAAGGATGT	240
Query	241	TTGTGTTTAAGATCACTATGACCAAACAGCAGGACCACTTCTTCCAGGCAGCCTTCCTGG	300
Sbjct	241	TTGTGTTTAAGATCACTATGACCAAACAGCAGGACCACTTCTTCCAGGCAGCCTTCCTGG	300
Query	301	AGGAGAGAGATGCCTGGGTTCGGGATATCAATAAGGCCATTAAATGCATTGAAGGAGGCC	360
Sbjct	301	AGGAGAGAGATGCCTGGGTTCGGGATATCAATAAGGCCATTAAATGCATTGAAGGAGGCC	360
Query	361	AGAAATTTGCCAGGAAATCTACCAGGAGGTCCATTGCGACTGCCAGAAACCATTGACTTAG	420
Sbjct	361	AGAAATTTGCCAGGAAATCTACCAGGAGGTCCATTGCGACTGCCAGAAACCATTGACTTAG	420
Query	421	GTGCCTTATATTTGTCCATGAAAGACACTGAAAAAGGAATAAAAGAACTGAAT	473
Sbjct	421	GTGCCTTATATTTGTCCATGAAAGACACTGAAAAAGGAATAAAAGAACTGAAT	473

Sequence 621 matched with Sequence 223

Query= Sequence ID 621
Length=392

SEQ ID NO: 223

ALIGNMENTS

Identities = 392/392 (100%), Gaps = 0/392 (0%)

Query	1	TGGTACTGAACCTACGAGTACACCGACTACGGCGGACTAATCTTCAACTCCTACATACTT	60
Sbjct	1	TGGTACTGAACCTACGAGTACACCGACTACGGCGGACTAATCTTCAACTCCTACATACTT	60
Query	61	CCCCATTATTCTAGAACCCAGGCGACCTGCGACTCCTTGACGTTGACAATCGAGTAGTA	120
Sbjct	61	CCCCATTATTCTAGAACCCAGGCGACCTGCGACTCCTTGACGTTGACAATCGAGTAGTA	120
Query	121	CTCCCGATTGAAGCCCCCATTCGTATAATAATTACATCACAAGACGTCTTGCACTCATGA	180
Sbjct	121	CTCCCGATTGAAGCCCCCATTCGTATAATAATTACATCACAAGACGTCTTGCACTCATGA	180
Query	181	GCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACGTCTAAACCAAACCACT	240
Sbjct	181	GCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACGTCTAAACCAAACCACT	240
Query	241	TTCACCGCTACACGACCGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAAC	300
Sbjct	241	TTCACCGCTACACGACCGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAAC	300
Query	301	CACAGTTTCATGCCCATCGTCCTAGAATTAATTCCCCTAAAAATCTTTGAAATAGGGCCC	360
Sbjct	301	CACAGTTTCATGCCCATCGTCCTAGAATTAATTCCCCTAAAAATCTTTGAAATAGGGCCC	360
Query	361	GTATTTACCCTATAGCACCCCTCTACCCCT	392
Sbjct	361	GTATTTACCCTATAGCACCCCTCTACCCCT	392

Sequence 622 matched with Sequence 224

Query= Sequence ID 622
Length=618

SEQ ID NO: 224

ALIGNMENTS

Identities = 618/618 (100%), Gaps = 0/618 (0%)

Query	1	TTTTTCTTGTTTTGTGTGTCTACCTTGGCATATACTAAAGGAAGGTGTGTATTCATTTA	60
Sbjct	1	TTTTTCTTGTTTTGTGTGTCTACCTTGGCATATACTAAAGGAAGGTGTGTATTCATTTA	60
Query	61	TTACATGATATCTCTGGGTTATAATTATTTACATATATGAATTTGAAAGAAAGATTGAGA	120
Sbjct	61	TTACATGATATCTCTGGGTTATAATTATTTACATATATGAATTTGAAAGAAAGATTGAGA	120
Query	121	GGGATATGTGTGACCTTTGTTTCATTATGATCATTTACATGACTAAAGATAAAGATCATA	180
Sbjct	121	GGGATATGTGTGACCTTTGTTTCATTATGATCATTTACATGACTAAAGATAAAGATCATA	180
Query	181	TGTCTGATTTTCAGTTTAATGGCAAGTTACTTAAAATAAATGAAATATGTTTTTATTGTT	240
Sbjct	181	TGTCTGATTTTCAGTTTAATGGCAAGTTACTTAAAATAAATGAAATATGTTTTTATTGTT	240
Query	241	TTCGTGGGTTTGATGCTTTGTGTTTTATTTCAAGTAACTTGAGAATGCATTGTGTTTGGT	300
Sbjct	241	TTCGTGGGTTTGATGCTTTGTGTTTTATTTCAAGTAACTTGAGAATGCATTGTGTTTGGT	300
Query	301	ACTGTTTTTTATGAATATCATTAAAAATTTATTTAAGGAGAGAGTAATTTTGCaataata	360
Sbjct	301	ACTGTTTTTTATGAATATCATTAAAAATTTATTTAAGGAGAGAGTAATTTTGCAATAATA	360
Query	361	tttttgatttatttgaaaataaaaattcaagataaatgaaataattgaaattttCTAAAGA	420
Sbjct	361	TTTTTGATTTATTTGAAAATAAAATTCAAGATAAATGAAATAATTGAAATTTTCTAAAGA	420
Query	421	AGGAATTGAATATATTTTTACATTTGAATGAACTAAGGATTAAGTGAACCATTTATATAT	480
Sbjct	421	AGGAATTGAATATATTTTTACATTTGAATGAACTAAGGATTAAGTGAACCATTTATATAT	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGTACTTTCAGAACTGAATGTCTTAAATGATAAAGCTCTAATTGGTTAAAGTGACTTTCT	540
Sbjct	481	AGTACTTTCAGAACTGAATGTCTTAAATGATAAAGCTCTAATTGGTTAAAGTGACTTTCT	540
Query	541	TTCAAGTCAAAGAACCCAGAACTGAATAGATGATCTAACTACTGCCACTGAGGTTTTGG	600
Sbjct	541	TTCAAGTCAAAGAACCCAGAACTGAATAGATGATCTAACTACTGCCACTGAGGTTTTGG	600
Query	601	ATTAGTGAGTATAAATTT	618
Sbjct	601	ATTAGTGAGTATAAATTT	618

Sequence 624 matched with Sequence 225

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 624
Length=17

SEQ ID NO: 225

34.2 1e-08

ALIGNMENTS

Identities = 17/17 (100%), Gaps = 0/17 (0%)

```
Query 1  TGCAGGATCCGTCGACT 17
          |||||
Sbjct 1  TGCAGGATCCGTCGACT 17
```


Sequence 625 matched with Sequence 226

Query= Sequence ID 625
Length=396

SEQ ID NO: 226

ALIGNMENTS

Identities = 396/396 (100%), Gaps = 0/396 (0%)

```
Query 1      GACAATCAGAGCAGATCTTGGGCTTCTGTGGCTCATCTCAGCCCTTTATAACTGGCCTGA  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1      GACAATCAGAGCAGATCTTGGGCTTCTGTGGCTCATCTCAGCCCTTTATAACTGGCCTGA  60

Query 61     GAAGAGGGTTTATCTACTTGTGCAAGTGGCCCAGAAATCTCACTCGTACATGAGGCTTTG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61     GAAGAGGGTTTATCTACTTGTGCAAGTGGCCCAGAAATCTCACTCGTACATGAGGCTTTG  120

Query 121    GAACATCCTTGCAAAGGTACGCTGAAAGCAAATTGCTGTTTTCTGGTGGTTCTGCACGT  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121    GAACATCCTTGCAAAGGTACGCTGAAAGCAAATTGCTGTTTTCTGGTGGTTCTGCACGT  180

Query 181    TTCCTAACTTTTATCATAGTTTGATTTTCATTATTTAAGaaaaataaaaaaTCCAAAGA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181    TTCCTAACTTTTATCATAGTTTGATTTTCATTATTTAAGAAAAAATAAAAAATCCAAAGA  240

Query 241    CCATAAGATGGCATTAGATTTTTTACCATTAAATTATTAATGCCTATTTGGTGCTCATAA  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241    CCATAAGATGGCATTAGATTTTTTACCATTAAATTATTAATGCCTATTTGGTGCTCATAA  300

Query 301    AGATTAATCATGTCACGCATGTTTCCAATCTTTCTTTTGCAGTATATTATTTTCTAAAAA  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301    AGATTAATCATGTCACGCATGTTTCCAATCTTTCTTTTGCAGTATATTATTTTCTAAAAA  360

Query 361    TTGTTACATGCAAATTTAAACCAAGATTTATCAGTA  396
          ||||||||||||||||||||||||||||
Sbjct 361    TTGTTACATGCAAATTTAAACCAAGATTTATCAGTA  396
```

Sequence 626 matched with Sequence 227

Query= Sequence ID 626
Length=535

SEQ ID NO: 227

ALIGNMENTS

Identities = 535/535 (100%), Gaps = 0/535 (0%)

Query	1	TTGGAAGAAATAAACCAAGGCAGAAAAATTTTAAATGGCCAAAATAAATTGTATTGCTAA	60
Sbjct	1	TTGGAAGAAATAAACCAAGGCAGAAAAATTTTAAATGGCCAAAATAAATTGTATTGCTAA	60
Query	61	CTTAGATGGCCACAGATGGGGGCAGGGGTGGAGAGAGGAGAAATTGAAAACNCCACAAAG	120
Sbjct	61	CTTAGATGGCCACAGATGGGGGCAGGGGTGGAGAGAGGAGAAATTGAAAACNCCACAAAG	120
Query	121	ACCCCGCAATGGCTAGAACTTGAAATCTCTGGATATTGCAACAATAGCAGCCTCCTTAAG	180
Sbjct	121	ACCCCGCAATGGCTAGAACTTGAAATCTCTGGATATTGCAACAATAGCAGCCTCCTTAAG	180
Query	181	TCAGCAAAAAGATAAAGATTGATCCAATGTTCTATATTACAGAACAGAGCAGATTGTCAA	240
Sbjct	181	TCAGCAAAAAGATAAAGATTGATCCAATGTTCTATATTACAGAACAGAGCAGATTGTCAA	240
Query	241	TATAGCAAATAAAGTTACCGTTGAGTGGACTGCGCTGTNTAAGCTGCTTGGTTGGCCTTA	300
Sbjct	241	TATAGCAAATAAAGTTACCGTTGAGTGGACTGCGCTGTNTAAGCTGCTTGGTTGGCCTTA	300
Query	301	AGTGCCGACAATTAAGAGATGAAGGCAATGAGAACTGAAACAAACATTTAAGTTCAAGAC	360
Sbjct	301	AGTGCCGACAATTAAGAGATGAAGGCAATGAGAACTGAAACAAACATTTAAGTTCAAGAC	360
Query	361	CCAGTTTACTGACACTGGGACTATTACTATATCTCTTTGGGCCTCAGTTTACTTATCTGT	420
Sbjct	361	CCAGTTTACTGACACTGGGACTATTACTATATCTCTTTGGGCCTCAGTTTACTTATCTGT	420
Query	421	AACATTAAGAGGTTGGATTACATGATGTCTCACGATTCTtttttttttATTTAGAGATGGG	480
Sbjct	421	AACATTAAGAGGTTGGATTACATGATGTCTCACGATTCTTTTTTTTTTATTTAGAGATGGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTTTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCATGATCATAGCTCACAGCAG	535
Sbjct	481	GTTTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCATGATCATAGCTCACAGCAG	535

Sequence 627 matched with Sequence 228

Query= Sequence ID 627
Length=392

SEQ ID NO: 228

ALIGNMENTS

Identities = 392/392 (100%), Gaps = 0/392 (0%)

Query	1	CCAGCCTGTCACTGGCCTGGCCAAGGAGGAGAGACAGGCCAGGGATTCTGGTCCTAACTC	60
Sbjct	1	CCAGCCTGTCACTGGCCTGGCCAAGGAGGAGAGACAGGCCAGGGATTCTGGTCCTAACTC	60
Query	61	TACTGGCCACACTGTGTGGCCTGAGACCCCCCTTTCCCTCCCAAGCCCCTGCCTCCGCAT	120
Sbjct	61	TACTGGCCACACTGTGTGGCCTGAGACCCCCCTTTCCCTCCCAAGCCCCTGCCTCCGCAT	120
Query	121	CTGCGTGGTGAAGGCCATTGGCCCTCATCGGTGGATCTGCGTTTCCTCGGGCCTACACTG	180
Sbjct	121	CTGCGTGGTGAAGGCCATTGGCCCTCATCGGTGGATCTGCGTTTCCTCGGGCCTACACTG	180
Query	181	TCTAGGATTGTGCGGGGCTGGTGAGAGAACAAGATCTCTTCCGTGTTCAAGGCAGACTTC	240
Sbjct	181	TCTAGGATTGTGCGGGGCTGGTGAGAGAACAAGATCTCTTCCGTGTTCAAGGCAGACTTC	240
Query	241	CTGCCCCCTGCACCCTGCTCTCTCCCAGGCCTTGAGGTCAGTGTGAGCCCCAAGGGCAAG	300
Sbjct	241	CTGCCCCCTGCACCCTGCTCTCTCCCAGGCCTTGAGGTCAGTGTGAGCCCCAAGGGCAAG	300
Query	301	AACACTTCTGGAAGGGAGAGTGGATTTGGCTGGGCCATCTGGATGGAAGGTaaaaaaaG	360
Sbjct	301	AACACTTCTGGAAGGGAGAGTGGATTTGGCTGGGCCATCTGGATGGAAGGTAAAAAAAAG	360
Query	361	AAAATCCCTTGAAAGGAGATTGAGGGAAGTTT	392
Sbjct	361	AAAATCCCTTGAAAGGAGATTGAGGGAAGTTT	392

Sequence 628 matched with Sequence 229

Query= Sequence ID - 628 nt: 419
Length=419

SEQ ID NO: 229 nt: 419

ALIGNMENTS

Identities = 419/419 (100%), Gaps = 0/419 (0%)

Query	1	AAGAGAAAGGACTCAGTGTGTGATCCGGTTTCTTTTTGCTCGCCCCTGTTTTTTGTAGAA	60
Sbjct	1	AAGAGAAAGGACTCAGTGTGTGATCCGGTTTCTTTTTGCTCGCCCCTGTTTTTTGTAGAA	60
Query	61	TCTCTTCATGCTTGACATACCTACCAGTATTATTCCCGACGACACATATACATATGAGAA	120
Sbjct	61	TCTCTTCATGCTTGACATACCTACCAGTATTATTCCCGACGACACATATACATATGAGAA	120
Query	121	TATACCTTATTTATTTTTGTGTAGGTGTCTGCCTTCACAAATGTCATTGTCTACTCCTAG	180
Sbjct	121	TATACCTTATTTATTTTTGTGTAGGTGTCTGCCTTCACAAATGTCATTGTCTACTCCTAG	180
Query	181	AAGAACCAAATACCTCAATTTTTGTTTTGAGTACTGTACTATCCTGTAAATATATCTTA	240
Sbjct	181	AAGAACCAAATACCTCAATTTTTGTTTTGAGTACTGTACTATCCTGTAAATATATCTTA	240
Query	241	AGCAGGTTTGTTTTCAGCACTGATGGAAAATACCAGTGTGGGtttttttttAGTTGCCA	300
Sbjct	241	AGCAGGTTTGTTTTCAGCACTGATGGAAAATACCAGTGTGGGTTTTTTTTTAGTTGCCA	300
Query	301	ACAGTTGTATGTTTGCTGATTATTTATGACCTGAAATAATATATTTCTTCTTCTAAGAAG	360
Sbjct	301	ACAGTTGTATGTTTGCTGATTATTTATGACCTGAAATAATATATTTCTTCTTCTAAGAAG	360
Query	361	ACATTTTGTTACATAAGGATGACTTTTTTATACAATGGGAATAAATTATGGCATTTTTT	419
Sbjct	361	ACATTTTGTTACATAAGGATGACTTTTTTATACAATGGGAATAAATTATGGCATTTTTT	419

Sequence 629 matched with Sequence 230

Query= Sequence ID 629
Length=622

SEQ ID NO: 230

ALIGNMENTS

Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query	1	CTGAGAGTCACTGTGTTTTAGCCAAATCTAAGGGAGAAAATGAATATTGATAGCAGCAT	60
Sbjct	1	CTGAGAGTCACTGTGTTTTAGCCAAATCTAAGGGAGAAAATGAATATTGATAGCAGCAT	60
Query	61	GCTGTAGCCAGCTCCTTAAAGGAAGGATGGTGCCTGGTACAGAGTTAGAGTTAGTGCTTC	120
Sbjct	61	GCTGTAGCCAGCTCCTTAAAGGAAGGATGGTGCCTGGTACAGAGTTAGAGTTAGTGCTTC	120
Query	121	AGTAAATAATGAATGTGTGCTAGGTAGGTTCTGCTGGGTAGGCTGCATGCATTGACCAAT	180
Sbjct	121	AGTAAATAATGAATGTGTGCTAGGTAGGTTCTGCTGGGTAGGCTGCATGCATTGACCAAT	180
Query	181	TTATTCCTCCTTGTTTCAAAACAGGATTTAAGGGCACTtatatatatatatTTTTtagtt	240
Sbjct	181	TTATTCCTCCTTGTTTCAAAACAGGATTTAAGGGCACTTATATATATATATTTTTTAGTT	240
Query	241	TTTTAATGTAAATGAGAGAATAAAGatatatatatatgtctatatatgtatatatgtat	300
Sbjct	241	TTTTTAATGTAAATGAGAGAATAAAGATATATATATATGTCTATATATGTATATATGTAT	300
Query	301	atatatgtctatatgtctatatgtatatatgtctatatgtatatatgtgtgtgtatat	360
Sbjct	301	ATATATGTCTATATGTCTATATGTATATATGTCTATATGTATATATGTGTGTGTATAT	360
Query	361	atatatatatatatatataAGTTTTCTGTTGCTAGCATAACAACTACCAGAACTTAGCAA	420
Sbjct	361	ATATATATATATATATAAGTTTTCTGTTGCTAGCATAACAACTACCAGAACTTAGCAA	420
Query	421	CTGAAACAACATGAATTTATCTTACGGTTCTATAGTTCAGAAGTCTAACGTGTCACTGGG	480
Sbjct	421	CTGAAACAACATGAATTTATCTTACGGTTCTATAGTTCAGAAGTCTAACGTGTCACTGGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATGAAATCCAGGTTTCAACAGGACTGGGTTCCCTTCTAGCTCATTGAGCTACCTGGCTCA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATGAAATCCAGGTTTCAACAGGACTGGGTTCCCTTCTAGCTCATTGAGCTACCTGGCTCA  540

Query  541  TTCAGGTTGTNGGCAGAAATATACTTCCATGAAACTGTAGGGCTGAGACCCCGTTCCTTCC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TTCAGGTTGTNGGCAGAAATATACTTCCATGAAACTGTAGGGCTGAGACCCCGTTCCTTCC  600

Query  601  TGGCTATCATCTGAAAACTTTC  622
          ||||||||||||||||
Sbjct   601  TGGCTATCATCTGAAAACTTTC  622
```

Sequence 630 matched with Sequence 231

Query= Sequence ID 630
Length=350

SEQ ID NO: 231

ALIGNMENTS

Identities = 350/350 (100%), Gaps = 0/350 (0%)

```
Query 1  AGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCTGTACGTGC  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  AGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCTGTACGTGC  60

Query 61  CGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  CGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGA  120

Query 121  TGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAAATGGCCAGTTTAAACTTATG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  TGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAAATGGCCAGTTTAAACTTATG  180

Query 181  CTATCTGCGGGGCCATTTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCGATTGGCCA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  CTATCTGCGGGGCCATTTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCGATTGGCCA  240

Query 241  AGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAGAATCACAGATGTGGAATATT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  AGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAGAATCACAGATGTGGAATATT  300

Query 301  TGTCATAAATAAATAATGAAAACCTaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  350
          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  TGTCATAAATAAATAATGAAAACCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  350
```


Sequence 631 matched with Sequence 232

Query= Sequence ID 631
Length=493

SEQ ID NO: 232

ALIGNMENTS

Identities = 493/493 (100%), Gaps = 0/493 (0%)

```
Query 1      TNCACTCACACACTCCCAAACCTTAACAAACACATACATGTGCAGCCAACCCAATGGGCCAG 62
|||||
Sbjct 1      TNCACTCACACACTCCCAAACCTTAACAAACACATACATGTGCAGCCAACCCAATGGGCCAG 62

Query 63     CCTCTTTTATGCTCCTCACATGTTTCCTTTAACTGGAATACCCATGACAGCTCCCTACAT 122
|||||
Sbjct 63     CCTCTTTTATGCTCCTCACATGTTTCCTTTAACTGGAATACCCATGACAGCTCCCTACAT 122

Query 123    AGTTACTTGTAACCTCCTCCTCTGTATAAGTTTTCTGAAttttttGATAAAATTAA 182
|||||
Sbjct 123    AGTTACTTGTAACCTCCTCCTCTGTATAAGTTTTCTGAATTTTTTTGATAAAATTAA 182

Query 183    GTTGTGCCACCCCTTTATGCTCTCTTANAACCTTTGTTCTGTTCTCATGGCTGTTCTGCAA 242
|||||
Sbjct 183    GTTGTGCCACCCCTTTATGCTCTCTTANAACCTTTGTTCTGTTCTCATGGCTGTTCTGCAA 242

Query 243    CGAATCTCATTGTGTTCTCCTACTCAATTACATTCTGCGTCTCCCACTAGATGGCAGAC 302
|||||
Sbjct 243    CGAATCTCATTGTGTTCTCCTACTCAATTACATTCTGCGTCTCCCACTAGATGGCAGAC 302

Query 303    TCTTTGAGAGTAGGAGATTCCCTTGTTATCTCTGGATCCCTGGCACTTGACAGAAAGCCTG 362
|||||
Sbjct 303    TCTTTGAGAGTAGGAGATTCCCTTGTTATCTCTGGATCCCTGGCACTTGACAGAAAGCCTG 362

Query 363    TTACGTAATAATTGCTCAACAATTAGTTTTTAAATAAATGAATTATTTTTAAACGCCAA 422
|||||
Sbjct 363    TTACGTAATAATTGCTCAACAATTAGTTTTTAAATAAATGAATTATTTTTAAACGCCAA 422

Query 423    AATTACAATGATTGTGCATTAAGTGAAAGATGACCATCTAAAAACATAAAGCCATGCTTC 482
|||||
Sbjct 423    AATTACAATGATTGTGCATTAAGTGAAAGATGACCATCTAAAAACATAAAGCCATGCTTC 482
```

```
Query  483  ATGACATTGGC  493
          |||||
Sbjct  483  ATGACATTGGC  493
```

Blast comparison trimmed “TN” from the 5’ end of both sequences and reported 491 identities. The report has been manually corrected for this. “TN” has been prepended to both sequences and identity count has been increased to 493.

Sequence 632 matched with Sequence 233

Query= Sequence ID 632
Length=577

SEQ ID NO: 233

ALIGNMENTS

Identities = 577/577 (100%), Gaps = 0/577 (0%)

Query	1	GACCATTGAGGAAATTTTATAAAAAATGCAGATACTGTCTTGAGCAGATCGAAATGCCG	60
Sbjct	1	GACCATTGAGGAAATTTTATAAAAAATGCAGATACTGTCTTGAGCAGATCGAAATGCCG	60
Query	61	ATGAGGTGGATGCAATTTCTTTTGTGCAAGCAGTGACGGTGccccccTGGGTGTC	120
Sbjct	61	ATGAGGTGGATGCAATTTCTTTTGTGCAAGCAGTGACGGTGCCCCCCTGGGTGTC	120
Query	121	CGTGCTGTGCCTTAGCTTCCCCAGGTGCCGGGACTCACACCTGCTAGGGGCTGGGCAAGG	180
Sbjct	121	CGTGCTGTGCCTTAGCTTCCCCAGGTGCCGGGACTCACACCTGCTAGGGGCTGGGCAAGG	180
Query	181	CCCCGGCTCTGCTTTCTCTGAAGGGCTTGTCCAAGTTCATTGCCCTGTTACAGGTGGTCA	240
Sbjct	181	CCCCGGCTCTGCTTTCTCTGAAGGGCTTGTCCAAGTTCATTGCCCTGTTACAGGTGGTCA	240
Query	241	AGACGTCCGGCCGCCTTGACCCAGGCTACCCTTAGCCAATATCCTCTGCCCCTGGGTGGT	300
Sbjct	241	AGACGTCCGGCCGCCTTGACCCAGGCTACCCTTAGCCAATATCCTCTGCCCCTGGGTGGT	300
Query	301	TGGTGGCTGGGCCTCAGGGTGGGCAACGTTAGGGGTTTGGCGAAAGCCCGCCCATGGGA	360
Sbjct	301	TGGTGGCTGGGCCTCAGGGTGGGCAACGTTAGGGGTTTGGCGAAAGCCCGCCCATGGGA	360
Query	361	TTGAGGGACGGGGCTGCACTCCAACCGTCTGCACCTGCTCTTCCCCACCCCTGTGGGAC	420
Sbjct	361	TTGAGGGACGGGGCTGCACTCCAACCGTCTGCACCTGCTCTTCCCCACCCCTGTGGGAC	420
Query	421	CTCATCTTCACGTGCCATGTGTGCTGAAGGCCAGGGCCCAGCAGGGGGCAGTGGCACCT	480
Sbjct	421	CTCATCTTCACGTGCCATGTGTGCTGAAGGCCAGGGCCCAGCAGGGGGCAGTGGCACCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTGACGAAAAGCCGAGGTGCTTACCAATGGACCTTCTGGCCCGCCCTCCCCTGTACTT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTGACGAAAAGCCGAGGTGCTTACCAATGGACCTTCTGGCCCGCCCTCCCCTGTACTT  540

Query  541  GTCGGGCATTTCAGGGCCCCGACCTGTGCCTACCCGCA  577
          ||||||||||||||||||||||||||||
Sbjct  541  GTCGGGCATTTCAGGGCCCCGACCTGTGCCTACCCGCA  577
```

Sequence 633 matched with Sequence 234

Query= Sequence ID 633
Length=568

SEQ ID NO: 234

ALIGNMENTS

Identities = 568/568 (100%), Gaps = 0/568 (0%)

Query	1	CAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA	60
Sbjct	1	CAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA	60
Query	61	GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCT	120
Sbjct	61	GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCT	120
Query	121	GGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGTTCTTTGAGTCCTTTGGGGATCT	180
Sbjct	121	GGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGTTCTTTGAGTCCTTTGGGGATCT	180
Query	181	GTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGCT	240
Sbjct	181	GTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGCT	240
Query	241	CGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACT	300
Sbjct	241	CGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACT	300
Query	301	GAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGGCAA	360
Sbjct	301	GAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGGCAA	360
Query	361	CGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCACCAAGTGCAGGC	420
Sbjct	361	CGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCACCAAGTGCAGGC	420
Query	421	TGCCTATCANAAAGTGGTGGCTGGTGTGGGCTAATGCCTGGCCCCACAAGTATCACTAAG	480
Sbjct	421	TGCCTATCANAAAGTGGTGGCTGGTGTGGGCTAATGCCTGGCCCCACAAGTATCACTAAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTTCCTTTGTTCCCTAAGTCCAACACTACT  540
          |||
Sbjct  481  CTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTTCCTTTGTTCCCTAAGTCCAACACTACT  540

Query  541  AAAGTGGGGGATATTATGAAGGGCCTTG  568
          |||
Sbjct  541  AAAGTGGGGGATATTATGAAGGGCCTTG  568
```

Sequence 634 matched with Sequence 235

Query= Sequence ID - 634 nt: 511
Length=511

SEQ ID NO: 235 nt: 511

ALIGNMENTS

Identities = 511/511 (100%), Gaps = 0/511 (0%)

Query	1	TTTTTTAATTTACCAAAATTTGTTGACGTCCCTTGATTGCTGATAGGGACAATAATTA	60
Sbjct	1	TTTTTTAATTTACCAAAATTTGTTGACGTCCCTTGATTGCTGATAGGGACAATAATTA	60
Query	61	AATATTTTCCACTTGTTTTTATAAAAACTGTAATGGTGATTGTTTAACAGATGTTGACT	120
Sbjct	61	AATATTTTCCACTTGTTTTTATAAAAACTGTAATGGTGATTGTTTAACAGATGTTGACT	120
Query	121	TAGCACCTTCTCTCtttttttttttttttttttttGAGTTGGAGTCTTGCTCTGTCACCCAG	180
Sbjct	121	TAGCACCTTCTCTCTTTTTTTTTTTTTTTTTTTTGGAGTTGGAGTCTTGCTCTGTCACCCAG	180
Query	181	CTGGAGTGCAGTGGCACGATTTCGGCTCACTGCAACCTCCGCCTCCCAGGTTGGGGCGCT	240
Sbjct	181	CTGGAGTGCAGTGGCACGATTTCGGCTCACTGCAACCTCCGCCTCCCAGGTTGGGGCGCT	240
Query	241	TCTCCTGCCTCAGCCTCCCANATAGTTGGGATTACAGGTGCATGCCGCCACNCCTAGCTA	300
Sbjct	241	TCTCCTGCCTCAGCCTCCCANATAGTTGGGATTACAGGTGCATGCCGCCACNCCTAGCTA	300
Query	301	ATGTTTTTTGTATCTTGGTANANATGGNGTTTCACCTTGTTGCCCATGCCGCTCTTGAAC	360
Sbjct	301	ATGTTTTTTGTATCTTGGTANANATGGNGTTTCACCTTGTTGCCCATGCCGCTCTTGAAC	360
Query	361	TCCTTGGCCTCCCAAAGTGTTAGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAATTT	420
Sbjct	361	TCCTTGGCCTCCCAAAGTGTTAGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAATTT	420
Query	421	ANCACCTTACTGGGTGCTGAGGCTGTGAGCCATAGTAGAATGCATGTGATCCAGGGCCTT	480
Sbjct	421	ANCACCTTACTGGGTGCTGAGGCTGTGAGCCATAGTAGAATGCATGTGATCCAGGGCCTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCTGAATTCATGGGCTAATAGGGAGCCTGAC  511
          |||||||||||||||||||||||||||
Sbjct  481  GCTGAATTCATGGGCTAATAGGGAGCCTGAC  511
```


Sequence 635 matched with Sequence 236

Query= Sequence ID - 635 nt: 592
Length=592

SEQ ID NO: 236 nt: 592

ALIGNMENTS

Identities = 592/592 (100%), Gaps = 0/592 (0%)

Query	1	TGAGCGTTGGGCTGTAGGTCGCTGTGCTGTGTGATCCCCAGAGCCATGCCCGAGATAGT	60
Sbjct	1	TGAGCGTTGGGCTGTAGGTCGCTGTGCTGTGTGATCCCCAGAGCCATGCCCGAGATAGT	60
Query	61	GGATACCTGTTTCGTTGGCCTCTCCGGCTTCCGTCTGCCGGACCAAGCACCTGCACCTGCG	120
Sbjct	61	GGATACCTGTTTCGTTGGCCTCTCCGGCTTCCGTCTGCCGGACCAAGCACCTGCACCTGCG	120
Query	121	CTGCAGCGTCGACTTTACTCGCCGGACGCTGACCGGGACTGCTGCTCTCACGGTCCAGTC	180
Sbjct	121	CTGCAGCGTCGACTTTACTCGCCGGACGCTGACCGGGACTGCTGCTCTCACGGTCCAGTC	180
Query	181	TCAGGAGGACAATCTGCGCAGCCTGGTTTTGGATACAAAGGACCTTACAATAGAAAAAGT	240
Sbjct	181	TCAGGAGGACAATCTGCGCAGCCTGGTTTTGGATACAAAGGACCTTACAATAGAAAAAGT	240
Query	241	AGTGATCAATGGACAAGAAGTCAAATATGCTCTTGGAGAAAGACAAAGTTACAAGGGATC	300
Sbjct	241	AGTGATCAATGGACAAGAAGTCAAATATGCTCTTGGAGAAAGACAAAGTTACAAGGGATC	300
Query	301	GCCAATGGAAATCTCTCTTCCTATCGCTTTGAGCAAAAATCAAGAAATTGTTATAGAAAT	360
Sbjct	301	GCCAATGGAAATCTCTCTTCCTATCGCTTTGAGCAAAAATCAAGAAATTGTTATAGAAAT	360
Query	361	TTCTTTTGAGACCTCTCCAAAATCTTCTGCTCTCCAGTGGCTCACTCCTGAACAGACTTC	420
Sbjct	361	TTCTTTTGAGACCTCTCCAAAATCTTCTGCTCTCCAGTGGCTCACTCCTGAACAGACTTC	420
Query	421	TGGGAAGGAACACCCATATCTCTTTAGTCAGTGCCAGGCCATCCACTGCAGAGCAATCCT	480
Sbjct	421	TGGGAAGGAACACCCATATCTCTTTAGTCAGTGCCAGGCCATCCACTGCAGAGCAATCCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TCCTTGTCAGGACACTCCTTCTGNGAAATTAACCTATACTGCAGAGGTGTCTGTCCCTAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TCCTTGTCAGGACACTCCTTCTGNGAAATTAACCTATACTGCAGAGGTGTCTGTCCCTAA  540

Query  541  AGAACTGGTGGCACTTATGAGTGCTATTCGTGATGGAGAAACACCTGACCCA  592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AGAACTGGTGGCACTTATGAGTGCTATTCGTGATGGAGAAACACCTGACCCA  592
```

Sequence 636 matched with Sequence 237

Query= Sequence ID - 636 nt: 572
Length=572

SEQ ID NO: 237 nt: 572

ALIGNMENTS

Identities = 572/572 (100%), Gaps = 0/572 (0%)

Query	1	CTTANAAGAGTTGCTCATTACACCCACGCCCTTGCCCAAGGCTGGCCCACTCAGAGCGA	60
Sbjct	1	CTTANAAGAGTTGCTCATTACACCCACGCCCTTGCCCAAGGCTGGCCCACTCAGAGCGA	60
Query	61	AACTTAACTTTTGTCTGGATGGGAAGAGAAGTAAGTCTACCCCGAGGTTGCCATGTTGAA	120
Sbjct	61	AACTTAACTTTTGTCTGGATGGGAAGAGAAGTAAGTCTACCCCGAGGTTGCCATGTTGAA	120
Query	121	GAGTGAGAGGTCCAAGTGATTCTGTGCATTGAAACCAAGACACCCACCCAGAACACTTC	180
Sbjct	121	GAGTGAGAGGTCCAAGTGATTCTGTGCATTGAAACCAAGACACCCACCCAGAACACTTC	180
Query	181	TTCCCTCCCTCAGCCCAAACCAAAGGCTGGGGTTCTCATCTCCAAGTGGCTGTTCTCCAA	240
Sbjct	181	TTCCCTCCCTCAGCCCAAACCAAAGGCTGGGGTTCTCATCTCCAAGTGGCTGTTCTCCAA	240
Query	241	CTTTCCCAAGCCGCTTGCAATCCCCAGACTGGACTACTGTGGCGGTTAGGTTAGATTTGA	300
Sbjct	241	CTTTCCCAAGCCGCTTGCAATCCCCAGACTGGACTACTGTGGCGGTTAGGTTAGATTTGA	300
Query	301	AGACGGGGCCCAGGCTGGGTATGAACGGGTGCAGCCCTCTTCTCCTCTTcccccccACAT	360
Sbjct	301	AGACGGGGCCCAGGCTGGGTATGAACGGGTGCAGCCCTCTTCTCCTCTTCCCCCCCACAT	360
Query	361	CTCTCATGAGAGAGGTAGTGGCATTTCCTTCTCAGGGAGCTTCAATGGGAAAGGTCTCGA	420
Sbjct	361	CTCTCATGAGAGAGGTAGTGGCATTTCCTTCTCAGGGAGCTTCAATGGGAAAGGTCTCGA	420
Query	421	AAGCTTCAGGAGGAGCAGAATACCAACGCAGGGGGATGGCTGTAACGATCTCACCGTCTC	480
Sbjct	421	AAGCTTCAGGAGGAGCAGAATACCAACGCAGGGGGATGGCTGTAACGATCTCACCGTCTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTAACCTCAGTCCCTTTTTTGAGAGTGAATGGTGGAGGGTGGGAAAGGGACCCAAATTTG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTAACCTCAGTCCCTTTTTTGAGAGTGAATGGTGGAGGGTGGGAAAGGGACCCAAATTTG  540

Query  541  TAGATCTCTTTGTCTGGGGGAGGGGAANGATG  572
          |||||||||||||||||||||||||
Sbjct  541  TAGATCTCTTTGTCTGGGGGAGGGGAANGATG  572
```

Sequence 637 matched with Sequence 238

Query= Sequence ID - 637 nt: 482
Length=482

SEQ ID NO: 238 nt: 482

ALIGNMENTS

Identities = 482/482 (100%), Gaps = 0/482 (0%)

Query	1	TTAAACAGGCGCAGGGTAAAAATGAGAATGAATCTGAAAAAGAGAGTTGGTGTTTAA	60
Sbjct	1	TTAAACAGGCGCAGGGTAAAAATGAGAATGAATCTGAAAAAGAGAGTTGGTGTTTAA	60
Query	61	AGAGGATGGACAAGAGTATGCTCAGGTAATCAAAATGTTGGGAAATGGACGATTGGAAGC	120
Sbjct	61	AGAGGATGGACAAGAGTATGCTCAGGTAATCAAAATGTTGGGAAATGGACGATTGGAAGC	120
Query	121	ATTGTGTTTTGATGGTGTAAAGAGGTTATGCCATATCAGAGGAAATTGAGAAAAAGGT	180
Sbjct	121	ATTGTGTTTTGATGGTGTAAAGAGGTTATGCCATATCAGAGGAAATTGAGAAAAAGGT	180
Query	181	TTGGATAAATACATCAGACATTATATTGGTTGGTCTACGGGACTATCAGGATAACAAAGC	240
Sbjct	181	TTGGATAAATACATCAGACATTATATTGGTTGGTCTACGGGACTATCAGGATAACAAAGC	240
Query	241	TGATGTAATTTTAAAGTACAATGCAGATGAAGCTAGAAGCCTGAAGGCATATGGCGAGCT	300
Sbjct	241	TGATGTAATTTTAAAGTACAATGCAGATGAAGCTAGAAGCCTGAAGGCATATGGCGAGCT	300
Query	301	TCCAGAACATGCTAAATCAATGAAACAGACACATTTGGTCCTGGAGATGATGATGAAAT	360
Sbjct	301	TCCAGAACATGCTAAATCAATGAAACAGACACATTTGGTCCTGGAGATGATGATGAAAT	360
Query	361	CCAGTTTGACGATATTGGAGATGATGATGAAGACATTGATGATATCTAAATTGAACCAAG	420
Sbjct	361	CCAGTTTGACGATATTGGAGATGATGATGAAGACATTGATGATATCTAAATTGAACCAAG	420
Query	421	TGTTTTTACATGACAAGTTCTCTGAGGATGGTTCTACAGTTGGGATTTTGGCCATCATCA	480
Sbjct	421	TGTTTTTACATGACAAGTTCTCTGAGGATGGTTCTACAGTTGGGATTTTGGCCATCATCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AC	482
Sbjct	481	AC	482

Sequence 638 matched with Sequence 239

Query= Sequence ID - 638 nt: 545
Length=545

SEQ ID NO: 239 nt: 545

ALIGNMENTS

Identities = 545/545 (100%), Gaps = 0/545 (0%)

Query	1	TTTGAAGGCAAAGAGGGATTAATCTGTGCTGGCATCATGTAAGGAGACTTGATAGATAAG	60
Sbjct	1	TTTGAAGGCAAAGAGGGATTAATCTGTGCTGGCATCATGTAAGGAGACTTGATAGATAAG	60
Query	61	AAAAAGCTTTACCTAAGTTTGAAGAATAGGTTTTTCATAATGGAAAATTTAAGGGAAAA	120
Sbjct	61	AAAAAGCTTTACCTAAGTTTGAAGAATAGGTTTTTCATAATGGAAAATTTAAGGGAAAA	120
Query	121	ATCTCCAAAAAAGTGCTACTCAAGTTTTATCCATTTGTATTTCCAACACAGCCTAGGACA	180
Sbjct	121	ATCTCCAAAAAAGTGCTACTCAAGTTTTATCCATTTGTATTTCCAACACAGCCTAGGACA	180
Query	181	GTACCTGCACATAGTAGGTGATTAATAAAAAATTTAGAAAGCATTAATACTAAAGAGGAAA	240
Sbjct	181	GTACCTGCACATAGTAGGTGATTAATAAAAAATTTAGAAAGCATTAATACTAAAGAGGAAA	240
Query	241	AATAGCAATGGCAAGAAAACACATGTAGGGAACACATGTAGCCAAAAATAATATATAAT	300
Sbjct	241	AATAGCAATGGCAAGAAAACACATGTAGGGAACACATGTAGCCAAAAATAATATATAAT	300
Query	301	CAGAGAAATAATAGGACTTCTGGaaaaaaaGATGAGATCAGATTGGTTAGGATCTTTAC	360
Sbjct	301	CAGAGAAATAATAGGACTTCTGGAAAAAAAAGATGAGATCAGATTGGTTAGGATCTTTAC	360
Query	361	TAACATGACAAGAGCATGAAttttttttCTGTAGATAATAAGTATGAAAGAATTTTAGCT	420
Sbjct	361	TAACATGACAAGAGCATGAATTTTTTTTCTGTAGATAATAAGTATGAAAGAATTTTAGCT	420
Query	421	TAAAAATTAGCATAATTTGGATCCACATATGCAAATCAATGAATGTAATTCATAATATAA	480
Sbjct	421	TAAAAATTAGCATAATTTGGATCCACATATGCAAATCAATGAATGTAATTCATAATATAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ACAGAACTAAACACAAAAACCACGTGATTATCTCAATAGACACAGAAAAGGCCTTCaaa  540
          |||
Sbjct  481  ACAGAACTAAACACAAAAACCACGTGATTATCTCAATAGACACAGAAAAGGCCTTCAAAA  540

Query  541  aaaTT  545
          ||||
Sbjct  541  AAATT  545
```


Sequence 639 matched with Sequence 240

Query= Sequence ID - 639 nt: 624
Length=624

SEQ ID NO: 240 nt: 624

ALIGNMENTS

Identities = 624/624 (100%), Gaps = 0/624 (0%)

Query	1	GACACACGAGCATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA	60
Sbjct	1	GACACACGAGCATATTTACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA	60
Query	61	GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC	120
Sbjct	61	GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC	120
Query	121	TGAGCCCTAGGATTCATCTTTCTTTTACCGTAGGTGGCCTGACTGGCATTGTATTAGCA	180
Sbjct	121	TGAGCCCTAGGATTCATCTTTCTTTTACCGTAGGTGGCCTGACTGGCATTGTATTAGCA	180
Query	181	AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT	240
Sbjct	181	AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT	240
Query	241	GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA	300
Sbjct	241	GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA	300
Query	301	TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC	360
Sbjct	301	TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC	360
Query	361	GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT	420
Sbjct	361	GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT	420
Query	421	TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC	480
Sbjct	421	TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540

Query  541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGA CTATATGGATGCCCC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGA CTATATGGATGCCCC  600

Query  601  CCACCCTACCACACATTTCGAAGAA  624
          |||||||||||||||||||
Sbjct   601  CCACCCTACCACACATTTCGAAGAA  624
```

Sequence 641 matched with Sequence 241

Query= Sequence ID 641
Length=421

SEQ ID NO: 241

ALIGNMENTS

Identities = 421/421 (100%), Gaps = 0/421 (0%)

Query	1	CAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAGGGCCGCGCCACGTGCA	60
Sbjct	1	CAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAGGGCCGCGCCACGTGCA	60
Query	61	GCCTATTCGCTGCACTAACTGTGCCCAGATGCGTGCCCAAGGACAAGGCCATTAAGAAATT	120
Sbjct	61	GCCTATTCGCTGCACTAACTGTGCCCAGATGCGTGCCCAAGGACAAGGCCATTAAGAAATT	120
Query	121	CGTCATTCGAAACATAGTGGAGGCCGAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTT	180
Sbjct	121	CGTCATTCGAAACATAGTGGAGGCCGAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTT	180
Query	181	CGATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTACATTACTGTGTGAGTTGTGCAAT	240
Sbjct	181	CGATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTACATTACTGTGTGAGTTGTGCAAT	240
Query	241	TCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGCAAGGACCGAACACCCCCACC	300
Sbjct	241	TCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGCAAGGACCGAACACCCCCACC	300
Query	301	CCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCACCAAAGCCCATGTAAGGAGCTGA	360
Sbjct	301	CCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCACCAAAGCCCATGTAAGGAGCTGA	360
Query	361	GTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTTA	420
Sbjct	361	GTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTTA	420
Query	421	A	421
Sbjct	421	A	421

Sequence 642 matched with Sequence 242

Query= Sequence ID 642
Length=539

SEQ ID NO: 242

ALIGNMENTS

Identities = 539/539 (100%), Gaps = 0/539 (0%)

Query	1	TGCTTGGCCCTCTACCTCCTGCCCTCTTCCTGTTTCATCTCCCAACCACTGCACTCTTGAT	60
Sbjct	1	TGCTTGGCCCTCTACCTCCTGCCCTCTTCCTGTTTCATCTCCCAACCACTGCACTCTTGAT	60
Query	61	TTTTATACCACACAGAAGGTAAGAAAATTCTAGGAACCCTAAGGATCAATCCTCTCCATT	120
Sbjct	61	TTTTATACCACACAGAAGGTAAGAAAATTCTAGGAACCCTAAGGATCAATCCTCTCCATT	120
Query	121	TTCACTCAAATGCCTGGGGCCCAGCTCTGCAATGACTGACTCCAGGGCCTCTTTCCTCAC	180
Sbjct	121	TTCACTCAAATGCCTGGGGCCCAGCTCTGCAATGACTGACTCCAGGGCCTCTTTCCTCAC	180
Query	181	TGCCAGCATAGAAGTCAGGGGAGCCAGCTGGGCCCTGCGGTCAGGAAGGTTCTCATTTTT	240
Sbjct	181	TGCCAGCATAGAAGTCAGGGGAGCCAGCTGGGCCCTGCGGTCAGGAAGGTTCTCATTTTT	240
Query	241	GGAGCATTCCCTGAGCCCAGATCATAGGAGCAGCTGTCCCTGGTGGGACACAGGAGTCAT	300
Sbjct	241	GGAGCATTCCCTGAGCCCAGATCATAGGAGCAGCTGTCCCTGGTGGGACACAGGAGTCAT	300
Query	301	GACTCCTACCCTCCACCCTCCACACCCACCAGGCATTTAGCAGTCTGTCCTATGCAAGAC	360
Sbjct	301	GACTCCTACCCTCCACCCTCCACACCCACCAGGCATTTAGCAGTCTGTCCTATGCAAGAC	360
Query	361	AGATGAATTCTCAGCCAGGATACCTCAAGGCAGGCAAAGGTGAGTGGAGGGAAAAATTCAC	420
Sbjct	361	AGATGAATTCTCAGCCAGGATACCTCAAGGCAGGCAAAGGTGAGTGGAGGGAAAAATTCAC	420
Query	421	AAACATTGAGGTGTGTGGTGTGGCATCACCATGGCCAAATCCAAGAGGTCTTCCTGGA	480
Sbjct	421	AAACATTGAGGTGTGTGGTGTGGCATCACCATGGCCAAATCCAAGAGGTCTTCCTGGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGAGGGCCCAAAGTGAACCAAAAGAATGCTGTCAGCAGTTGGAATAGAGCTGTGAATT	539
Sbjct	481	AGAGGGCCCAAAGTGAACCAAAAGAATGCTGTCAGCAGTTGGAATAGAGCTGTGAATT	539

Sequence 643 matched with Sequence 243

Query= Sequence ID 643
Length=397

SEQ ID NO: 243

ALIGNMENTS

Identities = 397/397 (100%), Gaps = 0/397 (0%)

Query	1	CTTTCCAAGAGGAATCCTCGGCAGATAAACTGGACTGTCCTCTACAGAAGGAAGCACAAA	60
Sbjct	1	CTTTCCAAGAGGAATCCTCGGCAGATAAACTGGACTGTCCTCTACAGAAGGAAGCACAAA	60
Query	61	AAGGGACAGTCGGAAGAAATTCAAAAGAAAAGAACCCGCCGAGCAGTCAAATTCCAGAGG	120
Sbjct	61	AAGGGACAGTCGGAAGAAATTCAAAAGAAAAGAACCCGCCGAGCAGTCAAATTCCAGAGG	120
Query	121	GCCATTACTGGTGCATCTCTTGCTGATATAATGGCCAAGAGGAATCAGAAACCTGAAGTT	180
Sbjct	121	GCCATTACTGGTGCATCTCTTGCTGATATAATGGCCAAGAGGAATCAGAAACCTGAAGTT	180
Query	181	AGAAAGGCTCAACGAGAACAAGCTATCAGGGCTGCTAAGGAAGCAAAAAAGGCTAAGCAA	240
Sbjct	181	AGAAAGGCTCAACGAGAACAAGCTATCAGGGCTGCTAAGGAAGCAAAAAAGGCTAAGCAA	240
Query	241	GCATCTAAAAAGACTGCAATGGCTGCTGCTAAGGCACCTACAAAGGCAGCACCTAAGCAA	300
Sbjct	241	GCATCTAAAAAGACTGCAATGGCTGCTGCTAAGGCACCTACAAAGGCAGCACCTAAGCAA	300
Query	301	AAGATTGTGAAGCCTGTGAAAGTTTCAGCTCCCCGAGTTGGTGGAAAACGCTAAACTGGC	360
Sbjct	301	AAGATTGTGAAGCCTGTGAAAGTTTCAGCTCCCCGAGTTGGTGGAAAACGCTAAACTGGC	360
Query	361	AGATTAGATTTTTAAATAAAGATTGGATTATAACTCT	397
Sbjct	361	AGATTAGATTTTTAAATAAAGATTGGATTATAACTCT	397

Sequence 644 matched with Sequence 244

Query= Sequence ID 644
Length=542

SEQ ID NO: 244

ALIGNMENTS

Identities = 542/542 (100%), Gaps = 0/542 (0%)

Query	1	CTTTGATAGAGAAGAAAATTCTCCTAGGATACAAGAGCCTCAACATTTTAAAGATTTTCT	60
Sbjct	1	CTTTGATAGAGAAGAAAATTCTCCTAGGATACAAGAGCCTCAACATTTTAAAGATTTTCT	60
Query	61	GCATCTCAAAAGCGTAGGCTCCTTGCTGGGCAAGGTGAGCCTCTGTGAGTCCTCATAGGA	120
Sbjct	61	GCATCTCAAAAGCGTAGGCTCCTTGCTGGGCAAGGTGAGCCTCTGTGAGTCCTCATAGGA	120
Query	121	CCGAGCAAATCTGATTCACCCAGAAAATCCAATATCGAAGCTGAGCTTTGGCCTGAGCG	180
Sbjct	121	CCGAGCAAATCTGATTCACCCAGAAAATCCAATATCGAAGCTGAGCTTTGGCCTGAGCG	180
Query	181	GGTTCCATTTCTCCCCAGATCCTATTTAGGAAGTGTCTCCTGACAACCTCCAAAAGGTG	240
Sbjct	181	GGTTCCATTTCTCCCCAGATCCTATTTAGGAAGTGTCTCCTGACAACCTCCAAAAGGTG	240
Query	241	CTAACATGCAACGTTCTGAAGGGTTATTGCTCAAAAACAAGATTTTCCTTGTTGGTCAAGA	300
Sbjct	241	CTAACATGCAACGTTCTGAAGGGTTATTGCTCAAAAACAAGATTTTCCTTGTTGGTCAAGA	300
Query	301	CTCTGCGAGCCTCGAACACGATGAATCCGCTCGAATGGGCTTGGGCTTTGCCCGGGTGGC	360
Sbjct	301	CTCTGCGAGCCTCGAACACGATGAATCCGCTCGAATGGGCTTGGGCTTTGCCCGGGTGGC	360
Query	361	GCACGCTCACACGCTGGAAGCACAGCTTTGACGATCTCCACACACGCACAGGCACACACG	420
Sbjct	361	GCACGCTCACACGCTGGAAGCACAGCTTTGACGATCTCCACACACGCACAGGCACACACG	420
Query	421	CCACAGATGATGCCGGCTCATTCTCAGGGGGTGTCTAAGTTCTGCTTTAAATATTTACCC	480
Sbjct	421	CCACAGATGATGCCGGCTCATTCTCAGGGGGTGTCTAAGTTCTGCTTTAAATATTTACCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCTAATTGTACAAACAATAGGGGCATGAGCCTGGTACTCGATAAAATGGGGACTTNCTTAA	540
Sbjct	481	CCTAATTGTACAAACAATAGGGGCATGAGCCTGGTACTCGATAAAATGGGGACTTNCTTAA	540
Query	541	AA	542
Sbjct	541	AA	542

Sequence 645 matched with Sequence 245

Query= Sequence ID - 645 nt: 649
Length=649

SEQ ID NO: 245 nt: 649

ALIGNMENTS

Identities = 649/649 (100%), Gaps = 0/649 (0%)

Query	1	CTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTCGTCCCC	60
Sbjct	1	CTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTCGTCCCC	60
Query	61	GGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCGGGGT	120
Sbjct	61	GGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCGGGGT	120
Query	121	GCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAA	180
Sbjct	121	GCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAA	180
Query	181	GAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTA	240
Sbjct	181	GAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTA	240
Query	241	CATCGACAAGGTGCGCTTCCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCA	300
Sbjct	241	CATCGACAAGGTGCGCTTCCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCA	300
Query	301	GCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCTCTACGAGGAGGAGATGCGGGAGCT	360
Sbjct	301	GCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCTCTACGAGGAGGAGATGCGGGAGCT	360
Query	361	GCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCCGCGTCGAGGTGGAGCGCGACAA	420
Sbjct	361	GCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCCGCGTCGAGGTGGAGCGCGACAA	420
Query	421	CCTGGCCGAGGACATCATGCGCCTCCGGGAGAAATTGCAGGAGGAGATGCTTCAGAGAGA	480
Sbjct	421	CCTGGCCGAGGACATCATGCGCCTCCGGGAGAAATTGCAGGAGGAGATGCTTCAGAGAGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAAATCCAGGAGCTGCAGGCTCAGAT	540
Sbjct	481	GGAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAAATCCAGGAGCTGCAGGCTCAGAT	540
Query	541	TCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCTT	600
Sbjct	541	TCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCTT	600
Query	601	GCGTGACGTACGTANCAATATGAAAGTGTGGCTGCCAAAAACCTTGCA	649
Sbjct	601	GCGTGACGTACGTANCAATATGAAAGTGTGGCTGCCAAAAACCTTGCA	649

Sequence 646 matched with Sequence 246

Query= Sequence ID - 646 nt: 600
Length=600

SEQ ID NO: 246 nt: 600

ALIGNMENTS

Identities = 600/600 (100%), Gaps = 0/600 (0%)

Query	1	GAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAG	60
Sbjct	1	GAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAG	60
Query	61	GCTATCCAGCGTACTCCAAAGATTGAGGTTTACTCACGTCATCCAGCAGAGAATGGAAAG	120
Sbjct	61	GCTATCCAGCGTACTCCAAAGATTGAGGTTTACTCACGTCATCCAGCAGAGAATGGAAAG	120
Query	121	TCAAATTTCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTA	180
Sbjct	121	TCAAATTTCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTA	180
Query	181	CTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTGAGCTTGTCTTTCAGCAAGGAC	240
Sbjct	181	CTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTGAGCTTGTCTTTCAGCAAGGAC	240
Query	241	TGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATGCC	300
Sbjct	241	TGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATGCC	300
Query	301	TGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGATCGAGACATG	360
Sbjct	301	TGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGATCGAGACATG	360
Query	361	TAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTCTG	420
Sbjct	361	TAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTCTG	420
Query	421	CTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTAGG	480
Sbjct	421	CTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTAGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTC	540
Sbjct	481	GTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTC	540
Query	541	CATGTTTGATGTATCTGAGCAGGGTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACTTA	600
Sbjct	541	CATGTTTGATGTATCTGAGCAGGGTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACTTA	600

Sequence 647 matched with Sequence 247

Query= Sequence ID 647
Length=331

SEQ ID NO: 247

ALIGNMENTS

Identities = 331/331 (100%), Gaps = 0/331 (0%)

Query	1	CGAATGTGCAGGTTTGTACATAGGTATATATATGCCATGATGGAAATATTTAttttttt	60
Sbjct	1	CGAATGTGCAGGTTTGTACATAGGTATATATATGCCATGATGGAAATATTTATTTTTTT	60
Query	61	AAGCGTAATTTTGCCAAATAATAAAAAACAGAAGGAAATTGAGATTAGAGGGAGGTGTTTA	120
Sbjct	61	AAGCGTAATTTTGCCAAATAATAAAAAACAGAAGGAAATTGAGATTAGAGGGAGGTGTTTA	120
Query	121	AAGAGAGGTTATAGAGTAGAAGATTTGATGCTGGAGAGGTTAAGGTGCAATAAGAATTTA	180
Sbjct	121	AAGAGAGGTTATAGAGTAGAAGATTTGATGCTGGAGAGGTTAAGGTGCAATAAGAATTTA	180
Query	181	GGGAGAAATGTTGTTTCATTATTGGAGGGTAAATGATGTGGTGCCTGAGGTCTGTACGTTA	240
Sbjct	181	GGGAGAAATGTTGTTTCATTATTGGAGGGTAAATGATGTGGTGCCTGAGGTCTGTACGTTA	240
Query	241	CCTCTTAACAATTTCTGTCCTTCAGATGGAACTCTTTAACTTCTCGTAAAAGTCATATA	300
Sbjct	241	CCTCTTAACAATTTCTGTCCTTCAGATGGAACTCTTTAACTTCTCGTAAAAGTCATATA	300
Query	301	CCTATATAATAAAGCTACTGATTTCCAAAAA	331
Sbjct	301	CCTATATAATAAAGCTACTGATTTCCAAAAA	331

Sequence 648 matched with Sequence 248

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 648
Length=41

SEQ ID NO: 248

81.8 3e-22

ALIGNMENTS

Identities = 41/41 (100%), Gaps = 0/41 (0%)

Query	1	AA	41
Sbjct	1	AA	41

Sequence 649 matched with Sequence 249

Query= Sequence ID - 649 nt: 425
Length=425

SEQ ID NO: 249 nt: 425

ALIGNMENTS

Identities = 425/425 (100%), Gaps = 0/425 (0%)

```
Query 1  CaaaaaaaaCGAAGAAAAGTGACGACAGTCTGAGGGACTTATGGGAGATCATCAAGTGAAC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  CAAAAAACGAAGAAAAGTGACGACAGTCTGAGGGACTTATGGGAGATCATCAAGTGAAC 60

Query 61 CACTATATGTGTAATGTAAGTCTTGGAATgagaagagagaaggagaaggaggagagagCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 CACTATATGTGTAATGTAAGTCTTGGAATGAGAAGAGAGAAGGAGAAGGAGGAGAGAGCT 120

Query 121 TATTTGTAGAAATAATGGCTGAAAACATCCCAAACCTTCCTtttttttGAGGAAAGAAATA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TATTTGTAGAAATAATGGCTGAAAACATCCCAAACCTTCCTTTTTTTTGGAGAAAGAAATA 180

Query 181 GGCATACAAGTTCAAGAAACTCAAGGAACTCCAGAGAGGACAATTCTAAAGACACCCCCT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 GGCATACAAGTTCAAGAAACTCAAGGAACTCCAGAGAGGACAATTCTAAAGACACCCCCT 240

Query 241 CTAACATACATTATAATCAAATTGTCAAAAGTAAAATACAAAGAGAATCTTTTAAATTGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 CTAACATACATTATAATCAAATTGTCAAAAGTAAAATACAAAGAGAATCTTTTAAATTGA 300

Query 301 CAAGAGAAAAGCAGCTGGTCACGTTCAAGGGAGTTCTATAAGAATTTTCAGCAGATTTCTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 CAAGAGAAAAGCAGCTGGTCACGTTCAAGGGAGTTCTATAAGAATTTTCAGCAGATTTCTC 360

Query 361 AGCAGAAACCTTGCAGGCCAACAGGCAGTGGGATGATACATTCAAAGTGCaaaaaaaaa 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 AGCAGAAACCTTGCAGGCCAACAGGCAGTGGGATGATACATTCAAAGTGCAAAAAAAAAAA 420

Query 421 aaaaaa 425
          |||||
Sbjct 421 AAAAAA 425
```


Sequence 650 matched with Sequence 250

Query= Sequence ID 650
Length=633

SEQ ID NO: 250

ALIGNMENTS

Identities = 633/633 (100%), Gaps = 0/633 (0%)

Query	1	CGAGAGTTTACCAGTNGCCTAATAATGCAATAAAAAATGCTTTGAGATAGCTAACNGCCC	60
Sbjct	1	CGAGAGTTTACCAGTNGCCTAATAATGCAATAAAAAATGCTTTGAGATAGCTAACNGCCC	60
Query	61	ATAAAACAACTCAAATTGCTTATAAAGTTTCTTCCCATGTTCCCATTTGATGAAAAGTC	120
Sbjct	61	ATAAAACAACTCAAATTGCTTATAAAGTTTCTTCCCATGTTCCCATTTGATGAAAAGTC	120
Query	121	TTACATCACATATAACTGGGAAGCAGGGGTCCCTCCTCAATTTTCAGACATTTTGAAAGG	180
Sbjct	121	TTACATCACATATAACTGGGAAGCAGGGGTCCCTCCTCAATTTTCAGACATTTTGAAAGG	180
Query	181	ATGACAGTTCTGTTTGTTAGATGAGTAAACCTCTATATTCATAAGTTCTAAATCCTTCA	240
Sbjct	181	ATGACAGTTCTGTTTGTTAGATGAGTAAACCTCTATATTCATAAGTTCTAAATCCTTCA	240
Query	241	TTATGAGGGATTCAAAGTATTTATAAAAAACTGCCCTCTAAAAATTCCTCAGATCTGA	300
Sbjct	241	TTATGAGGGATTCAAAGTATTTATAAAAAACTGCCCTCTAAAAATTCCTCAGATCTGA	300
Query	301	AGTATGGNCTTGGNCCTGAATATACAGTGTTATCCTATGTTTAAAAGGGTGATCCAGACA	360
Sbjct	301	AGTATGGNCTTGGNCCTGAATATACAGTGTTATCCTATGTTTAAAAGGGTGATCCAGACA	360
Query	361	TGAGACGCAACTAGTTGGTGCATAAGAAGGCCCCACTTGGCTATTTTCATATCTACCTACA	420
Sbjct	361	TGAGACGCAACTAGTTGGTGCATAAGAAGGCCCCACTTGGCTATTTTCATATCTACCTACA	420
Query	421	ATTGACCaaaaaaaTTTTTTAGGCCAGCAATTATTATTAGCTTCGCTCTTTCTAGTGC	480
Sbjct	421	ATTGACCAAAAAAATTTTTTAGGCCAGCAATTATTATTAGCTTCGCTCTTTCTAGTGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAGAAACTGCAGGCTGGATCAGTAGTTCAACAGCTAAACAGTCATAAAATAGTCATTGGC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AAGAAACTGCAGGCTGGATCAGTAGTTCAACAGCTAAACAGTCATAAAATAGTCATTGGC  540

Query  541  ATGTTAAATTTCTTTCAATGCTTCAAAGATAAATTCCAATTCTATTTACTTATTCATTGN  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATGTTAAATTTCTTTCAATGCTTCAAAGATAAATTCCAATTCTATTTACTTATTCATTGN  600

Query  601  GACNGNATTACTAAACAGGTAAGGATGGGAATA  633
          ||||||||||||||||||||||||||||
Sbjct   601  GACNGNATTACTAAACAGGTAAGGATGGGAATA  633
```

Sequence 651 matched with Sequence 251

Query= Sequence ID - 651 nt: 251
Length=251

SEQ ID NO: 251 nt: 251

ALIGNMENTS

Identities = 251/251 (100%), Gaps = 0/251 (0%)

```
Query 1   CTTTGGGAGGCCGAGGCGGGCGGATCACTTGAGGTCAGGGGTTTCGAGACCAGTCTGGCCA 60
          |||
Sbjct 1   CTTTGGGAGGCCGAGGCGGGCGGATCACTTGAGGTCAGGGGTTTCGAGACCAGTCTGGCCA 60

Query 61  ACATGGTGAAACCCCAACTCTACTAAAAATACAAAAGTTAGCCAAGTGTGGTGGCAAGTG 120
          |||
Sbjct 61  ACATGGTGAAACCCCAACTCTACTAAAAATACAAAAGTTAGCCAAGTGTGGTGGCAAGTG 120

Query 121 CCTGTAATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATCACTTTGAACCTGGGAGGCG 180
          |||
Sbjct 121 CCTGTAATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATCACTTTGAACCTGGGAGGCG 180

Query 181 GAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTTCAGCCTGGGCAACAGAGCAAGATT 240
          |||
Sbjct 181 GAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTTCAGCCTGGGCAACAGAGCAAGATT 240

Query 241 CCGTCCATCTC 251
          |||
Sbjct 241 CCGTCCATCTC 251
```

Sequence 652 matched with Sequence 252

Query= Sequence ID 652
Length=593

SEQ ID NO: 252

ALIGNMENTS

Identities = 593/593 (100%), Gaps = 0/593 (0%)

Query	1	CTTTCTTCAGCCTTGCAGACACCTAAACATCATGTAATTACCTAAGGAATTCCCAAGTGC	60
Sbjct	1	CTTTCTTCAGCCTTGCAGACACCTAAACATCATGTAATTACCTAAGGAATTCCCAAGTGC	60
Query	61	CTCTTCCAGGTTATACGTGTAAATAGCTGTTTTTATGCAAGATTAGTTAGATACTGCTCT	120
Sbjct	61	CTCTTCCAGGTTATACGTGTAAATAGCTGTTTTTATGCAAGATTAGTTAGATACTGCTCT	120
Query	121	TTACAGGATGAGTGGTGTGTCTTTGGCTgggggggNCTTAAATGTGTTTCTAATGTGTG	180
Sbjct	121	TTACAGGATGAGTGGTGTGTCTTTGGCTGGGGGGGNCTTAAATGTGTTTCTAATGTGTG	180
Query	181	TGTCAAATAATTACCTGTAAACAGACTGCCAATCTGGCTGAAGCCAATGCTTCTGAAGA	240
Sbjct	181	TGTCAAATAATTACCTGTAAACAGACTGCCAATCTGGCTGAAGCCAATGCTTCTGAAGA	240
Query	241	AGATAAAATTAAAGCAATGATGTCGCAATCTGGCCATGAATACGACCCAATCAATTACAT	300
Sbjct	241	AGATAAAATTAAAGCAATGATGTCGCAATCTGGCCATGAATACGACCCAATCAATTACAT	300
Query	301	GAAGAAACCTCTAGGTCCACCACCTCCATCTTACACGTGTTTCCGTTGTGGTAAACCTGG	360
Sbjct	301	GAAGAAACCTCTAGGTCCACCACCTCCATCTTACACGTGTTTCCGTTGTGGTAAACCTGG	360
Query	361	ACATTATATTAAGAATTGCCCAACAAATGGGGATAAAAACTTTGAATCTGGTCCTAGGAT	420
Sbjct	361	ACATTATATTAAGAATTGCCCAACAAATGGGGATAAAAACTTTGAATCTGGTCCTAGGAT	420
Query	421	TAAAAAGAGCACTGGAATTTCCAGAAGTTTCATGATGGAAGTGAAAGATCCTAATATGAA	480
Sbjct	421	TAAAAAGAGCACTGGAATTTCCAGAAGTTTCATGATGGAAGTGAAAGATCCTAATATGAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGGTGCAATGCTTACCAACACTGGAAAATATGCAATCCAACCTATAGATGCAGAAGCATAT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGGTGCAATGCTTACCAACACTGGAAAATATGCAATCCAACCTATAGATGCAGAAGCATAT  540

Query  541  GCAATTGGGAAGAAAGAGAAACCTCCTTNTTACCAGAGAGCCATCTTNTTCT  593
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GCAATTGGGAAGAAAGAGAAACCTCCTTNTTACCAGAGAGCCATCTTNTTCT  593
```

Sequence 653 matched with Sequence 253

Query= Sequence ID 653
Length=211

SEQ ID NO: 253

ALIGNMENTS

Identities = 211/211 (100%), Gaps = 0/211 (0%)

```
Query 1      GTTGTGACTCGTTGGCATGTGATCTGAAGTTCCTGCCCTGCAGCTGACGAGCCAGTGTTT  60
            |||
Sbjct 1      GTTGTGACTCGTTGGCATGTGATCTGAAGTTCCTGCCCTGCAGCTGACGAGCCAGTGTTT  60

Query 61     CAATAATTAAAACAACTCAACTCACTGTCCTCCTGCCTTGAATTTGATCATTGCGCTTT  120
            |||
Sbjct 61     CAATAATTAAAACAACTCAACTCACTGTCCTCCTGCCTTGAATTTGATCATTGCGCTTT  120

Query 121    GCATGTATGTATCACAATACCACATGTACCCCATAAATATGTACAAAGATTATGTGTCAA  180
            |||
Sbjct 121    GCATGTATGTATCACAATACCACATGTACCCCATAAATATGTACAAAGATTATGTGTCAA  180

Query 181    TaaaaaacaaaaattaaaaTCCCAATTTTTA  211
            |||
Sbjct 181    TAAAAAACAAAAATTAAATCCCAATTTTTA  211
```

Sequence 654 matched with Sequence 254

Query= Sequence ID 654
Length=247

SEQ ID NO: 254

ALIGNMENTS

Identities = 247/247 (100%), Gaps = 0/247 (0%)

```
Query 1      GTTGCTAGTAGCGGCAGGAAGATGTCAGGCTCACTTTCCTCTGATTCCCGAAATGGGGGG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1      GTTGCTAGTAGCGGCAGGAAGATGTCAGGCTCACTTTCCTCTGATTCCCGAAATGGGGGG 60

Query 61     AACCTCTAACCATAAAGGAATGGTAGAACAGTCCATTCTCGGATCAGAGAAAAATGCAG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61     AACCTCTAACCATAAAGGAATGGTAGAACAGTCCATTCTCGGATCAGAGAAAAATGCAG 120

Query 121    ACATGGTGTACCTGGAtttttttCTGCCCATGAATGTTGCCAGTCAGTACCTGTCCTCC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121    ACATGGTGTACCTGGATTTTTTCTGCCCATGAATGTTGCCAGTCAGTACCTGTCCTCC 180

Query 181    TTGTTTCTCTATTTTTTGTTATGAATGTTGGGGTTACCACCTGCATTTAGGGGAAAATTG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181    TTGTTTCTCTATTTTTTGTTATGAATGTTGGGGTTACCACCTGCATTTAGGGGAAAATTG 240

Query 241    TGTTCTG 247
             |||||
Sbjct 241    TGTTCTG 247
```


Sequence 655 matched with Sequence 255

Query= Sequence ID 655
Length=244

SEQ ID NO: 255

ALIGNMENTS

Identities = 244/244 (100%), Gaps = 0/244 (0%)

Query	1	GTCCCGGGAATCGCGCCGCGTCGACGGTTTATTTTCAGTGCTTGAAGATACATTCA	60
Sbjct	1	GTCCCGGGAATCGCGCCGCGTCGACGGTTTATTTTCAGTGCTTGAAGATACATTCA	60
Query	61	AATACTTGTTTGGGAAGACACCGTTTAATTTTAAGTTAACTTGCATGTTGTAAATGCGT	120
Sbjct	61	AATACTTGTTTGGGAAGACACCGTTTAATTTTAAGTTAACTTGCATGTTGTAAATGCGT	120
Query	121	TTTATGTTTAAATAAAGAGGAAAAATTTTTTGaaaaaaaaaaaaaaaaaaaaaaaaa	180
Sbjct	121	TTTATGTTTAAATAAAGAGGAAAAATTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAA	180
Query	181	aaaT	240
Sbjct	181	AAAT	240
Query	241	TTTT 244	
Sbjct	241	TTTT 244	

Sequence 656 matched with Sequence 256

Query= Sequence ID 656
Length=433

SEQ ID NO: 256

ALIGNMENTS

Identities = 433/433 (100%), Gaps = 0/433 (0%)

Query	1	TAGAGGCCTGAATAGGTAGACAATGGCAGCAGCGTTTTTAATCACAGTCCTATTCATGCC	60
Sbjct	1	TAGAGGCCTGAATAGGTAGACAATGGCAGCAGCGTTTTTAATCACAGTCCTATTCATGCC	60
Query	61	CTAATTCGGGAGTGATGATTAAAGGACATTAGAGGGAGCACTTTGACATCTGATCCTTTG	120
Sbjct	61	CTAATTCGGGAGTGATGATTAAAGGACATTAGAGGGAGCACTTTGACATCTGATCCTTTG	120
Query	121	AACTGACGTCTGTGCAGGCTGCACTCCATAGAGCTCACTTGGCCAAACTGATTCCTTAA	180
Sbjct	121	AACTGACGTCTGTGCAGGCTGCACTCCATAGAGCTCACTTGGCCAAACTGATTCCTTAA	180
Query	181	ATAAAGTGCTGTGATTTCCAATGTAGGAAATATTACATTAGAGCCTATTGAAATGATTAG	240
Sbjct	181	ATAAAGTGCTGTGATTTCCAATGTAGGAAATATTACATTAGAGCCTATTGAAATGATTAG	240
Query	241	GAATTGAGGAGCTTTTCTTTAGGTGGGAATGTGGTGTATGCTGTATACTCACAAAAGTGA	300
Sbjct	241	GAATTGAGGAGCTTTTCTTTAGGTGGGAATGTGGTGTATGCTGTATACTCACAAAAGTGA	300
Query	301	GATCATTAAATATTGCATGTACTACTTTGAATATCAGGGACCACAGAGAAATAGCATGAGA	360
Sbjct	301	GATCATTAAATATTGCATGTACTACTTTGAATATCAGGGACCACAGAGAAATAGCATGAGA	360
Query	361	AACGCCTTCCTGCAGTCATGCACTTAAAATGAATATGAACAAAAATGTGGAACCTCTGCTG	420
Sbjct	361	AACGCCTTCCTGCAGTCATGCACTTAAAATGAATATGAACAAAAATGTGGAACCTCTGCTG	420
Query	421	TCATAGCTCTCCG	433
Sbjct	421	TCATAGCTCTCCG	433

Sequence 657 matched with Sequence 257

Query= Sequence ID 657
Length=380

SEQ ID NO: 257

ALIGNMENTS

Identities = 380/380 (100%), Gaps = 0/380 (0%)

Query	1	GGGGCTTCTGCTGAGGGGCGAGCGGAGCTTGAGGAAACCGCAGATAAGtttttttCTCT	60
Sbjct	1	GGGGCTTCTGCTGAGGGGCGAGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTTCTCT	60
Query	61	TTGAAAGATAGAGATTAATACAACCTCTAAAAAATATAGTCAATAGGTTACTAAGATATT	120
Sbjct	61	TTGAAAGATAGAGATTAATACAACCTCTAAAAAATATAGTCAATAGGTTACTAAGATATT	120
Query	121	GCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATATGAA	180
Sbjct	121	GCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATATGAA	180
Query	181	GACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGAGGT	240
Sbjct	181	GACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGAGGT	240
Query	241	TGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAAAGGAC	300
Sbjct	241	TGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAAAGGAC	300
Query	301	TACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAAATGAAGGTGA	360
Sbjct	301	TACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAAATGAAGGTGA	360
Query	361	CTTAAACAGCTTAAAGTTTA	380
Sbjct	361	CTTAAACAGCTTAAAGTTTA	380

Sequence 658 matched with Sequence 258

Query= Sequence ID 658
Length=572

SEQ ID NO: 258

ALIGNMENTS

Identities = 572/572 (100%), Gaps = 0/572 (0%)

Query	1	GACCTTTGAGAAAATTAATTTAAATCCTAGAACTTTGGGTGAACCGAAGAAATTTATAAT	60
Sbjct	1	GACCTTTGAGAAAATTAATTTAAATCCTAGAACTTTGGGTGAACCGAAGAAATTTATAAT	60
Query	61	ATTTGTTTAGTTAATAACAGATAAAAAAGGAAAGATTCAAGCCTATTGGATGAGAATTTGT	120
Sbjct	61	ATTTGTTTAGTTAATAACAGATAAAAAAGGAAAGATTCAAGCCTATTGGATGAGAATTTGT	120
Query	121	ACATTATTTTAGAGCTAATAATAATGGTTTTTCAGTTTAGTGAGGATTTAAAAAATGTTTT	180
Sbjct	121	ACATTATTTTAGAGCTAATAATAATGGTTTTTCAGTTTAGTGAGGATTTAAAAAATGTTTT	180
Query	181	TGAATCAAACtttttttCTTTATAATCCTTTTTAACTAACTCAGGAAATAAGGTATTATG	240
Sbjct	181	TGAATCAAACTTTTTTTCTTTATAATCCTTTTTAACTAACTCAGGAAATAAGGTATTATG	240
Query	241	AAATCCACACACTGTTACCTCCTTAAAGTATGAGGATACTTCCCACTGTTTGGTCCACTA	300
Sbjct	241	AAATCCACACACTGTTACCTCCTTAAAGTATGAGGATACTTCCCACTGTTTGGTCCACTA	300
Query	301	GTGGCTGATTATTTTGTGTTGTGGATTATTTGTAATTTTCTTTTAAATCTTCCTTAAAGA	360
Sbjct	301	GTGGCTGATTATTTTGTGTTGTGGATTATTTGTAATTTTCTTTTAAATCTTCCTTAAAGA	360
Query	361	GCATGGCATTGAGTCACAGACCTATATTTGAATCCTGTCATTTACTAGCGTTTTGACC	420
Sbjct	361	GCATGGCATTGAGTCACAGACCTATATTTGAATCCTGTCATTTACTAGCGTTTTGACC	420
Query	421	TTGAACAATTATGCTCAGAGTCTCAGTTTTTTCTTGTAAGTGATGATGATACTACTTAA	480
Sbjct	421	TTGAACAATTATGCTCAGAGTCTCAGTTTTTTCTTGTAAGTGATGATGATACTACTTAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTCACAGGGTTGTAGTGAAGATCAAATGAGATCATGTCTGTANAACACCCTGCCCGGCAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CTCACAGGGTTGTAGTGAAGATCAAATGAGATCATGTCTGTANAACACCCTGCCCGGCAC  540

Query  541  TCAATAAGTATTAATAGGAACCCATATACCTC  572
          ||||||||||||||||||||||||
Sbjct   541  TCAATAAGTATTAATAGGAACCCATATACCTC  572
```

Sequence 660 matched with Sequence 259

Query= Sequence ID 660
Length=477

SEQ ID NO: 259

ALIGNMENTS

Identities = 477/477 (100%), Gaps = 0/477 (0%)

```
Query 1      TGttttttattttttAAAAGGTATAAACACCaaaaaaaTTAACATTGTATGAAGATGG  60
          |||
Sbjct 1      TGTtttttATTTTtAAAAGGTATAAACACCAAAAAAAAAATTAACATTGTATGAAGATGG  60

Query 61     AAAATAAGAAGATGCACTTTCTGTAACCTTTGTCTAAGGATTTAAATTACTAACTTATGAA  120
          |||
Sbjct 61     AAAATAAGAAGATGCACTTTCTGTAACCTTTGTCTAAGGATTTAAATTACTAACTTATGAA  120

Query 121    CTCCAATTTGAATTGAACTTAACTATCGGCTTTCTTACTGGTAAAATTATATGGTTTATT  180
          |||
Sbjct 121    CTCCAATTTGAATTGAACTTAACTATCGGCTTTCTTACTGGTAAAATTATATGGTTTATT  180

Query 181    TTAAATGCGTACATATTGACCAATGGCCTCTGAAAAAGCACATTTTAGATACTGAAATTG  240
          |||
Sbjct 181    TTAAATGCGTACATATTGACCAATGGCCTCTGAAAAAGCACATTTTAGATACTGAAATTG  240

Query 241    AAGGAAAGAAAATGCATCTTCAAACATTTTTTGAATCTCACCACATATACTttgttana  300
          |||
Sbjct 241    AAGGAAAGAAAATGCATCTTCAAACATTTTTTGAATCTCACCACATATACTTTGTTANA  300

Query 301    tttgtgtattgtagggtgtttgttttgtatttttgtattgtatatgaacttttttAAAT  360
          |||
Sbjct 301    TTTGTGTATTGTAGGGTGTtTGTtTTGTATTtTTGTATTGTATATGAACTTTtTTTAAAT  360

Query 361    GTGACAGTTAAACACATCTTTAAAAGCATAGTCACAGACAAAAGCATACAGTATAAAAAAT  420
          |||
Sbjct 361    GTGACAGTTAAACACATCTTTAAAAGCATAGTCACAGACAAAAGCATACAGTATAAAAAAT  420

Query 421    TTCCTTGAAAACCTCTACAATATTATATTTGGAGGCAGCTTCAGACTGTTTTATTGG  477
          |||
Sbjct 421    TTCCTTGAAAACCTCTACAATATTATATTTGGAGGCAGCTTCAGACTGTTTTATTGG  477
```


Sequence 661 matched with Sequence 260

Query= Sequence ID 661
Length=256

SEQ ID NO: 260

ALIGNMENTS

Identities = 256/256 (100%), Gaps = 0/256 (0%)

```
Query 1   CTCTGGCACACATTAGTTCCTCTTATATTACATTGATATAAGCAAGTCATATGGATTTAT  60
          |||
Sbjct 1   CTCTGGCACACATTAGTTCCTCTTATATTACATTGATATAAGCAAGTCATATGGATTTAT  60

Query 61  CTGAGTGTAAGGAGAGCTGGAAAAAATAGTTTCTAGCAGGTCAGCCACCTCCCAGTGAGG  120
          |||
Sbjct 61  CTGAGTGTAAGGAGAGCTGGAAAAAATAGTTTCTAGCAGGTCAGCCACCTCCCAGTGAGG  120

Query 121 GCTGCATACCATAGAAGGGGAGAATGAATTTTGGGAAAACAGGTAATTATCTCTGTCACA  180
          |||
Sbjct 121 GCTGCATACCATAGAAGGGGAGAATGAATTTTGGGAAAACAGGTAATTATCTCTGTCACA  180

Query 181 GAAGGGGATGAAAAGTATGGTAGTTACNCAAGTTANACATCTGTATGGAAAATACCACTT  240
          |||
Sbjct 181 GAAGGGGATGAAAAGTATGGTAGTTACNCAAGTTANACATCTGTATGGAAAATACCACTT  240

Query 241 GGTTCACAAATGNGG  256
          |||
Sbjct 241 GGTTCACAAATGNGG  256
```

Blast comparison trimmed “NGG” from the 3’ end of both sequences and reported 253 identities. The report has been manually corrected for this. “NGG” has been appended to both sequences and identity count has been increased to 256.

Sequence 663 matched with Sequence 261

Query= Sequence ID - 663 nt: 627
Length=627

SEQ ID NO: 261 nt: 627

ALIGNMENTS

Identities = 627/627 (100%), Gaps = 0/627 (0%)

Query	1	GCCTCCCGGGTTCAGGGATTTCTCCTGCCTCAGCCTCCTGAGTGGCTGCATTGCAGGCAC	60
Sbjct	1	GCCTCCCGGGTTCAGGGATTTCTCCTGCCTCAGCCTCCTGAGTGGCTGCATTGCAGGCAC	60
Query	61	CTGCCACCACGCCTTGCAAATTTTGTGTTTTTAGTGGAGATGGGGTTTGCCATGTTGG	120
Sbjct	61	CTGCCACCACGCCTTGCAAATTTTGTGTTTTAGTGGAGATGGGGTTTGCCATGTTGG	120
Query	121	CCAGGCTGGTCTCGGACTCCTGACCTCAGGTGATCCGCCCGCCTCAGCCTCCAGAGGGC	180
Sbjct	121	CCAGGCTGGTCTCGGACTCCTGACCTCAGGTGATCCGCCCGCCTCAGCCTCCAGAGGGC	180
Query	181	TGGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAAGTTTTGCATCTTTAATGCCCTC	240
Sbjct	181	TGGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAAGTTTTGCATCTTTAATGCCCTC	240
Query	241	TGAACAAATACATAGAGAAAACCTCAGAACAATTAACCTGCAGAGCAACAGTGTCTCT	300
Sbjct	241	TGAACAAATACATAGAGAAAACCTCAGAACAATTAACCTGCAGAGCAACAGTGTCTCT	300
Query	301	CCATGTCTTAGGTTTCAAGTTTGCCTCTAAAATTCTAATCCATATTTTCTACTTCTCAG	360
Sbjct	301	CCATGTCTTAGGTTTCAAGTTTGCCTCTAAAATTCTAATCCATATTTTCTACTTCTCAG	360
Query	361	ATAATTTATGTGTGTGTACTCTTCCTAGACGTACAAGAGACTTTTAAATGCTAAATATTT	420
Sbjct	361	ATAATTTATGTGTGTGTACTCTTCCTAGACGTACAAGAGACTTTTAAATGCTAAATATTT	420
Query	421	GTCAGTGCTTAACAAAACTCAATTTACATTACTCATattgttttgttttaattgaat	480
Sbjct	421	GTCAGTGCTTAACAAAACTCAATTTACATTACTCATATTGTTTTGTTTAAATTGAAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  gtgaattaaattttttattagttatttgatttggaatggtatgtATGCCATTAACACTATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTGAATTAAATTTTATTAGTTATTTGATTTGGAATGTTATGTATGCCATTAACACTATT  540

Query  541  AGGGGAATCTCTAGCATTTCTGTATTTTAAAGAATTTGATTCTTTGTANATTCTGCCT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AGGGGAATCTCTAGCATTTCTGTATTTTAAAGAATTTGATTCTTTGTANATTCTGCCT  600

Query  601  GTGTGGCATTTTAAACATGTGTGACAT  627
          ||||||||||||||||||||
Sbjct   601  GTGTGGCATTTTAAACATGTGTGACAT  627
```

Sequence 665 matched with Sequence 262

Query= Sequence ID - 665 nt: 345
Length=345

SEQ ID NO: 262 nt: 345

ALIGNMENTS

Identities = 345/345 (100%), Gaps = 0/345 (0%)

```
Query 1 ACCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAATACGGGACCCGC 60
      |||
Sbjct 1 ACCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAATACGGGACCCGC 60

Query 61 TATGGGGCCTCCCTCCGAAAAATGGTGAAGAAAATTGAAATCAGCCAGCACGCCAAGTAC 120
      |||
Sbjct 61 TATGGGGCCTCCCTCCGAAAAATGGTGAAGAAAATTGAAATCAGCCAGCACGCCAAGTAC 120

Query 121 ACTTGCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGGATCTGGCACTGT 180
      |||
Sbjct 121 ACTTGCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGGATCTGGCACTGT 180

Query 181 GGTTCCCTGCATGAAGACAGTGGCTGGCGGTGCCTGGACGTACAATACCACTTCCGCTGTC 240
      |||
Sbjct 181 GGTTCCCTGCATGAAGACAGTGGCTGGCGGTGCCTGGACGTACAATACCACTTCCGCTGTC 240

Query 241 ACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGAAAGACCAGTAGACGCTCCTCTAC 300
      |||
Sbjct 241 ACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGAAAGACCAGTAGACGCTCCTCTAC 300

Query 301 TCTTTGAGACATCACTGGCCTATAATAAATGGGTTAATTTATGTA 345
      |||
Sbjct 301 TCTTTGAGACATCACTGGCCTATAATAAATGGGTTAATTTATGTA 345
```

Sequence 666 matched with Sequence 263

Query= Sequence ID - 666 nt: 252
Length=252

SEQ ID NO: 263 nt: 252

ALIGNMENTS

Identities = 252/252 (100%), Gaps = 0/252 (0%)

```
Query 1   ATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGTTGATG  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   ATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGTTGATG  60

Query 61  AAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCCAGAAAGCAGTTAACA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  AAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCCAGAAAGCAGTTAACA  120

Query 121 GTGCCACCGGTGTTCCAACTGTTTAAAATTGATCAGGGACCATGAAAAGAACTTGTGCT  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 GTGCCACCGGTGTTCCAACTGTTTAAAATTGATCAGGGACCATGAAAAGAACTTGTGCT  180

Query 181 TCACCGAAGaaaaatatctaaacatcgaaaaacttaaatattatggaaaaaaaaacattgc  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 TCACCGAAGAAAAATATCTAAACATCGAAAAACTTAAATATTATGGAAAAAAAACATTGC  240

Query 241 aaaatataaaaT 252
          ||||||||||||
Sbjct 241 AAAATATAAAAT 252
```

Sequence 669 matched with Sequence 264

Query= Sequence ID 669
Length=294

SEQ ID NO: 264

ALIGNMENTS

Identities = 294/294 (100%), Gaps = 0/294 (0%)

Query	1	TTACTTTTAACCAGNGAAATTGACCTGCCCCTGAANAGGCGGGCNTGACACAGCAAGACG	60
Sbjct	1	TTACTTTTAACCAGNGAAATTGACCTGCCCCTGAANAGGCGGGCNTGACACAGCAAGACG	60
Query	61	AGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACGGTACCTAACAAACCCACAGGTC	120
Sbjct	61	AGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACGGTACCTAACAAACCCACAGGTC	120
Query	121	CTAAACTACCAAACCTGCATTAAAAATTTTCGGTTGGGGCGACCTCGGAGCAGAACCCAAC	180
Sbjct	121	CTAAACTACCAAACCTGCATTAAAAATTTTCGGTTGGGGCGACCTCGGAGCAGAACCCAAC	180
Query	181	CTCCGAGCAGTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGATC	240
Sbjct	181	CTCCGAGCAGTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGATC	240
Query	241	CAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAACAGCGCAATCCTATT	294
Sbjct	241	CAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAACAGCGCAATCCTATT	294

Sequence 670 matched with Sequence 265

Query= Sequence ID 670
Length=370

SEQ ID NO: 265

ALIGNMENTS

Identities = 370/370 (100%), Gaps = 0/370 (0%)

Query	1	GGCTGATTCCTGAGCTATAAAAGCATAATTGCTTTATATTTTGGATCATTTTTTACTGGG	60
Sbjct	1	GGCTGATTCCTGAGCTATAAAAGCATAATTGCTTTATATTTTGGATCATTTTTTACTGGG	60
Query	61	GGCGGACTTggggggggTTGCATACAAAGATAACATATATATCCAACCTTCTGAAATGAA	120
Sbjct	61	GGCGGACTTGGGGGGGGTTGCATACAAAGATAACATATATATCCAACCTTCTGAAATGAA	120
Query	121	ATGTTTTTAGATTACTTTTTCAACTGTAAATAATGTACATTTAATGTCACAAGaaaaaaa	180
Sbjct	121	ATGTTTTTAGATTACTTTTTCAACTGTAAATAATGTACATTTAATGTCACAAGAAAAAAA	180
Query	181	TGTCTTCTGCAAATTTTCTAGTATAACAGAAATTTTGTAGATGaaaaaaaTCATTATGT	240
Sbjct	181	TGTCTTCTGCAAATTTTCTAGTATAACAGAAATTTTGTAGATGAAAAAATCATTATGT	240
Query	241	TTAGAGGTCTAATGCTATGTTTTCATATTACAGAGTGAATTTGTATTTAAACAAAAATTT	300
Sbjct	241	TTAGAGGTCTAATGCTATGTTTTCATATTACAGAGTGAATTTGTATTTAAACAAAAATTT	300
Query	301	AAATTTTGGAATCCTCTAAACATTTTGTATCTTTAATTGGTTTATTATTAAATAAATCA	360
Sbjct	301	AAATTTTGGAATCCTCTAAACATTTTGTATCTTTAATTGGTTTATTATTAAATAAATCA	360
Query	361	TATAAAAATT 370	
Sbjct	361	TATAAAAATT 370	

Sequence 671 matched with Sequence 266

Query= Sequence ID 671
Length=353

SEQ ID NO: 266

ALIGNMENTS

Identities = 353/353 (100%), Gaps = 0/353 (0%)

Query	1	CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC	60
Sbjct	1	CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC	60
Query	61	TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT	120
Sbjct	61	TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT	120
Query	121	TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTACCTGAAAGAAACT	180
Sbjct	121	TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTACCTGAAAGAAACT	180
Query	181	ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTGAGAACCACTTCTAC	240
Sbjct	181	ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTGAGAACCACTTCTAC	240
Query	241	CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA	300
Sbjct	241	CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA	300
Query	301	TAAATGTTGATGGTAATACAGCATTATCTATCACCATAACCCTTCAGCACTA	353
Sbjct	301	TAAATGTTGATGGTAATACAGCATTATCTATCACCATAACCCTTCAGCACTA	353

Sequence 672 matched with Sequence 267

Query= Sequence ID 672
Length=433

SEQ ID NO: 267

ALIGNMENTS

Identities = 433/433 (100%), Gaps = 0/433 (0%)

Query	1	CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC	60
Sbjct	1	CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC	60
Query	61	TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT	120
Sbjct	61	TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT	120
Query	121	TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTACCTGAAAGAAACT	180
Sbjct	121	TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTACCTGAAAGAAACT	180
Query	181	ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTCAAAACCATTCTAC	240
Sbjct	181	ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTCAAAACCATTCTAC	240
Query	241	CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA	300
Sbjct	241	CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA	300
Query	301	TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTAGATCCCT	360
Sbjct	301	TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTAGATCCCT	360
Query	361	ATCAGTCCAATGGAAATGTTGGATTANAACCAGGCATTGTTTCAATANACTCTCGCTCTG	420
Sbjct	361	ATCAGTCCAATGGAAATGTTGGATTANAACCAGGCATTGTTTCAATANACTCTCGCTCTG	420
Query	421	TGAACACACATGG	433
Sbjct	421	TGAACACACATGG	433

Sequence 673 matched with Sequence 268

Query= Sequence ID 673
Length=683

SEQ ID NO: 268

ALIGNMENTS

Identities = 683/683 (100%), Gaps = 0/683 (0%)

Query	1	GGGTTTTCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACT	60
Sbjct	1	GGGTTTTCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACT	60
Query	61	GCTAAACAGAATACTGCTATTTTGAGAGAGTCAAGACTCTTCTTAAGGGCCAAGAAAGC	120
Sbjct	61	GCTAAACAGAATACTGCTATTTTGAGAGAGTCAAGACTCTTCTTAAGGGCCAAGAAAGC	120
Query	121	CACNTGNCCCTNGGNCTAATCTGGCTGAGTAGTCAGTTATAAAAGCCNTAATNGCTTNN	180
Sbjct	121	CACNTGNCCCTNGGNCTAATCTGGCTGAGTAGTCAGTTATAAAAGCCNTAATNGCTTNN	180
Query	181	TNTTTGGNNTCNTTTTTNNCNGGGGNCGGNCTTGGGGGGGGTTGCNTCCAAAGATANCAT	240
Sbjct	181	TNTTTGGNNTCNTTTTTNNCNGGGGNCGGNCTTGGGGGGGGTTGCNTCCAAAGATANCAT	240
Query	241	NTNTTCCAACTTTNTNAANNNAANNGTTTTAAAATCCCTTTTCCNCCNGAAAAANANGC	300
Sbjct	241	NTNTTCCAACTTTNTNAANNNAANNGTTTTAAAATCCCTTTTCCNCCNGAAAAANANGC	300
Query	301	CCTTTAAGNGCCNCAAAAAAAAAANNGTNTTCTGCANNTTTTCTANTATNACAAANNTTTT	360
Sbjct	301	CCTTTAAGNGCCNCAAAAAAAAAANNGTNTTCTGCANNTTTTCTANTATNACAAANNTTTT	360
Query	361	NGTAGAANAAAAATTTTTTTTTAGNGGCTACCCTTTNTTTNTTANNCANNGGAGTTTNTT	420
Sbjct	361	NGTAGAANAAAAATTTTTTTTTAGNGGCTACCCTTTNTTTNTTANNCANNGGAGTTTNTT	420
Query	421	TTTACAAAAAAAAAANATTGGGNCCCCTCCACAACCTTGGGTCTNTAATNGGGGGGTTTT	480
Sbjct	421	TTTACAAAAAAAAAANATTGGGNCCCCTCCACAACCTTGGGTCTNTAATNGGGGGGTTTT	480

```
Query  481  TAAATAAANCNTNTNTAAATCCCCNNNNNNNNNNNNNNNNNNNNNNCCNNNNNNNNNNNNNNN  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TAAATAAANCNTNTNTAAATCCCCNNNNNNNNNNNNNNNNNNNNNNCCNNNNNNNNNNNNNNN  540

Query  541  CCCNNNNAAAAAATTTTTNCTCCCCNCCCTTTTTCTTCCTGCCGGCCCAATTTAAGCC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CCCNNNNAAAAAATTTTTNCTCCCCNCCCTTTTTCTTCCTGCCGGCCCAATTTAAGCC  600

Query  601  CNGGCGCTTGGGGCAAATCCCCCTTTAGNGGGGGGGTTTANAAAAACCNGGGGCGGGGNT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  CNGGCGCTTGGGGCAAATCCCCCTTTAGNGGGGGGGTTTANAAAAACCNGGGGCGGGGNT  660

Query  661  TTAAAACNCGGGGNNNGGGGAA  683
          ||||||||||||||||
Sbjct   661  TTAAAACNCGGGGNNNGGGGAA  683
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

Sequence 674 matched with Sequence 269

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 674
Length=49

SEQ ID NO: 269

97.6 8e-27

ALIGNMENTS

Identities = 49/49 (100%), Gaps = 0/49 (0%)

Query	1	ACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATG	49
Sbjct	1	ACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATG	49

Sequence 675 matched with Sequence 270

Query= Sequence ID - 675 nt: 591
Length=591

SEQ ID NO: 270 nt: 591

ALIGNMENTS

Identities = 591/591 (100%), Gaps = 0/591 (0%)

Query	1	GTATAGAAAATAATGTCCCCAGNGCATAGAAAAAATGAGTCTCTGGGCCAGTGAATACAA	60
Sbjct	1	GTATAGAAAATAATGTCCCCAGNGCATAGAAAAAATGAGTCTCTGGGCCAGTGAATACAA	60
Query	61	AACATCATGTCGAGAATCATTGGAAGATATACAGAGTTCGTATTTTCAGCTTTGTTTATCC	120
Sbjct	61	AACATCATGTCGAGAATCATTGGAAGATATACAGAGTTCGTATTTTCAGCTTTGTTTATCC	120
Query	121	TTCCTGTTAAGAGCCTCTGAGTTTTTAGTTTTTAAAAGGATGAAAAGCTTATGCAACATGC	180
Sbjct	121	TTCCTGTTAAGAGCCTCTGAGTTTTTAGTTTTTAAAAGGATGAAAAGCTTATGCAACATGC	180
Query	181	TCAGCAGGAGCTTCATCAACGATATATGTCAGATCTAAAGGTATATTTTCATTCTGTAAT	240
Sbjct	181	TCAGCAGGAGCTTCATCAACGATATATGTCAGATCTAAAGGTATATTTTCATTCTGTAAT	240
Query	241	TATGTTACATAAAAGCAATGTAAATCAGAATAAATATGTTAGACCAGAATAAAATTAATT	300
Sbjct	241	TATGTTACATAAAAGCAATGTAAATCAGAATAAATATGTTAGACCAGAATAAAATTAATT	300
Query	301	ATATTCTGGTCTTCAAAGGACACACAGAACAGATATCAGCAGAATCACTTAATACTTCAT	360
Sbjct	301	ATATTCTGGTCTTCAAAGGACACACAGAACAGATATCAGCAGAATCACTTAATACTTCAT	360
Query	361	AGAACAAAAATCACTCAAAACCTGTTTATAACCAAAGAATTCATGAAAAAGAAAGCCTTT	420
Sbjct	361	AGAACAAAAATCACTCAAAACCTGTTTATAACCAAAGAATTCATGAAAAAGAAAGCCTTT	420
Query	421	GCCATTTGTCTTAGAAAGTTATTTTTTaaaaaaaTCATACTTACTATTAGTATCTATG	480
Sbjct	421	GCCATTTGTCTTAGAAAGTTATTTTTTAAAAAAAATCATACTTACTATTAGTATCTATG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAAGTATATGTAACAATTTTATGTAAAGGTCATCTTCTGTGATAGTAAAAAATATGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GAAGTATATGTAACAATTTTATGTAAAGGTCATCTTCTGTGATAGTAAAAAATATGT  540

Query  541  CTTTACTAAGTTGAAATGAATACTTTCTGNCTTTGCTAATGGATAGTTATT  591
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CTTTACTAAGTTGAAATGAATACTTTCTGNCTTTGCTAATGGATAGTTATT  591
```

Sequence 676 matched with Sequence 271

Query= Sequence ID 676
Length=329

SEQ ID NO: 271

ALIGNMENTS

Identities = 329/329 (100%), Gaps = 0/329 (0%)

Query	1	CTCAATTCTACTAAAAAGCCCCCAAGAAAAGCGAATGAGAAAACAGAGTCATCCTCTGC	60
Sbjct	1	CTCAATTCTACTAAAAAGCCCCCAAGAAAAGCGAATGAGAAAACAGAGTCATCCTCTGC	60
Query	61	ACAGCAAGTAGCAGTGTACGCCTTAGCGCTTCCAGCTCCAGCTCAGATTCCAGCTCCTC	120
Sbjct	61	ACAGCAAGTAGCAGTGTACGCCTTAGCGCTTCCAGCTCCAGCTCAGATTCCAGCTCCTC	120
Query	121	CTCTTCCTCGTCGTCGTCTTCAGACACCAGTGATTTCAGACTCAGGCTAAGGGGTCAGGCC	180
Sbjct	121	CTCTTCCTCGTCGTCGTCTTCAGACACCAGTGATTTCAGACTCAGGCTAAGGGGTCAGGCC	180
Query	181	AGATGGGGCAGGAAGGCTNCGCAGGACCGGACCCCTAGACCACCCTGCCCCACCTGCCCC	240
Sbjct	181	AGATGGGGCAGGAAGGCTNCGCAGGACCGGACCCCTAGACCACCCTGCCCCACCTGCCCC	240
Query	241	TTCCCCCTTTGCTGTGACACTTCTTCATCTCAccccccctgccccccTCTAGGAGAGCT	300
Sbjct	241	TTCCCCCTTTGCTGTGACACTTCTTCATCTCACCCCCCCTGCCCCCCTCTAGGAGAGCT	300
Query	301	GGCTCTGCAGTGGGGGAGGGATGCAGGGA	329
Sbjct	301	GGCTCTGCAGTGGGGGAGGGATGCAGGGA	329

Sequence 679 matched with Sequence 272

Query= Sequence ID 679
Length=688

SEQ ID NO: 272

ALIGNMENTS

Identities = 688/688 (100%), Gaps = 0/688 (0%)

Query	1	GNANCNTTTCCTNTCGNAAANCGCGCCTTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACaaa	66
Sbjct	1	GNANCNTTTCCTNTCGNAAANCGCGCCTTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACAAA	66
Query	67	aaaaaaaaaaaaaaaaaaaaaaaaaTNTAGACTCGANCAAGCTTATGCANGCNTGCGG	126
Sbjct	67	AAAAAAAAAAAAAAAAAAAAAAAAAANTNTAGACTCGANCAAGCTTATGCANGCNTGCGG	126
Query	127	CCGCAATTCGAGCTCGGCCGACTTGGCCAATTCGCCCTATAGNGAGTCGTATTACAATTC	186
Sbjct	127	CCGCAATTCGAGCTCGGCCGACTTGGCCAATTCGCCCTATAGNGAGTCGTATTACAATTC	186
Query	187	ACTGGCCGTCGTTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCAACCTTAATCG	246
Sbjct	187	ACTGGCCGTCGTTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCAACCTTAATCG	246
Query	247	CCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATANCGAANAGGCCCGCACCGATCG	306
Sbjct	247	CCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATANCGAANAGGCCCGCACCGATCG	306
Query	307	CCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAANGGAAATTGTAAGCGTTAATATTTTG	366
Sbjct	307	CCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAANGGAAATTGTAAGCGTTAATATTTTG	366
Query	367	TTAAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATC	426
Sbjct	367	TTAAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATC	426
Query	427	GGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGNGTTGTTCCAGTT	486
Sbjct	427	GGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGNGTTGTTCCAGTT	486

PATENT SEQUENCE ALIGNMENT

```
Query  487  TGGAACAANAGTCCACTNTTAAAGAACGNGGACTCCAACGTCAAAGGGCGAAAAACCGTC  546
          |||
Sbjct  487  TGGAACAANAGTCCACTNTTAAAGAACGNGGACTCCAACGTCAAAGGGCGAAAAACCGTC  546

Query  547  TATCAGGGCGATGGCCCACTACGTGAACCATCNCCTAATCAAGTTTTTTGGGGTCGAGG  606
          |||
Sbjct  547  TATCAGGGCGATGGCCCACTACGTGAACCATCNCCTAATCAAGTTTTTTGGGGTCGAGG  606

Query  607  NGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAAAGCTTGACGGGGA  666
          |||
Sbjct  607  NGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAAAGCTTGACGGGGA  666

Query  667  AAGCCCGGCGAACGTGGCGAAA  688
          |||
Sbjct  667  AAGCCCGGCGAACGTGGCGAAA  688
```

Blast comparison trimmed “GNANCN” from the 5’ end of both sequences and reported 682 identities. The report has been manually corrected for this. “GNANCN” has been prepended to both sequences and identity count has been increased to 688.

Sequence 682 matched with Sequence 273

Query= Sequence ID 682
Length=271

SEQ ID NO: 273

ALIGNMENTS

Identities = 271/271 (100%), Gaps = 0/271 (0%)

Query	1	CACCTGCAGTCCAAGTACATCGGCACGGGCCACGCCGACACCACCAAGTGGGAGTGGCTG	60
Sbjct	1	CACCTGCAGTCCAAGTACATCGGCACGGGCCACGCCGACACCACCAAGTGGGAGTGGCTG	60
Query	61	GTGAACCAACACCGCGACTCGTACTGCTCCTACATGGGCCACTTCGACCTTCTCAACTAC	120
Sbjct	61	GTGAACCAACACCGCGACTCGTACTGCTCCTACATGGGCCACTTCGACCTTCTCAACTAC	120
Query	121	TTCGCCATTGCGGAGAATGAGAGCAAAGCGCGAGTCCGCTTCAACTTGATGGAAAAGATG	180
Sbjct	121	TTCGCCATTGCGGAGAATGAGAGCAAAGCGCGAGTCCGCTTCAACTTGATGGAAAAGATG	180
Query	181	CTTCAGCCTTGTGGACCGCCAGCCGACAAGCCCGAGGAAAAGTGAACCTTTGCTTAACNA	240
Sbjct	181	CTTCAGCCTTGTGGACCGCCAGCCGACAAGCCCGAGGAAAAGTGAACCTTTGCTTAACNA	240
Query	241	CCGAATGGNGGGGANCTTTTCCAACGNTTTT	271
Sbjct	241	CCGAATGGNGGGGANCTTTTCCAACGNTTTT	271

Sequence 683 matched with Sequence 274

Query= Sequence ID 683
Length=213

SEQ ID NO: 274

ALIGNMENTS

Identities = 213/213 (100%), Gaps = 0/213 (0%)

Query	1	TTGGTTTCATACTGNTGGGGNTTGAATGNTCCCTNCAACACTNATGTTGANACTTAATCC	60
Sbjct	1	TTGGTTTCATACTGNTGGGGNTTGAATGNTCCCTNCAACACTNATGTTGANACTTAATCC	60
Query	61	CTAATGNNGCAATACTGAAAGGTGGGGCCTTTGAGATGTGATTGGATCGTAAGGCTGTGC	120
Sbjct	61	CTAATGNNGCAATACTGAAAGGTGGGGCCTTTGAGATGTGATTGGATCGTAAGGCTGTGC	120
Query	121	CTTCATTCATGGGTAAATGGATTAATGGGTTATCACAGGAATGGGACTGGTGGCTTTATA	180
Sbjct	121	CTTCATTCATGGGTAAATGGATTAATGGGTTATCACAGGAATGGGACTGGTGGCTTTATA	180
Query	181	AGAAGAGGAAAAGAGAACTGAGCTTGCATGCCC	213
Sbjct	181	AGAAGAGGAAAAGAGAACTGAGCTTGCATGCCC	213

Sequence 684 matched with Sequence 275

Query= Sequence ID - 684 nt: 545
Length=545

SEQ ID NO: 275 nt: 545

ALIGNMENTS

Identities = 545/545 (100%), Gaps = 0/545 (0%)

Query	1	GTGGAAGNGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC	60
Sbjct	1	GTGGAAGNGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC	60
Query	61	CANGGAAGACAGGGCGACCTGGAAGTCCAATACTTCTTAAGATCATCCAATACTATTGGA	120
Sbjct	61	CANGGAAGACAGGGCGACCTGGAAGTCCAATACTTCTTAAGATCATCCAATACTATTGGA	120
Query	121	TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA	180
Sbjct	121	TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA	180
Query	181	GATCCGCATGTCCCTTCNCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG	240
Sbjct	181	GATCCGCATGTCCCTTCNCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG	240
Query	241	CAAGGCCATCCGAGGGCACCTGAAAAACAACCCAGCTCTGGAGAACTGCTGCCTCATAT	300
Sbjct	241	CAAGGCCATCCGAGGGCACCTGAAAAACAACCCAGCTCTGGAGAACTGCTGCCTCATAT	300
Query	301	CCGGGGGAATGTGGGCTTTGTGTTACCAAGGAGGACCTCACTGANATCAGGGACATGTT	360
Sbjct	301	CCGGGGGAATGTGGGCTTTGTGTTACCAAGGAGGACCTCACTGANATCAGGGACATGTT	360
Query	361	GCTGGCCAATAAGGTGCCAGCTGCTGCCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCAC	420
Sbjct	361	GCTGGCCAATAAGGTGCCAGCTGCTGCCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCAC	420
Query	421	TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGATAAGACCTCCTTTTCCAGGCTTTAGG	480
Sbjct	421	TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGATAAGACCTCCTTTTCCAGGCTTTAGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TATCACCCTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TATCACCCTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540

Query  541  ACTGG  545
          ||||
Sbjct   541  ACTGG  545
```

Sequence 685 matched with Sequence 276

Query= Sequence ID 685
Length=260

SEQ ID NO: 276

ALIGNMENTS

Identities = 260/260 (100%), Gaps = 0/260 (0%)

```
Query 1  GGAAAGGGCCATTTTATTGCCTAAAACACCTGGNTTTTNAGGTAACAGTTCCAACATGT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  GGAAAGGGCCATTTTATTGCCTAAAACACCTGGNTTTTNAGGTAACAGTTCCAACATGT  60

Query 61 CCTTTTTTGAATAGCTGTTCTAATTATTATATATTCAGCTGATTAATAGGAGTACTTGAT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 CCTTTTTTGAATAGCTGTTCTAATTATTATATATTCAGCTGATTAATAGGAGTACTTGAT  120

Query 121 AGGTGGACTGTGTCAGGTAGCCTCAGGCAATCCTACTTCAACAAGCTGTCAGGGAGCCAT  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AGGTGGACTGTGTCAGGTAGCCTCAGGCAATCCTACTTCAACAAGCTGTCAGGGAGCCAT  180

Query 181 GCCATGCTTCTTTATGACATAGGTGAATTTGATAGGCTCACTAGCAGAACATGGGATCAC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 GCCATGCTTCTTTATGACATAGGTGAATTTGATAGGCTCACTAGCAGAACATGGGATCAC  240

Query 241 AAGGTGGAACCNTTCCNTTT  260
          ||||||||||||||||
Sbjct 241 AAGGTGGAACCNTTCCNTTT  260
```

Sequence 686 matched with Sequence 277

Query= Sequence ID 686
Length=603

SEQ ID NO: 277

ALIGNMENTS

Identities = 603/603 (100%), Gaps = 0/603 (0%)

Query	1	GACCCCTTCCTTACACCTTATACAAAAAACTGAAACTGGACCCCTTCCTTACACCTTAT	60
Sbjct	1	GACCCCTTCCTTACACCTTATACAAAAAACTGAAACTGGACCCCTTCCTTACACCTTAT	60
Query	61	ACAAAAATTAACCTCAATTTTATTATGTTGTATTAAATTAAGTTGGGTTTAATTAAGATGG	120
Sbjct	61	ACAAAAATTAACCTCAATTTTATTATGTTGTATTAAATTAAGTTGGGTTTAATTAAGATGG	120
Query	121	ATTAAAGACTTAATTATAAGACCTAAAACCATAAAAACCCTAGAAGAAAACCTAGGCCAT	180
Sbjct	121	ATTAAAGACTTAATTATAAGACCTAAAACCATAAAAACCCTAGAAGAAAACCTAGGCCAT	180
Query	181	ACCATTTCAGGACACGGGTATGGGCAAAGACTTCATAACTAAAACACCAAAAGCAATGGCA	240
Sbjct	181	ACCATTTCAGGACACGGGTATGGGCAAAGACTTCATAACTAAAACACCAAAAGCAATGGCA	240
Query	241	ACGAAGTCCAAATAGACAAATTGGACCTGATTAAACTAAAGAGCTTCAGCACAGCAGAAG	300
Sbjct	241	ACGAAGTCCAAATAGACAAATTGGACCTGATTAAACTAAAGAGCTTCAGCACAGCAGAAG	300
Query	301	AGACTATCGTCAGAGTGAACAGGCAACCCACAGAATGGAAGAAAATTCTTGCAATCTATC	360
Sbjct	301	AGACTATCGTCAGAGTGAACAGGCAACCCACAGAATGGAAGAAAATTCTTGCAATCTATC	360
Query	361	CATCTGACAAGGGGCTAATATCCAAAATCTACAAAGAACTTAAACAAATTTACAAGGAAA	420
Sbjct	361	CATCTGACAAGGGGCTAATATCCAAAATCTACAAAGAACTTAAACAAATTTACAAGGAAA	420
Query	421	AACACAAACAACCCCATCAAAAAGTGGGCTAAGGATGTGAACAGACACTTCTCAAAAGAA	480
Sbjct	421	AACACAAACAACCCCATCAAAAAGTGGGCTAAGGATGTGAACAGACACTTCTCAAAAGAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AACATTTATGCAGCCAACAAACATGAAAAAAGTTCATCATCACTGCTCATTAGAGACAT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AACATTTATGCAGCCAACAAACATGAAAAAAGTTCATCATCACTGCTCATTAGAGACAT  540

Query  541  GCAAATCAAAACCACAATGAGATCCCATCCCACACCAGTTAGAATGGCAATCATTAAAAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GCAAATCAAAACCACAATGAGATCCCATCCCACACCAGTTAGAATGGCAATCATTAAAAA  600

Query  601  TGT   603
          |||
Sbjct   601  TGT   603
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

Sequence 687 matched with Sequence 278

Query= Sequence ID - 687 nt: 268
Length=268

SEQ ID NO: 278 nt: 268

ALIGNMENTS

Identities = 268/268 (100%), Gaps = 0/268 (0%)

Query	1	TTTATGTGTTTTTGCTTGGGGGGCGCTGGGCCTAGCCCAGAGTAGTGCTTGCTCCCCCTG	60
Sbjct	1	TTTATGTGTTTTTGCTTGGGGGGCGCTGGGCCTAGCCCAGAGTAGTGCTTGCTCCCCCTG	60
Query	61	CCTTGTCCCACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTGTCAATTTTGT	120
Sbjct	61	CCTTGTCCCACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTGTCAATTTTGT	120
Query	121	TGACATGCATTCTCCTTTTGTCACTTTGTTGGGGGGAGGGGATTAACCAAAGGCCACCC	180
Sbjct	121	TGACATGCATTCTCCTTTTGTCACTTTGTTGGGGGGAGGGGATTAACCAAAGGCCACCC	180
Query	181	TGACTTTGTTTTTGTGGACACACAATAAAAGCCCCGTTTATTTGTaaaaaaaaaaaaaaaa	240
Sbjct	181	TGACTTTGTTTTTGTGGACACACAATAAAAGCCCCGTTTATTTGTAAAAAAAAAAAAAAAA	240
Query	241	aaaaaaaaaaaaaaaaaaaaaaaaaaaaa	268
Sbjct	241	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	268

Sequence 688 matched with Sequence 279

Query= Sequence ID - 688 nt: 569
Length=569

SEQ ID NO: 279 nt: 569

ALIGNMENTS

Identities = 569/569 (100%), Gaps = 0/569 (0%)

Query	1	CTTTAGCCAGCCTGATCAGaaaaaaCAAAAGAAGAGGAAAGACGTAGATTACCAACATC	60
Sbjct	1	CTTTAGCCAGCCTGATCAGAAAAAACAAGAGGAAAGACGTAGATTACCAACATC	60
Query	61	AAGAATGTGAGTTATGATATCACTACAGACTCTCCAGGTATTTAAAGCATAATTAGAGAA	120
Sbjct	61	AAGAATGTGAGTTATGATATCACTACAGACTCTCCAGGTATTTAAAGCATAATTAGAGAA	120
Query	121	TGATATGAGCAGCTATATGCAAATAAGTTCAACATTGGACAAATGGACAAATTTCTTGAA	180
Sbjct	121	TGATATGAGCAGCTATATGCAAATAAGTTCAACATTGGACAAATGGACAAATTTCTTGAA	180
Query	181	AGATAAATTATGAAATTTTCATTCTGAAAGAACTACATGACCTTAATTGTCTTACATCTAT	240
Sbjct	181	AGATAAATTATGAAATTTTCATTCTGAAAGAACTACATGACCTTAATTGTCTTACATCTAT	240
Query	241	TAAATAAGTGGAATTGTAGTTTAGAACTTTCCACAAAGAAACTCTAGGCCAGATG	300
Sbjct	241	TAAATAAGTGGAATTGTAGTTTAGAACTTTCCACAAAGAAACTCTAGGCCAGATG	300
Query	301	GCATCAAAATAATATTCAGATGAATGAAATGGAGAAAGGATAGCCTTTTCAACAAATGGT	360
Sbjct	301	GCATCAAAATAATATTCAGATGAATGAAATGGAGAAAGGATAGCCTTTTCAACAAATGGT	360
Query	361	GGTGAACAATTGGATTTCCATATGCaaaaaaTAGAGATGGACGCAGAGGTGTGTGCTT	420
Sbjct	361	GGTGAACAATTGGATTTCCATATGCAAAAAAATAGAGATGGACGCAGAGGTGTGTGCTT	420
Query	421	AGGAGGCTGAGGTGAGAGGATTGTTTGAGGCCAGCCTGGGCAACATAGCAAGACCCCATT	480
Sbjct	421	AGGAGGCTGAGGTGAGAGGATTGTTTGAGGCCAGCCTGGGCAACATAGCAAGACCCCATT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TCAAAAACAAAATAAAGAACTTGTAGCCTTACCTTGTGCCATATTATGAAAATGTATCA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TCAAAAACAAAATAAAGAACTTGTAGCCTTACCTTGTGCCATATTATGAAAATGTATCA  540

Query  541  TAGGCTTAAATGTGAAACGTAAAACAAAA  569
          ||||||||||||||||||||
Sbjct   541  TAGGCTTAAATGTGAAACGTAAAACAAAA  569
```

Sequence 689 matched with Sequence 280

Query= Sequence ID 689
Length=492

SEQ ID NO: 280

ALIGNMENTS

Identities = 492/492 (100%), Gaps = 0/492 (0%)

Query	1	CGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGttttttt	60
Sbjct	1	CGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTT	60
Query	61	CTCTTTGAAAGATAGAGATTAATACAACACTTTAAAAAATATAGTCAATAGGTTACTAAG	120
Sbjct	61	CTCTTTGAAAGATAGAGATTAATACAACACTTTAAAAAATATAGTCAATAGGTTACTAAG	120
Query	121	ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT	180
Sbjct	121	ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT	180
Query	181	ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAAACATGACG	240
Sbjct	181	ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAAACATGACG	240
Query	241	GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAAATTGAGAGAA	300
Sbjct	241	GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAAATTGAGAGAA	300
Query	301	AGGACTACAGAGCCCCGAATTAATACTAATAGAGGGCAATGCTTTTAGATTAAAATGAA	360
Sbjct	301	AGGACTACAGAGCCCCGAATTAATACTAATAGAGGGCAATGCTTTTAGATTAAAATGAA	360
Query	361	GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAAATAATTTGAAG	420
Sbjct	361	GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAAATAATTTGAAG	420
Query	421	GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAGACCTTGAAATCCATGACGC	480
Sbjct	421	GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAGACCTTGAAATCCATGACGC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGGGAGAATTGC	492
Sbjct	481	AGGGAGAATTGC	492

Sequence 690 matched with Sequence 281

Query= Sequence ID 690
Length=355

SEQ ID NO: 281

ALIGNMENTS

Identities = 355/355 (100%), Gaps = 0/355 (0%)

Query	1	CGAAAAGCAAATATAACTTGCCACTAACCAAGATCACCTCTGCAAAAAGAAATGAAAACA	60
Sbjct	1	CGAAAAGCAAATATAACTTGCCACTAACCAAGATCACCTCTGCAAAAAGAAATGAAAACA	60
Query	61	ACTTTTGGCAGGATTCTGTTTCATCTGACAGAATTCAGAAGCAGGaaaaaaGCCTTTTA	120
Sbjct	61	ACTTTTGGCAGGATTCTGTTTCATCTGACAGAATTCAGAAGCAGGAAAAAAGCCTTTTA	120
Query	121	AAAATACCGAGAACATTAAAAATTCGCATTTGAAGAAATCAGCATTCTAACTGAAGTGA	180
Sbjct	121	AAAATACCGAGAACATTAAAAATTCGCATTTGAAGAAATCAGCATTCTAACTGAAGTGA	180
Query	181	GCCAAAAGGAAAATTATGCTGGGGCAAAGTTTAGTGATCCACCTTCTCCTAGTGTTCTTC	240
Sbjct	181	GCCAAAAGGAAAATTATGCTGGGGCAAAGTTTAGTGATCCACCTTCTCCTAGTGTTCTTC	240
Query	241	CAAAGCCTCCTAGTCACTGGATGGGAAGCACTGTTGAAAATTCCAACCAAAACAGGGAGC	300
Sbjct	241	CAAAGCCTCCTAGTCACTGGATGGGAAGCACTGTTGAAAATTCCAACCAAAACAGGGAGC	300
Query	301	TGATGGCAGTACACTTAAAAACGCTCCTCAAAGTTCAAACCTTAGATTTTCAGATTT	355
Sbjct	301	TGATGGCAGTACACTTAAAAACGCTCCTCAAAGTTCAAACCTTAGATTTTCAGATTT	355

Sequence 691 matched with Sequence 282

Query= Sequence ID 691
Length=619

SEQ ID NO: 282

ALIGNMENTS

Identities = 619/619 (100%), Gaps = 0/619 (0%)

Query	1	CCGGTCTCTACACAATATATAGAAATCTGGGCATGGTGGTGCCTGGCTGTAGTCTCAGCT	60
Sbjct	1	CCGGTCTCTACACAATATATAGAAATCTGGGCATGGTGGTGCCTGGCTGTAGTCTCAGCT	60
Query	61	ACCTAGTTGGGTGAGGTGGGAGAGTCGCTTGAGTCCTGGAGGTTGAGGCTGTAGTGAGCC	120
Sbjct	61	ACCTAGTTGGGTGAGGTGGGAGAGTCGCTTGAGTCCTGGAGGTTGAGGCTGTAGTGAGCC	120
Query	121	AGGGCTGCACCACTGCATTCCAGCCTGGGTAACAGAGTGAGACCCTGTCTCaaaaagaaa	180
Sbjct	121	AGGGCTGCACCACTGCATTCCAGCCTGGGTAACAGAGTGAGACCCTGTCTCAAAAAGAAA	180
Query	181	aaaaaaaaTTGCTAATTTTAAACAAATCACAAAACCTGACTCAGGCAAGTTGTCTGACTCAA	240
Sbjct	181	AAAAAAAAATTGCTAATTTTAAACAAATCACAAAACCTGACTCAGGCAAGTTGTCTGACTCAA	240
Query	241	AAGCCCTTGAAAAACCATCAAAGACAGTAGAATGTTAACTGGTCATTTACGTAAAATAGT	300
Sbjct	241	AAGCCCTTGAAAAACCATCAAAGACAGTAGAATGTTAACTGGTCATTTACGTAAAATAGT	300
Query	301	G TTCATTAAATTTTGGTTCATTTAGGATAATCATTTTAAATGAGACTGTATTTGAGACT	360
Sbjct	301	G TTCATTAAATTTTGGTTCATTTAGGATAATCATTTTAAATGAGACTGTATTTGAGACT	360
Query	361	GtatacacatacatatacatgttttacacacatatagtcacaatatatgtacatTCTATCT	420
Sbjct	361	GTATACACATACATATACATGTTTACACACATATACGTACAATATATGTACATTCTATCT	420
Query	421	AAAAGATCATACATGTGTGTACATATATGTTTTTAAAGTCAAACCTGACATATTAATGGA	480
Sbjct	421	AAAAGATCATACATGTGTGTACATATATGTTTTTAAAGTCAAACCTGACATATTAATGGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AACAGTGCTTACATCTCTGGTAGTGATTTTCTATTAGCAGCAGCCCTACATATGCTGCGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AACAGTGCTTACATCTCTGGTAGTGATTTTCTATTAGCAGCAGCCCTACATATGCTGCGT  540

Query  541  CTCTGAACAGCATGTCAGTGCCATGACTGTCTAAACATGCAAATATGACTGACAGACTCT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CTCTGAACAGCATGTCAGTGCCATGACTGTCTAAACATGCAAATATGACTGACAGACTCT  600

Query  601  TGAGACAGCTTTCACCTTG  619
          ||||||||||||||||
Sbjct   601  TGAGACAGCTTTCACCTTG  619
```

Sequence 692 matched with Sequence 283

Query= Sequence ID 692
Length=328

SEQ ID NO: 283

ALIGNMENTS

Identities = 328/328 (100%), Gaps = 0/328 (0%)

Query	1	AATTCGNGGCCGCGTCNNCCTANGAGGCACCAGGAAATCCCGCGGGGTGGCCCATGCAGA	60
Sbjct	1	AATTCGNGGCCGCGTCNNCCTANGAGGCACCAGGAAATCCCGCGGGGTGGCCCATGCAGA	60
Query	61	CCAGGCGCACGTGGCTCATGGGGCANAATTGCCAAGGACAGCTCACGACAGTGCCACCTT	120
Sbjct	61	CCAGGCGCACGTGGCTCATGGGGCANAATTGCCAAGGACAGCTCACGACAGTGCCACCTT	120
Query	121	CTCACCATTCCAGCCAAGGAGAGATGTGACGTTGGAAGTCTCTGGCACTTCTGTCAAGC	180
Sbjct	121	CTCACCATTCCAGCCAAGGAGAGATGTGACGTTGGAAGTCTCTGGCACTTCTGTCAAGC	180
Query	181	CTCCCCGCCCCAATTGCCTTGAGATCTCTGCTCTTTGTCAGAGATTGCAAAGACTCAC	240
Sbjct	181	CTCCCCGCCCCAATTGCCTTGAGATCTCTGCTCTTTGTCAGAGATTGCAAAGACTCAC	240
Query	241	GTTTTTGTTGTTTTCTCATCATTCCATTGTGATACTAAGAACTAAGAAGCTTAATGAAA	300
Sbjct	241	GTTTTTGTTGTTTTCTCATCATTCCATTGTGATACTAAGAACTAAGAAGCTTAATGAAA	300
Query	301	AGAAATAAAATGCCTATGTTGTTGTTCT	328
Sbjct	301	AGAAATAAAATGCCTATGTTGTTGTTCT	328

Sequence 693 matched with Sequence 284

Query= Sequence ID 693
Length=563

SEQ ID NO: 284

ALIGNMENTS

Identities = 563/563 (100%), Gaps = 0/563 (0%)

Query	1	CTAGAACCCATGACTCCTAGGTCTTATACTGCAACCACAGTATCAGCAAATAATCTTTCA	60
Sbjct	1	CTAGAACCCATGACTCCTAGGTCTTATACTGCAACCACAGTATCAGCAAATAATCTTTCA	60
Query	61	TAAGGGGATTATTCTCTGATTAACAGGAAATACAGGAATTTAATTTGTGAACACGCTAGG	120
Sbjct	61	TAAGGGGATTATTCTCTGATTAACAGGAAATACAGGAATTTAATTTGTGAACACGCTAGG	120
Query	121	TAGAAGCAGAAACCCAAATCCAAATCCAAATTTAAACATTTAAAATTCATTCTATAACTA	180
Sbjct	121	TAGAAGCAGAAACCCAAATCCAAATCCAAATTTAAACATTTAAAATTCATTCTATAACTA	180
Query	181	AGATCTAACAGTCATTTTCTTCCCAGTAAGAAATAACCAAAGCATGCTAAAAATCACTGG	240
Sbjct	181	AGATCTAACAGTCATTTTCTTCCCAGTAAGAAATAACCAAAGCATGCTAAAAATCACTGG	240
Query	241	ACTAAATTGGTGTCAAAACTGCCACATTGCCAGGCATgggggggTCATACTTGTAATCCC	300
Sbjct	241	ACTAAATTGGTGTCAAAACTGCCACATTGCCAGGCATGGGGGGGTCATACTTGTAATCCC	300
Query	301	AGCACTTTGGGAGGCCGAGGTGGGAAAATTGCTTGAGGCCAGGAGTTCGAAACCAGCCTG	360
Sbjct	301	AGCACTTTGGGAGGCCGAGGTGGGAAAATTGCTTGAGGCCAGGAGTTCGAAACCAGCCTG	360
Query	361	GGCAACACAGTGAGACCCCATCTCCACaaaaaaaaaattaaaaaacaaaacaaaCAT	420
Sbjct	361	GGCAACACAGTGAGACCCCATCTCCACAAAAAAAAAAAAATTAAAAACAAAACAAACAT	420
Query	421	TAGCTGGGCATGGTGGTACACGCCTGTAGTCCCAGCTACTCAGGAGCCTGAAGTGAGAGG	480
Sbjct	421	TAGCTGGGCATGGTGGTACACGCCTGTAGTCCCAGCTACTCAGGAGCCTGAAGTGAGAGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATCACTGAAGCCCAGGAGGTAGAGCTATGACTGTAGTGAGCTATGACTGTGCCACTACAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATCACTGAAGCCCAGGAGGTAGAGCTATGACTGTAGTGAGCTATGACTGTGCCACTACAC  540

Query  541  TCCACCTGGGTGACAGGGGACTC  563
          ||||||||||||||||
Sbjct   541  TCCACCTGGGTGACAGGGGACTC  563
```

Sequence 694 matched with Sequence 285

Query= Sequence ID 694
Length=257

SEQ ID NO: 285

ALIGNMENTS

Identities = 257/257 (100%), Gaps = 0/257 (0%)

Query	1	CGACTTCCATTTGTATTAATGGAATACTAAGTCCCTCTGTGATTTCTGAACCAAGCTATT	60
Sbjct	1	CGACTTCCATTTGTATTAATGGAATACTAAGTCCCTCTGTGATTTCTGAACCAAGCTATT	60
Query	61	CCTAGGCCTGAGTTTTATTTGTTGACACAGAAATAAATTANAAGGCCAAGCGTGGTGGC	120
Sbjct	61	CCTAGGCCTGAGTTTTATTTGTTGACACAGAAATAAATTANAAGGCCAAGCGTGGTGGC	120
Query	121	ATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAGGAGTTCAAGGC	180
Sbjct	121	ATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAGGAGTTCAAGGC	180
Query	181	TGCAGCAAGCTTTGATTGCGCCACTGCACTCCAGCCTTGGCGACAGACTAAGACGCTGTC	240
Sbjct	181	TGCAGCAAGCTTTGATTGCGCCACTGCACTCCAGCCTTGGCGACAGACTAAGACGCTGTC	240
Query	241	TCaaaaaaaaacaaaaa	257
Sbjct	241	TCAAAAAAAAAACAAAAA	257

Sequence 696 matched with Sequence 286

Query= Sequence ID 696
Length=602

SEQ ID NO: 286

ALIGNMENTS

Identities = 602/602 (100%), Gaps = 0/602 (0%)

Query	1	GGTTATCAATGAGATTAAGAGACAACTAGAGTaaaaacaaaagaaaagaaaangaa	60
Sbjct	1	GGTTATCAATGAGATTAAGAGACAACTAGAGTAAAAACAAAAGAAAAGAAAANGAA	60
Query	61	aaCAACAGAAGCTCTATTAAGTACCTCTAACCAATACAACAGGTAACTGATGTTCTCC	120
Sbjct	61	AACAACAGAAGCTCTATTAAGTACCTCTAACCAATACAACAGGTAACTGATGTTCTCC	120
Query	121	ATTCTGTATATAAAAAATCCAGTGGACACCCACAACACAGGCTTCAGGCTTGTAGGACAC	180
Sbjct	121	ATTCTGTATATAAAAAATCCAGTGGACACCCACAACACAGGCTTCAGGCTTGTAGGACAC	180
Query	181	TTTCTAGTTCATCTGAGCACTTTTGTCTCAGCAGTTGAGCTGTATACTTAGCAACATTT	240
Sbjct	181	TTTCTAGTTCATCTGAGCACTTTTGTCTCAGCAGTTGAGCTGTATACTTAGCAACATTT	240
Query	241	GGTGCTTCCAAACCCATTTGTGCCTGTAGCACTTACTATTGAAATACATAATTTAATTAA	300
Sbjct	241	GGTGCTTCCAAACCCATTTGTGCCTGTAGCACTTACTATTGAAATACATAATTTAATTAA	300
Query	301	ATATTATATAAAGGAATGGAATACGAGTTGGACAAGAAAAAGAGTTAAATCTGAAGGTTA	360
Sbjct	301	ATATTATATAAAGGAATGGAATACGAGTTGGACAAGAAAAAGAGTTAAATCTGAAGGTTA	360
Query	361	GGTAAAAAGAGCAACTTCTTTTCTCTGTTTTGCAGGTTGGCAAAATCATTTAAAAACAAT	420
Sbjct	361	GGTAAAAAGAGCAACTTCTTTTCTCTGTTTTGCAGGTTGGCAAAATCATTTAAAAACAAT	420
Query	421	TGGAAGTATTATATGTTCTGCATTAAGTTGTCATTTTACTTAAAACTAGGCATCAAAGA	480
Sbjct	421	TGGAAGTATTATATGTTCTGCATTAAGTTGTCATTTTACTTAAAACTAGGCATCAAAGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TGATGCATAATAAATTTAGTGTATGCAAGAATGACTGCTTGGGACCTCAATATATGAATT  540
          |||
Sbjct   481  TGATGCATAATAAATTTAGTGTATGCAAGAATGACTGCTTGGGACCTCAATATATGAATT  540

Query  541  CTTAATCCAAGGAAAGTCCTTGGCCTTACATTTAAAAGTCGGCAAATAAGTGTACGTTCA  600
          |||
Sbjct   541  CTTAATCCAAGGAAAGTCCTTGGCCTTACATTTAAAAGTCGGCAAATAAGTGTACGTTCA  600

Query  601  TT   602
          ||
Sbjct   601  TT   602
```

Sequence 697 matched with Sequence 287

Query= Sequence ID 697
Length=306

SEQ ID NO: 287

ALIGNMENTS

Identities = 306/306 (100%), Gaps = 0/306 (0%)

```
Query 1   GAACATTTAAAAATAATGCAAATAAGGCTGGGCGTGGGGGCTCACACCTGTAATCCCAGC  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   GAACATTTAAAAATAATGCAAATAAGGCTGGGCGTGGGGGCTCACACCTGTAATCCCAGC  60

Query 61  ACTTTGGGAGGCCGAGGCAGGCAGATCACGAGGTCAGGAGATTGAGACCATCCTGGCTAA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  ACTTTGGGAGGCCGAGGCAGGCAGATCACGAGGTCAGGAGATTGAGACCATCCTGGCTAA  120

Query 121 CACAGTGAAACCCTGTCTCTACTTaaaaataaaaaaaTTAGCCAGGCGTGGTGGTGGGC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 CACAGTGAAACCCTGTCTCTACTTAAAAAATAAAAAAATTAGCCAGGCGTGGTGGTGGGC  180

Query 181 GCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 GCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCG  240

Query 241 GAGCTTGCANTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGAGCGACAGAGCGAGACT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 GAGCTTGCANTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGAGCGACAGAGCGAGACT  300

Query 301 CTGTCT  306
          |||||
Sbjct 301 CTGTCT  306
```


Sequence 698 matched with Sequence 288

Query= Sequence ID 698
Length=419

SEQ ID NO: 288

ALIGNMENTS

Identities = 419/419 (100%), Gaps = 0/419 (0%)

Query	1	TCATTAGAATCCAAGCTTTGAAAATTTCTGATTAATGCTCATGTATTCTTTATCTTTGT	60
Sbjct	1	TCATTAGAATCCAAGCTTTGAAAATTTCTGATTAATGCTCATGTATTCTTTATCTTTGT	60
Query	61	TTTTCCTTGTGAAGAAAGACTTTCACCACTGTCTGAGTGATGATGCTGTTGATAAGGATG	120
Sbjct	61	TTTTCCTTGTGAAGAAAGACTTTCACCACTGTCTGAGTGATGATGCTGTTGATAAGGATG	120
Query	121	ATGTCGATGACTACTATATTGCATCTCTCAGGAACAGCTGATGGGAAGGGAGGGGCTGCT	180
Sbjct	121	ATGTCGATGACTACTATATTGCATCTCTCAGGAACAGCTGATGGGAAGGGAGGGGCTGCT	180
Query	181	GAGTTCCTTGTTCCTAGCTAGCAGCACGCTCCTCANAGAGGGGGCCGAGTTACAGACAGC	240
Sbjct	181	GAGTTCCTTGTTCCTAGCTAGCAGCACGCTCCTCANAGAGGGGGCCGAGTTACAGACAGC	240
Query	241	AGCCGCATTCTCATGCAAAATTAGTTTTAAACTGCTAGTGTGGGCATCGGTACCTTTTGC	300
Sbjct	241	AGCCGCATTCTCATGCAAAATTAGTTTTAAACTGCTAGTGTGGGCATCGGTACCTTTTGC	300
Query	301	CTGGGTGATACCGAAGAATTGTTGAGGATTTAGTATGCTCCGTAGAGACAGTTCAGCCAG	360
Sbjct	301	CTGGGTGATACCGAAGAATTGTTGAGGATTTAGTATGCTCCGTAGAGACAGTTCAGCCAG	360
Query	361	TCATTTCTGCATTGGAGAGACTTCTCATACTTTCTTTGAAGACTCATAGAAAGCTGGAT	419
Sbjct	361	TCATTTCTGCATTGGAGAGACTTCTCATACTTTCTTTGAAGACTCATAGAAAGCTGGAT	419

Sequence 699 matched with Sequence 289

Query= Sequence ID 699
Length=626

SEQ ID NO: 289

ALIGNMENTS

Identities = 626/626 (100%), Gaps = 0/626 (0%)

Query	1	ATTAAGGTTTGTNCCCAACAAGAATAGATGTAATTAGaaaaanTGNCCTCCTTACCTAT	60
Sbjct	1	ATTAAGGTTTGTNCCCAACAAGAATAGATGTAATTAGAAAAANTGNCTTCCTTACCTAT	60
Query	61	TGCCTCTGATNTTTACTTGCTTAAAttttttttATTGNAAATCCAGAAAAAGNGGATTTA	120
Sbjct	61	TGCCTCTGATNTTTACTTGCTTAAATTTTTTTTATTGNAAATCCAGAAAAAGNGGATTTA	120
Query	121	GAGAACAACACTAACTCCCACCTAATCTATGACAganatgtacaananagtacctgtgaa	180
Sbjct	121	GAGAACAACACTAACTCCCACCTAATCTATGACAGANATGTACAANANACTACCTGTGAA	180
Query	181	aaatgtgaaagnatntgaaaaatgtAACCTTTGGCAGCCTGAGCATAGTCAACCAGAAAA	240
Sbjct	181	AAATGTGAAAGNATNTGAAAAATGTAACCTTTGGCAGCCTGAGCATAGTCAACCAGAAAA	240
Query	241	ACTATCTGAATTAAAATAATTGGTCCATAGGTACTATTTTATTTGGTCCATAAGGATTAt	300
Sbjct	241	ACTATCTGAATTAAAATAATTGGTCCATAGGTACTATTTTATTTGGTCCATAAGGATTAT	300
Query	301	tttttcaacttttttttCAAGTGATTATTATGTCATTTCACGTAGGTTACTGATACC	360
Sbjct	301	TTTTTCAACTTTTTTTTCAAGTGATTATTATGTCATTTCACGTAGGTTACTGATACC	360
Query	361	TGAAGACTTTTTNCACCTTTAACCTTNCTCGTTGAGGAGCTTTGTANTCTAATAAAAGAG	420
Sbjct	361	TGAAGACTTTTTNCACCTTTAACCTTNCTCGTTGAGGAGCTTTGTANTCTAATAAAAGAG	420
Query	421	AAATATAAGTAAATGTTAGATATATGGGNGGATAATGGTAACTATGTGCTTAAAGAGGTA	480
Sbjct	421	AAATATAAGTAAATGTTAGATATATGGGNGGATAATGGTAACTATGTGCTTAAAGAGGTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAAAAGAAGGGTAGGGAGCAGATAAGACAAAGGAAGGGCTATATTATAANGAAGAATATT	540
Sbjct	481	TAAAAGAAGGGTAGGGAGCAGATAAGACAAAGGAAGGGCTATATTATAANGAAGAATATT	540
Query	541	CCAAGTAGGGAAGAGAAAAAGATATGTTATCCATATAATATTTTATGTGCAGTAGAGAAC	600
Sbjct	541	CCAAGTAGGGAAGAGAAAAAGATATGTTATCCATATAATATTTTATGTGCAGTAGAGAAC	600
Query	601	ATGTTCTATAGAANAGACAGAAGATG	626
Sbjct	601	ATGTTCTATAGAANAGACAGAAGATG	626

Sequence 700 matched with Sequence 290

Query= Sequence ID 700
Length=623

SEQ ID NO: 290

ALIGNMENTS

Identities = 623/623 (100%), Gaps = 0/623 (0%)

Query	1	CTTGAGCCCAGGAATTCCAGCCTGGGCAATATAGTAAGACTCCGTCTCTACAAAAGATAC	60
Sbjct	1	CTTGAGCCCAGGAATTCCAGCCTGGGCAATATAGTAAGACTCCGTCTCTACAAAAGATAC	60
Query	61	AAAAATTAGCCAGATGTGGTGGTGCCTGTAGTTCCAGATACTGGAAAGACTGAGGC	120
Sbjct	61	AAAAATTAGCCAGATGTGGTGGTGCCTGTAGTTCCAGATACTGGAAAGACTGAGGC	120
Query	121	AGGAGGATTGCTTGAGCATGGGAAGTTGAGGCTGCAATGAGCTGTGATTACGCCACTACA	180
Sbjct	121	AGGAGGATTGCTTGAGCATGGGAAGTTGAGGCTGCAATGAGCTGTGATTACGCCACTACA	180
Query	181	CTCCAGCCTGGGCAACAGAGTAAGATCTTGTCTCaaaaaaaaattgaattcagctaaaa	240
Sbjct	181	CTCCAGCCTGGGCAACAGAGTAAGATCTTGTCTCAAAAAAAAAAATTGAATTCAGCTAAAA	240
Query	241	ataataaaatttttaaaataatttttaaaaaGCCCTCAACAGCTTTGTTTTTCTCTCCTTGC	300
Sbjct	241	ATAATAAAATTTTAAATAATTTTAAAAAGCCCTCAACAGCTTTGTTTTTCTCTCCTTGC	300
Query	301	CAGCTTCTCTGCAGCCTATAGCCTGCAGGCTGGCTGCTGCGAGCCAGGACAAGCGGTGGG	360
Sbjct	301	CAGCTTCTCTGCAGCCTATAGCCTGCAGGCTGGCTGCTGCGAGCCAGGACAAGCGGTGGG	360
Query	361	AAATGCAATCACAGCGTGAAATCTCTGTGTTTCAGAGACACGCAGGAAGCAGGTGAACCAT	420
Sbjct	361	AAATGCAATCACAGCGTGAAATCTCTGTGTTTCAGAGACACGCAGGAAGCAGGTGAACCAT	420
Query	421	GAAGGGCCAACACATGCCCCAGTTAGCAGGGTGTAGAGACCGGGGCAGGGCTTTCTTCT	480
Sbjct	421	GAAGGGCCAACACATGCCCCAGTTAGCAGGGTGTAGAGACCGGGGCAGGGCTTTCTTCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCCTTCTGGGTTATAAAATATCCATGTCCTGCCATTTGAAGCTGCAAGTGGCACACATGGA	540
Sbjct	481	TCCTTCTGGGTTATAAAATATCCATGTCCTGCCATTTGAAGCTGCAAGTGGCACACATGGA	540
Query	541	TGCTGGACAGGCGCTCGCACTTTCTGGGCAGGGCANGGGGCTCAAAGGCAGGACAGCTGG	600
Sbjct	541	TGCTGGACAGGCGCTCGCACTTTCTGGGCAGGGCANGGGGCTCAAAGGCAGGACAGCTGG	600
Query	601	GCAAAAGCACCTTGCGTGGGCCC	623
Sbjct	601	GCAAAAGCACCTTGCGTGGGCCC	623

Sequence 701 matched with Sequence 291

Query= Sequence ID - 701 nt: 579
Length=579

SEQ ID NO: 291 nt: 579

ALIGNMENTS

Identities = 579/579 (100%), Gaps = 0/579 (0%)

Query	1	CTTTGGAGCTTCTGTCTGTGCTGTGGACCTCAATGCAGATGGCTTCTCAGATCTGCTCGT	60
Sbjct	1	CTTTGGAGCTTCTGTCTGTGCTGTGGACCTCAATGCAGATGGCTTCTCAGATCTGCTCGT	60
Query	61	GGGAGCACCCATGCAGAGCACCATCAGAGAGGAAGGAAGAGTGTTTGTGTACATCAACTC	120
Sbjct	61	GGGAGCACCCATGCAGAGCACCATCAGAGAGGAAGGAAGAGTGTTTGTGTACATCAACTC	120
Query	121	TGGCTCGGGAGCAGTAATGAATGCAATGGAAACAAACCTCGTTGGAAGTGACAAATATGC	180
Sbjct	121	TGGCTCGGGAGCAGTAATGAATGCAATGGAAACAAACCTCGTTGGAAGTGACAAATATGC	180
Query	181	TGCAAGATTTGGGGAATCTATAGTTAATCTTGGCGACATTGACAATGATGGCTTTGAAGG	240
Sbjct	181	TGCAAGATTTGGGGAATCTATAGTTAATCTTGGCGACATTGACAATGATGGCTTTGAAGG	240
Query	241	TAATTTAAATTATCAAATTGGTGCTTGATTTCTGCTTTTAAATGGTTTATGGAAGAAAA	300
Sbjct	241	TAATTTAAATTATCAAATTGGTGCTTGATTTCTGCTTTTAAATGGTTTATGGAAGAAAA	300
Query	301	TATGATTAAAGTTTTGTATTGTTTTCTTCCTTCTATAGAAGATGGAGCCAGAATGGCATGCT	360
Sbjct	301	TATGATTAAAGTTTTGTATTGTTTTCTTCCTTCTATAGAAGATGGAGCCAGAATGGCATGCT	360
Query	361	AAGTTTTTTCTTTTCTTTAGTGTTATATATGACTTCTCCTCAATTGTCACCCATTGATCT	420
Sbjct	361	AAGTTTTTTCTTTTCTTTAGTGTTATATATGACTTCTCCTCAATTGTCACCCATTGATCT	420
Query	421	TTACCACTGTTAATAATGGATGATATTCAAATACCTTATTTCAAGTATTCTAAGGCACC	480
Sbjct	421	TTACCACTGTTAATAATGGATGATATTCAAATACCTTATTTCAAGTATTCTAAGGCACC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATTGATTAGAACTGCATTATTATTTATGTGTCCCTAAAAGCTACCTATTAAGCTGTTAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATTGATTAGAACTGCATTATTATTTATGTGTCCCTAAAAGCTACCTATTAAGCTGTTAC  540

Query  541  ACCCACCATTTTCTGTTAAGAAAATCCTGATTTTCAGAA  579
          ||||||||||||||||||||||||||||
Sbjct   541  ACCCACCATTTTCTGTTAAGAAAATCCTGATTTTCAGAA  579
```

Sequence 702 matched with Sequence 292

Query= Sequence ID 702
Length=709

SEQ ID NO: 292

ALIGNMENTS

Identities = 709/709 (100%), Gaps = 0/709 (0%)

Query	1	GTNNTCCTCTCGGAACGCGCCTTNTGTAGCCAGGTGCTACCAGACCNAATACACGGTTGTTCCA	64
Sbjct	1	GTNNTCCTCTCGGAACGCGCCTTNTGTAGCCAGGTGCTACCAGACCNAATACACGGTTGTTCCA	64
Query	65	GCTTGCGCATTACCGATGGCGTAGATATCCGGATCGGAAGTCTGGCAGGAATCATTAAAT	124
Sbjct	65	GCTTGCGCATTACCGATGGCGTAGATATCCGGATCGGAAGTCTGGCAGGAATCATTAAAT	124
Query	125	GACAATACCCCCACGCGGAGCAACGTCCAGACCACACTGGGTTGCCAGCTTATCGCGCGG	184
Sbjct	125	GACAATACCCCCACGCGGAGCAACGTCCAGACCACACTGGGTTGCCAGCTTATCGCGCGG	184
Query	185	ACGGATACCGGTAGAGAAGACGATAAAGTCGACTTCCAGTTCGCTGCCGTCGGCAAAACG	244
Sbjct	185	ACGGATACCGGTAGAGAAGACGATAAAGTCGACTTCCAGTTCGCTGCCGTCGGCAAAACG	244
Query	245	CATGGTTTTACGCGCTTCAACACCTTCCTGCACAATCTCAAGGGTGTTTTTGCTGGTGTG	304
Sbjct	245	CATGGTTTTACGCGCTTCAACACCTTCCTGCACAATCTCAAGGGTGTTTTTGCTGGTGTG	304
Query	305	AACGCGCACGCCCATACTTTTCGATTTTGCGACGCAGCTGCTCGCCGCCCATCTGATCAAG	364
Sbjct	305	AACGCGCACGCCCATACTTTTCGATTTTGCGACGCAGCTGCTCGCCGCCCATCTGATCAAG	364
Query	365	CTGTTCTGCCATCAGCATAGGGGCAAATTCGATAACGTGGGTTTCAATACCTAAGTTTTT	424
Sbjct	365	CTGTTCTGCCATCAGCATAGGGGCAAATTCGATAACGTGGGTTTCAATACCTAAGTTTTT	424
Query	425	CAGCGCGCCTGCGGCTTCCAGACCTAACAGGCCGCAATTCGAGCTCGGCCGACTTGGCCA	484
Sbjct	425	CAGCGCGCCTGCGGCTTCCAGACCTAACAGGCCGCAATTCGAGCTCGGCCGACTTGGCCA	484

PATENT SEQUENCE ALIGNMENT

```
Query  485  ATTCGCCCTATAGTGAGTCGTATTACAATTCAGTGGCCGTCGTTTTACAACGTCGTGACT  544
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   485  ATTCGCCCTATAGTGAGTCGTATTACAATTCAGTGGCCGTCGTTTTACAACGTCGTGACT  544

Query  545  GGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTCGCCAGCT  604
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   545  GGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTCGCCAGCT  604

Query  605  GCGTAATAGCGAAAGAGGCCCGCACCCGATCGCCCTTTCCAACAGTTGCGCACCTGAAT  664
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   605  GCGTAATAGCGAAAGAGGCCCGCACCCGATCGCCCTTTCCAACAGTTGCGCACCTGAAT  664

Query  665  GCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGT  709
          ||||||||||||||||||||||||||||||||||||||||
Sbjct   665  GCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGT  709
```

Blast comparison trimmed “GTNN” from the 5’ end of both sequences and reported 705 identities. The report has been manually corrected for this. “GTNN” has been prepended to both sequences and identity count has been increased to 709.

Sequence 703 matched with Sequence 293

Query= Sequence ID 703
Length=471

SEQ ID NO: 293

ALIGNMENTS

Identities = 471/471 (100%), Gaps = 0/471 (0%)

Query	1	CTGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCA	60
Sbjct	1	CTGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCA	60
Query	61	TGTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGA	120
Sbjct	61	TGTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGA	120
Query	121	CAGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAG	180
Sbjct	121	CAGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAG	180
Query	181	CAGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGC	240
Sbjct	181	CAGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGC	240
Query	241	CTTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAG	300
Sbjct	241	CTTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAG	300
Query	301	TTTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCT	360
Sbjct	301	TTTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCT	360
Query	361	GCCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTG	420
Sbjct	361	GCCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTG	420
Query	421	AAGGAAGAAGTGGGGTGGAAGAAGTGGGGGTGGGACGACAGTGAAATCTAA	471
Sbjct	421	AAGGAAGAAGTGGGGTGGAAGAAGTGGGGGTGGGACGACAGTGAAATCTAA	471

Sequence 704 matched with Sequence 294

Query= Sequence ID 704
Length=495

SEQ ID NO: 294

ALIGNMENTS

Identities = 495/495 (100%), Gaps = 0/495 (0%)

Query	1	CTTGTATTCAAGAACTACTGTAATGCATTAGTGGTCTGGCTTCATTTGTATGATGCCAG	60
Sbjct	1	CTTGTATTCAAGAACTACTGTAATGCATTAGTGGTCTGGCTTCATTTGTATGATGCCAG	60
Query	61	ATCCTTAATTTACCCAGCACAAATCATTTTCAGTAGTTTCCTATGGCTCCTGCAAAAATGCA	120
Sbjct	61	ATCCTTAATTTACCCAGCACAAATCATTTTCAGTAGTTTCCTATGGCTCCTGCAAAAATGCA	120
Query	121	AACAGAAACCACCACAGGAACAGCCCCTTGCTGCCTCCTGTTGCTGAGGTAGTAGTCGCT	180
Sbjct	121	AACAGAAACCACCACAGGAACAGCCCCTTGCTGCCTCCTGTTGCTGAGGTAGTAGTCGCT	180
Query	181	AAAGAAAATTGAAGGCTCCTTACAATCTATATTTGAAAAGTAGAACTTCTGTAGAAACAC	240
Sbjct	181	AAAGAAAATTGAAGGCTCCTTACAATCTATATTTGAAAAGTAGAACTTCTGTAGAAACAC	240
Query	241	ACAGATCCCGATCTTAGAAGTTGTACAGGACAATCTGGTAAAGTACATAATTGTGATT	300
Sbjct	241	ACAGATCCCGATCTTAGAAGTTGTACAGGACAATCTGGTAAAGTACATAATTGTGATT	300
Query	301	TATTAACATGAATTAAAAATGCCCAACCAGTGCTTCAGTGTGACAGTATATTTAAATATAA	360
Sbjct	301	TATTAACATGAATTAAAAATGCCCAACCAGTGCTTCAGTGTGACAGTATATTTAAATATAA	360
Query	361	AAAGAAATTAAAGGTCATATACTGTACTACTTTCACAAAGATCCACAGTTTGCAAAAGA	420
Sbjct	361	AAAGAAATTAAAGGTCATATACTGTACTACTTTCACAAAGATCCACAGTTTGCAAAAGA	420
Query	421	CTTGTCATATGTACAATGCTATATATCAAATGAGAAAAGCTGTAAGCAATTATATACGCA	480
Sbjct	421	CTTGTCATATGTACAATGCTATATATCAAATGAGAAAAGCTGTAAGCAATTATATACGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AAAGAAATGGCAGTA	495
Sbjct	481	AAAGAAATGGCAGTA	495

Sequence 705 matched with Sequence 295

Query= Sequence ID 705
Length=531

SEQ ID NO: 295

ALIGNMENTS

Identities = 531/531 (100%), Gaps = 0/531 (0%)

Query	1	TTCCAGTCCTTTCATTTAGTATAAAAGAAATACTGAACAAGCCAGTGGGATGGAATTGAA	60
Sbjct	1	TTCCAGTCCTTTCATTTAGTATAAAAGAAATACTGAACAAGCCAGTGGGATGGAATTGAA	60
Query	61	AGAACTAATCATGAGGACTCTGTCCTGACACAGGTCCTCAAAGCTAGCAGAGATACGCAG	120
Sbjct	61	AGAACTAATCATGAGGACTCTGTCCTGACACAGGTCCTCAAAGCTAGCAGAGATACGCAG	120
Query	121	ACATTGTGGCATCTGGGTAGAAGAATACTGTATtgtgtgtgcagtgcacagtgtgtggtg	180
Sbjct	121	ACATTGTGGCATCTGGGTAGAAGAATACTGTATTGTGTGTGCAGTGCACAGTGTGTGGTG	180
Query	181	tgtgCACACTCATTCTTCTGCTCTTGGGCACAGGCAGTGGGTGTAGAGGTAACCAGTAG	240
Sbjct	181	TGTGCACACTCATTCTTCTGCTCTTGGGCACAGGCAGTGGGTGTAGAGGTAACCAGTAG	240
Query	241	CTTTGAGAAGCTACATGTAGCTCACCAGTGGTTTTCTCTAAGGAATCACAAAGGTAAACT	300
Sbjct	241	CTTTGAGAAGCTACATGTAGCTCACCAGTGGTTTTCTCTAAGGAATCACAAAGGTAAACT	300
Query	301	ACCCAACCACATGCCACGTAATATTTTCAGCCATTTCAGAGGAACTGTTTTCTCTTTATTT	360
Sbjct	301	ACCCAACCACATGCCACGTAATATTTTCAGCCATTTCAGAGGAACTGTTTTCTCTTTATTT	360
Query	361	GCTTATATGTTAATATGGTTTTTAAATTGGTAACTTTTATATAGTATGGTAACAGTATGT	420
Sbjct	361	GCTTATATGTTAATATGGTTTTTAAATTGGTAACTTTTATATAGTATGGTAACAGTATGT	420
Query	421	TAATACACACATACATATGCACACATGCTTTGGGTCCTTCCATAATACTTTTATATTTGT	480
Sbjct	421	TAATACACACATACATATGCACACATGCTTTGGGTCCTTCCATAATACTTTTATATTTGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	AAATCAATGTTTTGGAGCAATCCCAAGTTTAAGGGAAATATTTTGTAAA	531
Sbjct	481	AAATCAATGTTTTGGAGCAATCCCAAGTTTAAGGGAAATATTTTGTAAA	531

Sequence 706 matched with Sequence 296

Query= Sequence ID - 706 nt: 496
Length=496

SEQ ID NO: 296 nt: 496

ALIGNMENTS

Identities = 496/496 (100%), Gaps = 0/496 (0%)

Query	1	CAACCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTCATGGCGT	60
Sbjct	1	CAACCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTCATGGCGT	60
Query	61	GCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAG	120
Sbjct	61	GCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAG	120
Query	121	AGGGTGACAAGTTCAAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGC	180
Sbjct	121	AGGGTGACAAGTTCAAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGC	180
Query	181	CCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCAGAAGCTGATGAGCAACTTGG	240
Sbjct	181	CCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCAGAAGCTGATGAGCAACTTGG	240
Query	241	ACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCTGTCCTGCATCG	300
Sbjct	241	ACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCTGTCCTGCATCG	300
Query	301	CCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAATGAA	360
Sbjct	301	CCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAATGAA	360
Query	361	AACTCCTCTGATGTGGTTGGGGGTCTGCCAGCTGGGGCCCTCCCTGTCGCCAGTGGGCA	420
Sbjct	361	AACTCCTCTGATGTGGTTGGGGGTCTGCCAGCTGGGGCCCTCCCTGTCGCCAGTGGGCA	420
Query	421	CtttttttttttCCACCCTGGCTCCTTCAACACGTGCTTGATGCTGAGCAAAGTTCAATAA	480
Sbjct	421	CTTTTTTTTTTCCACCCTGGCTCCTTCAACACGTGCTTGATGCTGAGCAAAGTTCAATAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	AGATTTTGGGAAGTTT	496
Sbjct	481	AGATTTTGGGAAGTTT	496

Sequence 707 matched with Sequence 297

Query= Sequence ID - 707 nt: 397
Length=397

SEQ ID NO: 297 nt: 397

ALIGNMENTS

Identities = 397/397 (100%), Gaps = 0/397 (0%)

Query	1	CGGATGTGGTGGCAGGCGCTCTAGTCCCAGCTACTCGGCAGGCTGAGGTAGGAGAATGG	60
Sbjct	1	CGGATGTGGTGGCAGGCGCTCTAGTCCCAGCTACTCGGCAGGCTGAGGTAGGAGAATGG	60
Query	61	CTTGAACCCAGGAGGTGGAGCTGACAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTG	120
Sbjct	61	CTTGAACCCAGGAGGTGGAGCTGACAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTG	120
Query	121	GGCGGCAGAGCGAGACTCCATCTCaaaaaaaaaaaaaaaaaaaaaTAGACTTTGAGACCAG	180
Sbjct	121	GGCGGCAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAATAGACTTTGAGACCAG	180
Query	181	CCTGACCAACATAGTGAAACCCGTCCTACTACTAAAAATACAAAAATTACCCGGGCGTGGTG	240
Sbjct	181	CCTGACCAACATAGTGAAACCCGTCCTACTACTAAAAATACAAAAATTACCCGGGCGTGGTG	240
Query	241	ACGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGACAGGAGAATCACTTGAACCAGG	300
Sbjct	241	ACGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGACAGGAGAATCACTTGAACCAGG	300
Query	301	GAGGCGGAGGTTGTAGTGAAGTGAATCGTGCCCCTGCACTCCAGCCTGGGTAACAAGAG	360
Sbjct	301	GAGGCGGAGGTTGTAGTGAAGTGAATCGTGCCCCTGCACTCCAGCCTGGGTAACAAGAG	360
Query	361	CGAAACTCCGTCTCaaaaataaataaataaataaaat	397
Sbjct	361	CGAAACTCCGTCTCAAAAATAAATAAATAAATAAAAT	397

Sequence 708 matched with Sequence 298

Query= Sequence ID - 708 nt: 293
Length=293

SEQ ID NO: 298 nt: 293

ALIGNMENTS

Identities = 293/293 (100%), Gaps = 0/293 (0%)

Query	1	CCAGCTTTTTATGGTGTTTAATCTAATACACTTAAGCTGCAGTCCCAAAATTAGGGGTCC	60
Sbjct	1	CCAGCTTTTTATGGTGTTTAATCTAATACACTTAAGCTGCAGTCCCAAAATTAGGGGTCC	60
Query	61	TTCAGTCTTGGAGACTATAAGGGAGCCTCTGCACCCAGGGAAAATGTTACCCTTTACAGG	120
Sbjct	61	TTCAGTCTTGGAGACTATAAGGGAGCCTCTGCACCCAGGGAAAATGTTACCCTTTACAGG	120
Query	121	GGGGAAGGGTAAACCAGTAGGGAATACAGTACAATCCCAACCCTACTGGGAGGGGCGGGA	180
Sbjct	121	GGGGAAGGGTAAACCAGTAGGGAATACAGTACAATCCCAACCCTACTGGGAGGGGCGGGA	180
Query	181	GGGAGGTGTTGCCGTCAGTGTATTAAGTCGATGTTGGGAAACGTTTAAACATCTGGAGCC	240
Sbjct	181	GGGAGGTGTTGCCGTCAGTGTATTAAGTCGATGTTGGGAAACGTTTAAACATCTGGAGCC	240
Query	241	TTTGTGGGTGGAAATATGTCTCCAGTTACAACCTCCGCAGTGGATGTGAAGAAG	293
Sbjct	241	TTTGTGGGTGGAAATATGTCTCCAGTTACAACCTCCGCAGTGGATGTGAAGAAG	293

Sequence 709 matched with Sequence 299

Query= Sequence ID 709
Length=452

SEQ ID NO: 299

ALIGNMENTS

Identities = 452/452 (100%), Gaps = 0/452 (0%)

Query	1	GGAAGCTACAATGATTTTGGGAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAG	60
Sbjct	1	GGAAGCTACAATGATTTTGGGAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAG	60
Query	61	GGAGGAAATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCCAATACTTTGCA	120
Sbjct	61	GGAGGAAATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCCAATACTTTGCA	120
Query	121	AAACCACGAAACCAAGGTGGCTATGGCGGTTCCAGCAGCAGCAGTAGCTATGGCAGTGGC	180
Sbjct	121	AAACCACGAAACCAAGGTGGCTATGGCGGTTCCAGCAGCAGCAGTAGCTATGGCAGTGGC	180
Query	181	AGAAGATTTTAATTAGGAAACAAAGCTTANCAGGAGAGGAGAGCCAGAGAAGTGACAGGG	240
Sbjct	181	AGAAGATTTTAATTAGGAAACAAAGCTTANCAGGAGAGGAGAGCCAGAGAAGTGACAGGG	240
Query	241	AAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCAGGGCCTAGC	300
Sbjct	241	AAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCAGGGCCTAGC	300
Query	301	TGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAAACTCGAGGA	360
Sbjct	301	TGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAAACTCGAGGA	360
Query	361	CTGTATTTGTGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGAAAGTGTA	420
Sbjct	361	CTGTATTTGTGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGAAAGTGTA	420
Query	421	AGCATTCCAACAAAGGGGTTTAAATGTANATT	452
Sbjct	421	AGCATTCCAACAAAGGGGTTTAAATGTANATT	452

Sequence 710 matched with Sequence 300

Query= Sequence ID 710
Length=480

SEQ ID NO: 300

ALIGNMENTS

Identities = 480/480 (100%), Gaps = 0/480 (0%)

Query	1	TGGATTCCCGTCGTAACCTAAAGGGAAACTTTACAATGTCCGGAGCCCTTGATGTCCTG	60
Sbjct	1	TGGATTCCCGTCGTAACCTAAAGGGAAACTTTACAATGTCCGGAGCCCTTGATGTCCTG	60
Query	61	CAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCGAGCAGGAACCCACTTAGGTGGCACC	120
Sbjct	61	CAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCGAGCAGGAACCCACTTAGGTGGCACC	120
Query	121	AATCTTGAAGTTCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATC	180
Sbjct	121	AATCTTGAAGTTCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATC	180
Query	181	ATAAATCTCAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCAATTGTTGCCATT	240
Sbjct	181	ATAAATCTCAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCAATTGTTGCCATT	240
Query	241	GAAAACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTG	300
Sbjct	241	GAAAACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTG	300
Query	301	AAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTC	360
Sbjct	301	AAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTC	360
Query	361	ACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTTGTTACTGACCCCAGG	420
Sbjct	361	ACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTTGTTACTGACCCCAGG	420
Query	421	GCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCCCTGTGT	480
Sbjct	421	GCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCCCTGTGT	480

Sequence 711 matched with Sequence 301

Query= Sequence ID - 711 nt: 498
Length=498

SEQ ID NO: 301 nt: 498

ALIGNMENTS

Identities = 498/498 (100%), Gaps = 0/498 (0%)

Query	1	GTGGTACATATACACAAAGGAAAACTATGTAGCCATTAAGAAAGGAACTCCTATCAT	60
Sbjct	1	GTGGTACATATACACAAAGGAAAACTATGTAGCCATTAAGAAAGGAACTCCTATCAT	60
Query	61	TTGTAACAACATAAATAAATCTGGAGGAGATTAGGCTAAGGTGAAATAAGCCAGGCACAA	120
Sbjct	61	TTGTAACAACATAAATAAATCTGGAGGAGATTAGGCTAAGGTGAAATAAGCCAGGCACAA	120
Query	121	AAAGACAACTACCATATGATCTTACTTATACGTGTGTGGAATCTAAAAAGGTGGAATTTA	180
Sbjct	121	AAAGACAACTACCATATGATCTTACTTATACGTGTGTGGAATCTAAAAAGGTGGAATTTA	180
Query	181	CAGAAGCAGAGAGTAGAATGGTGATTACCAGAGGCTGGGGAGTGAGGGCAGGAGGTTGGA	240
Sbjct	181	CAGAAGCAGAGAGTAGAATGGTGATTACCAGAGGCTGGGGAGTGAGGGCAGGAGGTTGGA	240
Query	241	GAAATGTTGGTCAAAGGATACAAAGTTTCAGTTATACAGGATGAATAAGTTCAAGAGATC	300
Sbjct	241	GAAATGTTGGTCAAAGGATACAAAGTTTCAGTTATACAGGATGAATAAGTTCAAGAGATC	300
Query	301	TATTGTACAACGTGGTGGCTATAGTTGATAACAATGTATTGTGTTCTTGAAAAATGCTGA	360
Sbjct	301	TATTGTACAACGTGGTGGCTATAGTTGATAACAATGTATTGTGTTCTTGAAAAATGCTGA	360
Query	361	GAGAGTAGATTTTAAGTGTCTCACCACAAAACATAAGTATGTGAGGTAATGCATGTGTT	420
Sbjct	361	GAGAGTAGATTTTAAGTGTCTCACCACAAAACATAAGTATGTGAGGTAATGCATGTGTT	420
Query	421	AATTANCTTAATTTAGACATTTTATAATGTATTATACATATTTCAAACACGTTGTACA	480
Sbjct	421	AATTANCTTAATTTAGACATTTTATAATGTATTATACATATTTCAAACACGTTGTACA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGAGAAAGATACACAATT	498
Sbjct	481	TGAGAAAGATACACAATT	498

Sequence 713 matched with Sequence 302

Query= Sequence ID 713
Length=474

SEQ ID NO: 302

ALIGNMENTS

Identities = 474/474 (100%), Gaps = 0/474 (0%)

Query	1	GCCCAGTCGACCCATGTTCTCCTTTCTACACCAGCATTAGACGCTGTCTTCACAGATTTG	60
Sbjct	1	GCCCAGTCGACCCATGTTCTCCTTTCTACACCAGCATTAGACGCTGTCTTCACAGATTTG	60
Query	61	GAAATCCTGGCTGCCATTTTTCAGCTGCCATCCATGACGTTGATCATCCTGGAGTCTCC	120
Sbjct	61	GAAATCCTGGCTGCCATTTTTCAGCTGCCATCCATGACGTTGATCATCCTGGAGTCTCC	120
Query	121	AATCAGTTTCTCATCAACACAAATTCAGAACTTGCTTTGATGTATAATGATGAATCTGTG	180
Sbjct	121	AATCAGTTTCTCATCAACACAAATTCAGAACTTGCTTTGATGTATAATGATGAATCTGTG	180
Query	181	TTGGAAAATCATCACCTTGCTGTGGGTTTCAAAGTCTGCAAGAAGAACTGTGACATC	240
Sbjct	181	TTGGAAAATCATCACCTTGCTGTGGGTTTCAAAGTCTGCAAGAAGAACTGTGACATC	240
Query	241	TTCATGAATCTCACCAAGAAGCAGCGTCAGAACTCAGGAAGATGGTTATTGACATGGTG	300
Sbjct	241	TTCATGAATCTCACCAAGAAGCAGCGTCAGAACTCAGGAAGATGGTTATTGACATGGTG	300
Query	301	TTAGCAACTGATATGTCTAAACATATGAGCCTGCTGGCAGACCTGAAGACAATGGTAGAA	360
Sbjct	301	TTAGCAACTGATATGTCTAAACATATGAGCCTGCTGGCAGACCTGAAGACAATGGTAGAA	360
Query	361	ACGAAGAAAGTTACAAGTTCAGGCGTTCTTCTCCTAGACAACTATACCCGATCGCATTCA	420
Sbjct	361	ACGAAGAAAGTTACAAGTTCAGGCGTTCTTCTCCTAGACAACTATACCCGATCGCATTCA	420
Query	421	GGTCCTTCGCAACATGGTCACTGTGCAGACCTGAGCAACCCACCAAGTCCTTG	474
Sbjct	421	GGTCCTTCGCAACATGGTCACTGTGCAGACCTGAGCAACCCACCAAGTCCTTG	474

Sequence 714 matched with Sequence 303

Query= Sequence ID 714
Length=535

SEQ ID NO: 303

ALIGNMENTS

Identities = 535/535 (100%), Gaps = 0/535 (0%)

Query	1	CTGTAACAGAGATTCCTTTTTTCAATAATCTTAATTCAAAGCATTATTAGACTTGAAAG	60
Sbjct	1	CTGTAACAGAGATTCCTTTTTTCAATAATCTTAATTCAAAGCATTATTAGACTTGAAAG	60
Query	61	GGTTTGATAATCTCCAGTCCTTAGTAAAGATTGAGAGAGGCTGGAGCAGTTTTCAGTTT	120
Sbjct	61	GGTTTGATAATCTCCAGTCCTTAGTAAAGATTGAGAGAGGCTGGAGCAGTTTTCAGTTT	120
Query	121	TAAATGAGTCTGCAGTTAATATCAAATGTGAGTTTGGGACTGCCTGGCAACATTTATATT	180
Sbjct	121	TAAATGAGTCTGCAGTTAATATCAAATGTGAGTTTGGGACTGCCTGGCAACATTTATATT	180
Query	181	TCTTATTCAGAACCCTTGATGAGACTATTTTAAACATACTAGTCTGCTGATAGAAAGCA	240
Sbjct	181	TCTTATTCAGAACCCTTGATGAGACTATTTTAAACATACTAGTCTGCTGATAGAAAGCA	240
Query	241	CTATACATCCTATTGTTTCTTCTTTCCAAAATCAGCCTTCTGTCTGTAACAAAAATGTA	300
Sbjct	241	CTATACATCCTATTGTTTCTTCTTTCCAAAATCAGCCTTCTGTCTGTAACAAAAATGTA	300
Query	301	CTTTATAGAGATGGAGGAAAAGGTCTAATACTACATAGCCTTAAGTGTTTCTGTCATTGT	360
Sbjct	301	CTTTATAGAGATGGAGGAAAAGGTCTAATACTACATAGCCTTAAGTGTTTCTGTCATTGT	360
Query	361	TCAAGTGATTTTCTGTAACAGAAACATATTTGGAATGTTTTCTTTCCCCTTATAAAT	420
Sbjct	361	TCAAGTGATTTTCTGTAACAGAAACATATTTGGAATGTTTTCTTTCCCCTTATAAAT	420
Query	421	TGTAATTCCTGAAATACTGCTGCTTTAAAAAGTCCCACTGTCAGATTATATTATCTAACA	480
Sbjct	421	TGTAATTCCTGAAATACTGCTGCTTTAAAAAGTCCCACTGTCAGATTATATTATCTAACA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATTGAATATTGNAATATACTTGGCTTACCTCTCAATAAAAGGGTCTTTTCTATT	535
Sbjct	481	ATTGAATATTGNAATATACTTGGCTTACCTCTCAATAAAAGGGTCTTTTCTATT	535

Sequence 717 matched with Sequence 304

Query= Sequence ID 717
Length=464

SEQ ID NO: 304

ALIGNMENTS

Identities = 464/464 (100%), Gaps = 0/464 (0%)

Query	1	TCCACCCACCTTGACCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCTCGCCCAGCC	60
Sbjct	1	TCCACCCACCTTGACCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCTCGCCCAGCC	60
Query	61	CGATACTAGGACTTATGCAGAAAAAACCTTGACATGGAGGAAAGTAAGATCTAAATAAAT	120
Sbjct	61	CGATACTAGGACTTATGCAGAAAAAACCTTGACATGGAGGAAAGTAAGATCTAAATAAAT	120
Query	121	ACTGTATTCATAGATTAAGAACTCAGCATAATAAATATACCATTCTCCCCAGATTGAT	180
Sbjct	121	ACTGTATTCATAGATTAAGAACTCAGCATAATAAATATACCATTCTCCCCAGATTGAT	180
Query	181	GTACAGATTTAACACAATTCCTATCAAGATCCCAGCAAGATTTTGTAGATATGTAAAAG	240
Sbjct	181	GTACAGATTTAACACAATTCCTATCAAGATCCCAGCAAGATTTTGTAGATATGTAAAAG	240
Query	241	ATTATTCAAAAATGTAAAAGGAAGGACAAAGGACTAGAATAGATAAAACAAAATGGAGAA	300
Sbjct	241	ATTATTCAAAAATGTAAAAGGAAGGACAAAGGACTAGAATAGATAAAACAAAATGGAGAA	300
Query	301	AGATTTAATAGGAATCACTGTAAGTATTTAAGACATACAGAACAATAATAGAACTGC	360
Sbjct	301	AGATTTAATAGGAATCACTGTAAGTATTTAAGACATACAGAACAATAATAGAACTGC	360
Query	361	TTGTATTAGTCCATTTTCACGCTGCTGATAAAGACATACCTGAGATTGGCAATTACAAAG	420
Sbjct	361	TTGTATTAGTCCATTTTCACGCTGCTGATAAAGACATACCTGAGATTGGCAATTACAAAG	420
Query	421	GAAAGANGTTTATTGGCTTACAGTTCCTATGGCTGGGGAGGCCT	464
Sbjct	421	GAAAGANGTTTATTGGCTTACAGTTCCTATGGCTGGGGAGGCCT	464

Sequence 718 matched with Sequence 305

Query= Sequence ID 718
Length=588

SEQ ID NO: 305

ALIGNMENTS

Identities = 588/588 (100%), Gaps = 0/588 (0%)

Query	1	CTCCTCTGGGTTGAAACCCGGGCGCCGCAAGATGCCGGCTTACCACTCTTCTCTCATGG	60
Sbjct	1	CTCCTCTGGGTTGAAACCCGGGCGCCGCAAGATGCCGGCTTACCACTCTTCTCTCATGG	60
Query	61	ATCCTGATACCAAACATCATCGGAAACATGGCACTGTTGCCTATCAGAAGTCAATTCAAAG	120
Sbjct	61	ATCCTGATACCAAACATCATCGGAAACATGGCACTGTTGCCTATCAGAAGTCAATTCAAAG	120
Query	121	GACCTGCCCCCAGAGAGACAAAAGATACAGATATTGTGGATGAAGCCATCTATTACTTCA	180
Sbjct	121	GACCTGCCCCCAGAGAGACAAAAGATACAGATATTGTGGATGAAGCCATCTATTACTTCA	180
Query	181	AGGCCAATGTCTTCTTCAAAAACATGAAATTAAGAATGAAGCTGATAGGACCTTGATAT	240
Sbjct	181	AGGCCAATGTCTTCTTCAAAAACATGAAATTAAGAATGAAGCTGATAGGACCTTGATAT	240
Query	241	ATATAACTCTCTACATTTCTGAATGTCTGAAGAACTGCAAAAGTGCAATTCCAAAAGCC	300
Sbjct	241	ATATAACTCTCTACATTTCTGAATGTCTGAAGAACTGCAAAAGTGCAATTCCAAAAGCC	300
Query	301	AAGGTGAGAAAGAAATGTATACGCTGGGAATCACTAATTTTCCCATTCTTGAGAGCCTG	360
Sbjct	301	AAGGTGAGAAAGAAATGTATACGCTGGGAATCACTAATTTTCCCATTCTTGAGAGCCTG	360
Query	361	GTTTTCCACTTAACGCAATTTATGCCAAACCTGCAAACAAACAGGAAGATGAAGTGATGA	420
Sbjct	361	GTTTTCCACTTAACGCAATTTATGCCAAACCTGCAAACAAACAGGAAGATGAAGTGATGA	420
Query	421	GAGCCTATTTACAACAGCTAAGGCAAGAGACTGGACTGAGACTTTGTGAGAAAAGTTTTC	480
Sbjct	421	GAGCCTATTTACAACAGCTAAGGCAAGAGACTGGACTGAGACTTTGTGAGAAAAGTTTTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GACCCTCAGAATGATAAACCAGCAAGTGGNGGGCTTGCTTTGTGAAGAGACAGTTCATG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GACCCTCAGAATGATAAACCAGCAAGTGGNGGGCTTGCTTTGTGAAGAGACAGTTCATG  540

Query  541  AACAAAGTCTTTCAGGACCTGGACAGTGAAGGGAGCCCGGCAGCCA  588
          ||||||||||||||||||||||||||||||||||||
Sbjct   541  AACAAAGTCTTTCAGGACCTGGACAGTGAAGGGAGCCCGGCAGCCA  588
```

Sequence 719 matched with Sequence 306

Query= Sequence ID 719
Length=492

SEQ ID NO: 306

ALIGNMENTS

Identities = 492/492 (100%), Gaps = 0/492 (0%)

```
Query 1   CGNGGCCGCGTNAACTTTGGATCGTCAGCTGGGGCTGGCAGGCACCTAAATGGGAAGGGTGAT 63
          |||
Sbjct 1   CGNGGCCGCGTNAACTTTGGATCGTCAGCTGGGGCTGGCAGGCACCTAAATGGGAAGGGTGAT 63

Query 64  AGCAGTGTGTTGGGGGAGTTTAGGGAACGGTCCTCTACCGATAGAGGCAGCANCTCATT 123
          |||
Sbjct 64  AGCAGTGTGTTGGGGGAGTTTAGGGAACGGTCCTCTACCGATAGAGGCAGCANCTCATT 123

Query 124  GGAATTTCTCCTGAAGTTGTCTTGCCCCTTGAATCCTGCAGGAAGGCTGGCAAATGGCC 183
          |||
Sbjct 124  GGAATTTCTCCTGAAGTTGTCTTGCCCCTTGAATCCTGCAGGAAGGCTGGCAAATGGCC 183

Query 184  ATTTCCCTTCCACTTGAATAGAGACCCATAACTCAAGTATCTGCCCTTAAGACACCACAG 243
          |||
Sbjct 184  ATTTCCCTTCCACTTGAATAGAGACCCATAACTCAAGTATCTGCCCTTAAGACACCACAG 243

Query 244  GACTGTTCTTCGCGGGCCCTGCCCTGGATTTGGGAGAGGCAGTCCANCTACCCAACTA 303
          |||
Sbjct 244  GACTGTTCTTCGCGGGCCCTGCCCTGGATTTGGGAGAGGCAGTCCANCTACCCAACTA 303

Query 304  GGCTCTGCANGGGGACCANGAGGGATGGGTTGTGTCCACAGGACCAGCCAGACTGATGAG 363
          |||
Sbjct 304  GGCTCTGCANGGGGACCANGAGGGATGGGTTGTGTCCACAGGACCAGCCAGACTGATGAG 363

Query 364  GGATGCGGCAAGCATATTCTCACCACCTTCTTTACGTTTACAACANACCAGCNTTCCCT 423
          |||
Sbjct 364  GGATGCGGCAAGCATATTCTCACCACCTTCTTTACGTTTACAACANACCAGCNTTCCCT 423

Query 424  GTGTGGCAGGGGTTACATTGGTCACCGAGGACCTANAATCATGGAGTGCTCTGGGGATCC 483
          |||
Sbjct 424  GTGTGGCAGGGGTTACATTGGTCACCGAGGACCTANAATCATGGAGTGCTCTGGGGATCC 483
```

PATENT SEQUENCE ALIGNMENT

```
Query  484  GGGCTTGGA  492
          |||||
Sbjct  484  GGGCTTGGA  492
```

Blast comparison trimmed “CGN” from the 5’ end of both sequences and reported 489 identities. The report has been manually corrected for this. “CGN” has been prepended to both sequences and identity count has been increased to 492.

Sequence 720 matched with Sequence 307

Query= Sequence ID 720
Length=430

SEQ ID NO: 307

ALIGNMENTS

Identities = 430/430 (100%), Gaps = 0/430 (0%)

Query	1	TCAGTGTTGAATTTTGTGACACTTTCTCTGCATCAATTGGTATGACCATGTGA	60
Sbjct	1	TCAGTGTTGAATTTTGTGACACTTTCTCTGCATCAATTGGTATGACCATGTGA	60
Query	61	tttCTGTAGCCTGTTAATATGGTTAATTTTCAAATATTGAGCTGATTAATTTTCAAATAT	120
Sbjct	61	TTTCTGTAGCCTGTTAATATGGTTAATTTTCAAATATTGAGCTGATTAATTTTCAAATAT	120
Query	121	TGAGCTCTCCTTGCATCTCTGGAATAAGTACCACTTGGTCGTGGTATATATTTCTTTTAA	180
Sbjct	121	TGAGCTCTCCTTGCATCTCTGGAATAAGTACCACTTGGTCGTGGTATATATTTCTTTTAA	180
Query	181	TATATTGCTGAATTCTGTTTGATCATGTTTTCTTAAAGACTTTCGTGTCTGTTTTCATGA	240
Sbjct	181	TATATTGCTGAATTCTGTTTGATCATGTTTTCTTAAAGACTTTCGTGTCTGTTTTCATGA	240
Query	241	TAGATACTGGTCTATAGTTTTGTTGTAATATCTTGGTTTGATTTTGATATCAGGATAATG	300
Sbjct	241	TAGATACTGGTCTATAGTTTTGTTGTAATATCTTGGTTTGATTTTGATATCAGGATAATG	300
Query	301	CTACCTTAATAGAATGAATTGGAGCCAAGTATGGTGGCAAATGCCTATAGTCCTAGCTAC	360
Sbjct	301	CTACCTTAATAGAATGAATTGGAGCCAAGTATGGTGGCAAATGCCTATAGTCCTAGCTAC	360
Query	361	TCAGGAGGCTGAGGTGGTGGGGACTGCTTGACCCANGAGTTCAAATCTAGCTTGGGCAAT	420
Sbjct	361	TCAGGAGGCTGAGGTGGTGGGGACTGCTTGACCCANGAGTTCAAATCTAGCTTGGGCAAT	420
Query	421	GTAGCAAGAC	430
Sbjct	421	GTAGCAAGAC	430

Sequence 721 matched with Sequence 308

Query= Sequence ID 721
Length=574

SEQ ID NO: 308

ALIGNMENTS

Identities = 574/574 (100%), Gaps = 0/574 (0%)

Query	1	TAGAAGGAATGACTATTCATGTCCAAAGTGAATGGTTTTGTGCAGTGAACAACACATGGC	60
Sbjct	1	TAGAAGGAATGACTATTCATGTCCAAAGTGAATGGTTTTGTGCAGTGAACAACACATGGC	60
Query	61	GAGGTACTAACTGAGAACTTTTCATGCTTTATGCCTACCTCTTGTAGTTGTTGCAGAG	120
Sbjct	61	GAGGTACTAACTGAGAACTTTTCATGCTTTATGCCTACCTCTTGTAGTTGTTGCAGAG	120
Query	121	CAAATATAAATTGTAATAAGATAGCTAGGCCTTGCAGAAACAAACAGAAAACTTaaaaa	180
Sbjct	121	CAAATATAAATTGTAATAAGATAGCTAGGCCTTGCAGAAACAAACAGAAAACTTAAAAA	180
Query	181	aaaaTGATATAAGAGCTGGAGTCTAGTATTTATATGAATCTGTGAGAGATAAttttttG	240
Sbjct	181	AAAATGATATAAGAGCTGGAGTCTAGTATTTATATGAATCTGTGAGAGATAATTTTTTTG	240
Query	241	GTCTCACTGCAATGAACCAAAAGCGGCTGAGTTTGGTTTTTAATTGTAGCCATGTATTGA	300
Sbjct	241	GTCTCACTGCAATGAACCAAAAGCGGCTGAGTTTGGTTTTTAATTGTAGCCATGTATTGA	300
Query	301	AGGCATCTTTTTGACCAACTCTTGTTGGTTCTGTCTTGAACCATTGTTAATCACTGTGCT	360
Sbjct	301	AGGCATCTTTTTGACCAACTCTTGTTGGTTCTGTCTTGAACCATTGTTAATCACTGTGCT	360
Query	361	GTAATTAGTATAGCTAAATCTTTTCCTTCCTTGCTCCTCCCCAGCCCACCCCGTCTTCC	420
Sbjct	361	GTAATTAGTATAGCTAAATCTTTTCCTTCCTTGCTCCTCCCCAGCCCACCCCGTCTTCC	420
Query	421	CTTAACATTTTTTCAGgggggTTGGGAGTGGTTTCATTTTAATGTGAGTGGATGTTTTG	480
Sbjct	421	CTTAACATTTTTTCAGGGGGGTTGGGAGTGGTTTCATTTTAATGTGAGTGGATGTTTTG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATAGTTGTAAGGAAAAAATGCATTTTCAGACACATTTTCACACATGAGCTATTTTCTTACAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATAGTTGTAAGGAAAAAATGCATTTTCAGACACATTTTCACACATGAGCTATTTTCTTACAC  540

Query  541  AGTATGTCTTATTGGTAATAAGAATGTAATTCAT  574
          ||||||||||||||||||||||||||||
Sbjct  541  AGTATGTCTTATTGGTAATAAGAATGTAATTCAT  574
```

Sequence 722 matched with Sequence 309

Query= Sequence ID 722
Length=327

SEQ ID NO: 309

ALIGNMENTS

Identities = 327/327 (100%), Gaps = 0/327 (0%)

```
Query 1  CNTTCCNTAAGAATACAAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCCATCTAC 62
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  CNTTCCNTAAGAATACAAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCCATCTAC 62

Query 63 TCAGGAAGCTGAGGCTGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCAGA 122
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 63 TCAGGAAGCTGAGGCTGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCAGA 122

Query 123 GATCACGCCACTGCAGTCCAGCCTGGGCAACAGTGCAGACTCTGTCTCaaaaaaaaaT 182
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 123 GATCACGCCACTGCAGTCCAGCCTGGGCAACAGTGCAGACTCTGTCTCAAAAAAAAAAAT 182

Query 183 AAATAAATTACCTGGGTGTGGCAGCGCGTGCCTGTAATCCCAGCTACCCAGGAGGCTGAG 242
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 183 AAATAAATTACCTGGGTGTGGCAGCGCGTGCCTGTAATCCCAGCTACCCAGGAGGCTGAG 242

Query 243 GCAAGAGAACTGCTTGAACCCAGGAGGCAGAGGTTGCATGGAGCTGAGATGGCGCCACTG 302
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 243 GCAAGAGAACTGCTTGAACCCAGGAGGCAGAGGTTGCATGGAGCTGAGATGGCGCCACTG 302

Query 303 CACTCCAGTCTGGTGACAGAGTGAG 327
      ||||||||||||||||||||
Sbjct 303 CACTCCAGTCTGGTGACAGAGTGAG 327
```

Blast comparison trimmed “CN” from the 5’ end of both sequences and reported 325 identities. The report has been manually corrected for this. “CN” has been prepended to both sequences and identity count has been increased to 327.

Sequence 724 matched with Sequence 310

Query= Sequence ID 724
Length=273

SEQ ID NO: 310

ALIGNMENTS

Identities = 273/273 (100%), Gaps = 0/273 (0%)

```
Query 1   CTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGNGGTGCATGCCTGTAAACCCAGCT  60
          |||
Sbjct 1   CTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGNGGTGCATGCCTGTAAACCCAGCT  60

Query 61  ACCAGGTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGTCGGAGGTTGCG  120
          |||
Sbjct 61  ACCAGGTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGTCGGAGGTTGCG  120

Query 121 GCGAGCTGAGATCATGCCACTGCACTGCGGCCTGGAGACAAGAGCAAGACTCCGTCTCaa  180
          |||
Sbjct 121 GCGAGCTGAGATCATGCCACTGCACTGCGGCCTGGAGACAAGAGCAAGACTCCGTCTCAA  180

Query 181 aaaaaaaaaaaaaaaaaaaaaaaaaaGACNTCACCTAATTGCAGNGNGNGGACCTTATTT  240
          |||
Sbjct 181 AAAAAAAAAAAAAAAAAAAAAAAAAAAGACNTCACCTAATTGCAGNGNGNGGACCTTATTT  240

Query 241 GGCTNTTAATTCAAAC TATTA AAAAATGTGAACN  273
          |||
Sbjct 241 GGCTNTTAATTCAAAC TATTA AAAAATGTGAACN  273
```

Blast comparison trimmed “N” from the 3’ end of both sequences and reported 272 identities. The report has been manually corrected for this. “N” has been appended to both sequences and identity count has been increased to 273.

Sequence 726 matched with Sequence 311

Query= Sequence ID - 726 nt: 260
Length=260

SEQ ID NO: 311 nt: 260

ALIGNMENTS

Identities = 260/260 (100%), Gaps = 0/260 (0%)

Query	1	CGGGGTCTGTACCGGGCTGGCCTGTGCCTATCACCTCTTATGCACACCTCCCACCCCCTG	60
Sbjct	1	CGGGGTCTGTACCGGGCTGGCCTGTGCCTATCACCTCTTATGCACACCTCCCACCCCCTG	60
Query	61	TATTCACACCTGGACTGGTGGCCCCTGCCTTGGGGAAGGTCTCCCATGTGCCTGCAC	120
Sbjct	61	TATTCACACCTGGACTGGTGGCCCCTGCCTTGGGGAAGGTCTCCCATGTGCCTGCAC	120
Query	121	CAGGAGACAGACAGAGAAGGCAGCAGGCGGCCTTTGTTGCTCAGCAAGGGGCTCTGCCCT	180
Sbjct	121	CAGGAGACAGACAGAGAAGGCAGCAGGCGGCCTTTGTTGCTCAGCAAGGGGCTCTGCCCT	180
Query	181	CCCTCCTTCCTTCTTGCTTCTCATAGCCCCGGTGTGCGGTGCATACACCCACCTCCTG	240
Sbjct	181	CCCTCCTTCCTTCTTGCTTCTCATAGCCCCGGTGTGCGGTGCATACACCCACCTCCTG	240
Query	241	CAATAAAATAGTAGCATCGG	260
Sbjct	241	CAATAAAATAGTAGCATCGG	260

Sequence 727 matched with Sequence 312

Query= Sequence ID 727
Length=538

SEQ ID NO: 312

ALIGNMENTS

Identities = 538/538 (100%), Gaps = 0/538 (0%)

Query	1	CTGAGTNTAGAAATGATGCCATTAATACTGATTGCAAAAACATTACAACCTCAGTACTGCA	60
Sbjct	1	CTGAGTNTAGAAATGATGCCATTAATACTGATTGCAAAAACATTACAACCTCAGTACTGCA	60
Query	61	GCTTTCATTCAAATAGGTTATATGTATAAACTGAGTTCAACAATATTGTATTTGAGATGG	120
Sbjct	61	GCTTTCATTCAAATAGGTTATATGTATAAACTGAGTTCAACAATATTGTATTTGAGATGG	120
Query	121	TAAAGTTAAAGAAATGCAATAATGTAAATAATACTTAAGAAAATAAGATCTCAGGAAACT	180
Sbjct	121	TAAAGTTAAAGAAATGCAATAATGTAAATAATACTTAAGAAAATAAGATCTCAGGAAACT	180
Query	181	GTATATACTCTGTACTTTTATGCAACTTTATCAGATCATTTTCAGTATATGCATCAAGGAT	240
Sbjct	181	GTATATACTCTGTACTTTTATGCAACTTTATCAGATCATTTTCAGTATATGCATCAAGGAT	240
Query	241	ATAGTGTATATGACATGAACTTTGAGTGCAAAAACGTACTATGTACCTTTTGTTTATTT	300
Sbjct	241	ATAGTGTATATGACATGAACTTTGAGTGCAAAAACGTACTATGTACCTTTTGTTTATTT	300
Query	301	TGCTGTCAACATCTAAATAAAGGtttttttgtttgtttttgttttttaattgttttgt	360
Sbjct	301	TGCTGTCAACATCTAAATAAAGGTTTTTTTGTTTGTTTTTTGTTTTTTAATTGTTTTGT	360
Query	361	tttaaagattgttttaattaattaaaaattaattgttttaattaacaattgtttaatt	420
Sbjct	361	TTTAAAGATTGTTTTAATTAATTAATAAATAATTGTTTTAATTAACAATTGTTTAATT	420
Query	421	gttttaaaGTCGCCAGGCTGAGGCAGGTGAATCACAAGCTTAGGAGTTGGAGGCTAGCCT	480
Sbjct	421	GTTTTAAAGTCGCCAGGCTGAGGCAGGTGAATCACAAGCTTAGGAGTTGGAGGCTAGCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCCAACATGGTGAACCCCGTCTCTACTAAAAATACaaaaaaTTAACTGGGTGTGGG	538
Sbjct	481	GCCAACATGGTGAACCCCGTCTCTACTAAAAATACAAAAAATTAACCTGGGTGTGGG	538

Sequence 728 matched with Sequence 313

Query= Sequence ID 728
Length=629

SEQ ID NO: 313

ALIGNMENTS

Identities = 629/629 (100%), Gaps = 0/629 (0%)

Query	1	CCCATCTGCACCAGTACACAGGCAGGCATTATCATTCTTCACCTACTTTTAAATAGTGG	60
Sbjct	1	CCCATCTGCACCAGTACACAGGCAGGCATTATCATTCTTCACCTACTTTTAAATAGTGG	60
Query	61	CAACTTGGGATTTCATTCTGGTGATTCTGAACCTTGCCTCATAGCTTAAAGTATAAAAAAG	120
Sbjct	61	CAACTTGGGATTTCATTCTGGTGATTCTGAACCTTGCCTCATAGCTTAAAGTATAAAAAAG	120
Query	121	ATTCAAGAGCAGTGAGGTTTGTCTTTCCAGTGAATGGTGGACTGAGTGGTGCAGGTGG	180
Sbjct	121	ATTCAAGAGCAGTGAGGTTTGTCTTTCCAGTGAATGGTGGACTGAGTGGTGCAGGTGG	180
Query	181	AGGGCTAACAAGAGGAAAGAACTACATTCTTCAGAATACAGTGATGAAAATTCATTTTGA	240
Sbjct	181	AGGGCTAACAAGAGGAAAGAACTACATTCTTCAGAATACAGTGATGAAAATTCATTTTGA	240
Query	241	AACTCAAATATTTTCATTTTGGATATTCTCCTGTTTTTATTAAACCAGTGATTACACCTG	300
Sbjct	241	AACTCAAATATTTTCATTTTGGATATTCTCCTGTTTTTATTAAACCAGTGATTACACCTG	300
Query	301	GCCATCCCTCTAAATGTTCTAGGAAGGCATGTCTATTGTGATTTTGATGAAGACAGAATT	360
Sbjct	301	GCCATCCCTCTAAATGTTCTAGGAAGGCATGTCTATTGTGATTTTGATGAAGACAGAATT	360
Query	361	ATTTTCTCTGTAGAAACACAGATACCACTTTATCAGGGGAAGTTAGTCAAATGAAATGG	420
Sbjct	361	ATTTTCTCTGTAGAAACACAGATACCACTTTATCAGGGGAAGTTAGTCAAATGAAATGG	420
Query	421	AAATTGGTAAATGGACAAAAGCTAGCTAGTAAAAAGGACGACCCAGCAACATGCTTTAAC	480
Sbjct	421	AAATTGGTAAATGGACAAAAGCTAGCTAGTAAAAAGGACGACCCAGCAACATGCTTTAAC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCCATTGTATGTTTGTGGAAAGAGCATAGTTTAAACATCTTGAGAAATTTGGGACATAAAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CCCATTGTATGTTTGTGGAAAGAGCATAGTTTAAACATCTTGAGAAATTTGGGACATAAAA  540

Query  541  GTTTTCATNGGTAGACAGTTCATGGCAGTATATGAATTGACATAATGGAAATAATCTGAT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GTTTTCATNGGTAGACAGTTCATGGCAGTATATGAATTGACATAATGGAAATAATCTGAT  600

Query  601  TTTATTTTTTACAACATAACATCCTTTCCCC  629
          ||||||||||||||||||||||||
Sbjct   601  TTTATTTTTTACAACATAACATCCTTTCCCC  629
```

Sequence 736 matched with Sequence 314

Query= Sequence ID - 736 nt: 641
Length=641

SEQ ID NO: 314 nt: 641

ALIGNMENTS

Identities = 641/641 (100%), Gaps = 0/641 (0%)

Query	1	GGAATTCCAAGTGCTTGGGGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACT	60
Sbjct	1	GGAATTCCAAGTGCTTGGGGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACT	60
Query	61	TGAGTGTGCAGCTGCATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATAC	120
Sbjct	61	TGAGTGTGCAGCTGCATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATAC	120
Query	121	CAGTAGGACAAGGCAGGAAAATACTACACTTTTCAGGATCAAGCCCCTCTGACTCTCATTT	180
Sbjct	121	CAGTAGGACAAGGCAGGAAAATACTACACTTTTCAGGATCAAGCCCCTCTGACTCTCATTT	180
Query	181	GGAAACTGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACT	240
Sbjct	181	GGAAACTGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACT	240
Query	241	CCCAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGG	300
Sbjct	241	CCCAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGG	300
Query	301	ACTTGAATAAAATTAACCATTGTCATGTTTTTCAGAACAACTAAGCTGTTTTATATTTTCAT	360
Sbjct	301	ACTTGAATAAAATTAACCATTGTCATGTTTTTCAGAACAACTAAGCTGTTTTATATTTTCAT	360
Query	361	GTGCATGAAAGCCCTAGAACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGT	420
Sbjct	361	GTGCATGAAAGCCCTAGAACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGT	420
Query	421	TAGATGATGTGGCCATTAGGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAG	480
Sbjct	421	TAGATGATGTGGCCATTAGGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CAGTACCTAATAAAATATAGTATACTGAAAGTGAACAGATACTTTGTCTCTTTCTTTGGC	540
Sbjct	481	CAGTACCTAATAAAATATAGTATACTGAAAGTGAACAGATACTTTGTCTCTTTCTTTGGC	540
Query	541	TGCTTGATCTTTATCTGTGTCTGCCGTACAGTGCACCCTTAAAGTATTCTACACCAGTGC	600
Sbjct	541	TGCTTGATCTTTATCTGTGTCTGCCGTACAGTGCACCCTTAAAGTATTCTACACCAGTGC	600
Query	601	TTCTCAAACCTGGAAATGTGCATGTAAGTCACCCANGGGTCT	641
Sbjct	601	TTCTCAAACCTGGAAATGTGCATGTAAGTCACCCANGGGTCT	641

Sequence 739 matched with Sequence 315

Query= Sequence ID 739
Length=645

SEQ ID NO: 315

ALIGNMENTS

Identities = 645/645 (100%), Gaps = 0/645 (0%)

Query	1	TGCATGCCCATAGTCCCAGCTATTTGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCGGG	60
Sbjct	1	TGCATGCCCATAGTCCCAGCTATTTGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCGGG	60
Query	61	AGCCAGAGGTTGCAGTGAGCCGAGATCGCACTCCAGCTTGGCGACAGAACAAGACTCTGT	120
Sbjct	61	AGCCAGAGGTTGCAGTGAGCCGAGATCGCACTCCAGCTTGGCGACAGAACAAGACTCTGT	120
Query	121	CTCaaaaaaaaaaaaaaaaaGAAATCTTGGGATCCTGAACCCCTTACTCGAAGGGCTAAGG	180
Sbjct	121	CTCAAAAAAAAAAAAAAAAAAGAAATCTTGGGATCCTGAACCCCTTACTCGAAGGGCTAAGG	180
Query	181	TAGCATCTCAGCATGTCTTATTCGAGACTTCGTANAACCAGACCTGCTGTTTGTAGATGT	240
Sbjct	181	TAGCATCTCAGCATGTCTTATTCGAGACTTCGTANAACCAGACCTGCTGTTTGTAGATGT	240
Query	241	TAATTAATCAAACCTTTCTCTACTCATTCTGGACCAGTTAAGGTTTTCTCCTTCTCCGTA	300
Sbjct	241	TAATTAATCAAACCTTTCTCTACTCATTCTGGACCAGTTAAGGTTTTCTCCTTCTCCGTA	300
Query	301	TGAGTTTTGATTTTCGTCCTCCTTGGTTGGAGATCACACTTTGGTCTGCTGCTAAGTTGG	360
Sbjct	301	TGAGTTTTGATTTTCGTCCTCCTTGGTTGGAGATCACACTTTGGTCTGCTGCTAAGTTGG	360
Query	361	ATGCCTCCCACTGTCTTTCCCTAAGTCTAGGGCTTCANACCCAGTGTTGGGAGAGGGAC	420
Sbjct	361	ATGCCTCCCACTGTCTTTCCCTAAGTCTAGGGCTTCANACCCAGTGTTGGGAGAGGGAC	420
Query	421	TTTCGTTTCCTGCCCCTCACCACATCAGACACAGGCAGGCAAGAATAAGATGGCCAAAAG	480
Sbjct	421	TTTCGTTTCCTGCCCCTCACCACATCAGACACAGGCAGGCAAGAATAAGATGGCCAAAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCCGATGAACTTCTTGACCTAGCCTGGGACATTACCTGTTACTAGGTGGACTTCACTGCC	540
Sbjct	481	GCCGATGAACTTCTTGACCTAGCCTGGGACATTACCTGTTACTAGGTGGACTTCACTGCC	540
Query	541	TGTGAATGGAAGCTGAAGGGCTGtttttttGGTTTGTATTTGGACAGGCCAGGCTTANAG	600
Sbjct	541	TGTGAATGGAAGCTGAAGGGCTGTTTTTTTGGTTTGTATTTGGACAGGCCAGGCTTANAG	600
Query	601	AGGGAGAGAACTGGGCTACTCTTCAGCAGTGATCTTTAAAATGCC	645
Sbjct	601	AGGGAGAGAACTGGGCTACTCTTCAGCAGTGATCTTTAAAATGCC	645

Sequence 747 matched with Sequence 316

Query= Sequence ID 747
Length=542

SEQ ID NO: 316

ALIGNMENTS

Identities = 542/542 (100%), Gaps = 0/542 (0%)

Query	1	CAGAGTGCAAGACGATGACTTGCAAAATGTGCGCAGCTGGAACGCAACATAGAGACCATCA	60
Sbjct	1	CAGAGTGCAAGACGATGACTTGCAAAATGTGCGCAGCTGGAACGCAACATAGAGACCATCA	60
Query	61	TCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGGG	120
Sbjct	61	TCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGGG	120
Query	121	AATTCAAAGAGCTGGTGCAGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAATAAGAATG	180
Sbjct	121	AATTCAAAGAGCTGGTGCAGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAATAAGAATG	180
Query	181	AAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGAGCT	240
Sbjct	181	AAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGAGCT	240
Query	241	TCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCACGAGAAGATGCACG	300
Sbjct	241	TCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCACGAGAAGATGCACG	300
Query	301	AGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCACCCCCTAAG	360
Sbjct	301	AGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCACCCCCTAAG	360
Query	361	ACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGGCCACGGCC	420
Sbjct	361	ACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGGCCACGGCC	420
Query	421	ACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTCTACCCAACCAGGGCCCCGGGGCCT	480
Sbjct	421	ACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTCTACCCAACCAGGGCCCCGGGGCCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTATGTCAAACGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTATGTCAAACGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTTCC  540

Query  541  TC    542
          ||
Sbjct  541  TC    542
```

Sequence 757 matched with Sequence 317

Query= Sequence ID - 757 nt: 583
Length=583

SEQ ID NO: 317 nt: 583

ALIGNMENTS

Identities = 583/583 (100%), Gaps = 0/583 (0%)

Query	1	GAACCCTGCGGAGGGACTTCAATCACATCAATGTAGAACTCAGCCTTCTTGAAAGaaaa	60
Sbjct	1	GAACCCTGCGGAGGGACTTCAATCACATCAATGTAGAACTCAGCCTTCTTGAAAGAAAA	60
Query	61	aaaaGAGGCTCCGGGTTGACAAATGGTGGGGTAACAGAAAGGAACTGGCTACCGTTCGGA	120
Sbjct	61	AAAAGAGGCTCCGGGTTGACAAATGGTGGGGTAACAGAAAGGAACTGGCTACCGTTCGGA	120
Query	121	CTATTTGTAGTCATGTACAGAACATGATCAAGGGTGTTAACTGGGCTTCCGTTACAAGA	180
Sbjct	121	CTATTTGTAGTCATGTACAGAACATGATCAAGGGTGTTAACTGGGCTTCCGTTACAAGA	180
Query	181	TGAGGTCTGTGTATGCTCACTTCCCCATCAACGTTGTTATCCAGGAGAATGGGTCTCTTG	240
Sbjct	181	TGAGGTCTGTGTATGCTCACTTCCCCATCAACGTTGTTATCCAGGAGAATGGGTCTCTTG	240
Query	241	TTGAAATCCGAAATTTCTTGGGTGAAAAATACATCCGCAGGGTTCGGATGAGACCAGGTG	300
Sbjct	241	TTGAAATCCGAAATTTCTTGGGTGAAAAATACATCCGCAGGGTTCGGATGAGACCAGGTG	300
Query	301	TTGCTTGTTTCAGTATCTCAAGCCCAGAAAGATGAATTAATCCTTGAAGGAAATGACATTG	360
Sbjct	301	TTGCTTGTTTCAGTATCTCAAGCCCAGAAAGATGAATTAATCCTTGAAGGAAATGACATTG	360
Query	361	AGCTTGTTTCAAATTCAGCGGCTTTGATTTCAGCAAGCCACAACAGTTAAAAACAAGGATA	420
Sbjct	361	AGCTTGTTTCAAATTCAGCGGCTTTGATTTCAGCAAGCCACAACAGTTAAAAACAAGGATA	420
Query	421	TCAGGAAATTTTGGATGGTATCTATGTCTCTGAAAAAGGAACTGTTTCAGCAGGCTGATG	480
Sbjct	421	TCAGGAAATTTTGGATGGTATCTATGTCTCTGAAAAAGGAACTGTTTCAGCAGGCTGATG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AATAAGATCTAAGAGTTACCTGGCTACAGAAAGAAGATGCCAGATGACACTTAAGACCTA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AATAAGATCTAAGAGTTACCTGGCTACAGAAAGAAGATGCCAGATGACACTTAAGACCTA  540

Query  541  CTTGTGATATTTAAATGATGCAATAAAAGACCTATTGATTGG  583
          ||||||||||||||||||||||||||||||||
Sbjct   541  CTTGTGATATTTAAATGATGCAATAAAAGACCTATTGATTGG  583
```

Sequence 758 matched with Sequence 318

Query= Sequence ID - 758 nt: 424
Length=424

SEQ ID NO: 318 nt: 424

ALIGNMENTS

Identities = 424/424 (100%), Gaps = 0/424 (0%)

Query	1	CTTGGCTCCTGTGGAGGCCTGCTGGGAACGGGACTTCTAAAAGGAACTATGTCTGGAAGG	60
Sbjct	1	CTTGGCTCCTGTGGAGGCCTGCTGGGAACGGGACTTCTAAAAGGAACTATGTCTGGAAGG	60
Query	61	CTGTGGTCCAAGGCCATTTTGTGCTGCTATAAGCGGGTCTCCGGAACCAAAGGGAGCAC	120
Sbjct	61	CTGTGGTCCAAGGCCATTTTGTGCTGCTATAAGCGGGTCTCCGGAACCAAAGGGAGCAC	120
Query	121	ACAGCTCTTCTTAAAATTGAAGGTGTTTACGCCCAGATGAAACAGAATTCTATTTGGGC	180
Sbjct	121	ACAGCTCTTCTTAAAATTGAAGGTGTTTACGCCCAGATGAAACAGAATTCTATTTGGGC	180
Query	181	AAGAGATGCGCTTATGTATATAAAGCAAAGAACAACACAGTCACTCCTGGCGGCAAACCA	240
Sbjct	181	AAGAGATGCGCTTATGTATATAAAGCAAAGAACAACACAGTCACTCCTGGCGGCAAACCA	240
Query	241	AACAAAACCAGAGTCATCTGGGGAAAAGTAACTCGGGCCCATGGAAACAGTGGCATGGTT	300
Sbjct	241	AACAAAACCAGAGTCATCTGGGGAAAAGTAACTCGGGCCCATGGAAACAGTGGCATGGTT	300
Query	301	CGTGCCAAATTCCGAAGCAATCTTCTGCTAAGGCCATTGGACACAGAATCCGAGTGATG	360
Sbjct	301	CGTGCCAAATTCCGAAGCAATCTTCTGCTAAGGCCATTGGACACAGAATCCGAGTGATG	360
Query	361	CTGTACCCCTCAAGGATTTAAACTAACGAAAAATCAATAAATAAATGTGGATTTGTGCTC	420
Sbjct	361	CTGTACCCCTCAAGGATTTAAACTAACGAAAAATCAATAAATAAATGTGGATTTGTGCTC	420
Query	421	TTGT 424	
Sbjct	421	TTGT 424	

Sequence 764 matched with Sequence 319

Query= Sequence ID - 764 nt: 626
Length=626

SEQ ID NO: 319 nt: 626

ALIGNMENTS

Identities = 626/626 (100%), Gaps = 0/626 (0%)

Query	1	GAttttttttttttttttttGAGATGGAGTCTTTCTCTGTGCGCCAGGCTGGAGTGCAGTGG	60
Sbjct	1	GATTTTtttttttttttttttttGAGATGGAGTCTTTCTCTGTGCGCCAGGCTGGAGTGCAGTGG	60
Query	61	TGAAATCTCGACTCACTGCAACCTCCGTCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGC	120
Sbjct	61	TGAAATCTCGACTCACTGCAACCTCCGTCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGC	120
Query	121	CTCCTGAGTAGCTGGGATTACAGGCACCAGCCACCACGCCCCGGCTAATTTTGTATTTT	180
Sbjct	121	CTCCTGAGTAGCTGGGATTACAGGCACCAGCCACCACGCCCCGGCTAATTTTGTATTTT	180
Query	181	AGTAGAGACAGGTTTTTACCATGTTGGCTAGGCTGATTTTGAAGTCATGACCCCAAGTGA	240
Sbjct	181	AGTAGAGACAGGTTTTTACCATGTTGGCTAGGCTGATTTTGAAGTCATGACCCCAAGTGA	240
Query	241	TCTGCCCCGCTCGGCCTCCCAAAGTGCTGGAATTACAGGTGTGAGCTACCACTCCCAGCC	300
Sbjct	241	TCTGCCCCGCTCGGCCTCCCAAAGTGCTGGAATTACAGGTGTGAGCTACCACTCCCAGCC	300
Query	301	AATGATTACATTTATAAGGTAAAAATAACTTGTGCCAATCTGTACAAGTGAATTCAGATTT	360
Sbjct	301	AATGATTACATTTATAAGGTAAAAATAACTTGTGCCAATCTGTACAAGTGAATTCAGATTT	360
Query	361	AAAATTTTAATTGTAAAAAGATATCCAGGTGATATTTCTCCCTGAATAATTTAGTTTCCT	420
Sbjct	361	AAAATTTTAATTGTAAAAAGATATCCAGGTGATATTTCTCCCTGAATAATTTAGTTTCCT	420
Query	421	TTTCTATTTCTTGATATAAAAGTACTCAGCATTGAAGTAATTGCTATCTTCACATTTCTT	480
Sbjct	421	TTTCTATTTCTTGATATAAAAGTACTCAGCATTGAAGTAATTGCTATCTTCACATTTCTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCTATTTGAGCTGTCTAAATAAGTAGTCCTACATATTTTCCCCCAACACAAAAAACCCA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CCTATTTGAGCTGTCTAAATAAGTAGTCCTACATATTTTCCCCCAACACAAAAAACCCA  540

Query  541  GAAAAGAATTATTTTATACTGGAtttttttGGTTGTAGCAGGAACCTAAAGNGCCAATT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GAAAAGAATTATTTTATACTGGATTTTTTTGGTTGTAGCAGGAACCTAAAGNGCCAATT  600

Query  601  GTAACATGCATGTTCTTTTTGGCAAA  626
          |||||||||||||||||||
Sbjct   601  GTAACATGCATGTTCTTTTTGGCAAA  626
```

Sequence 766 matched with Sequence 320

Query= Sequence ID 766
Length=618

SEQ ID NO: 320

ALIGNMENTS

Identities = 618/618 (100%), Gaps = 0/618 (0%)

Query	1	GTCCATCCTGCAGGCCACAAGCTCTGGATGAGGAACCTGAGGCAAGTCACCAGCCCCTGA	60
Sbjct	1	GTCCATCCTGCAGGCCACAAGCTCTGGATGAGGAACCTGAGGCAAGTCACCAGCCCCTGA	60
Query	61	TCATTTGCGCTAAAAGAGCAAGGACTAGAGTTCCTGACCTCCAGGCCAGTCCCTGATCCC	120
Sbjct	61	TCATTTGCGCTAAAAGAGCAAGGACTAGAGTTCCTGACCTCCAGGCCAGTCCCTGATCCC	120
Query	121	TGACCTAATGTTATCGCGGAATGATGATATATGTATCTACGGGGGCTGGGGCTGGGCGG	180
Sbjct	121	TGACCTAATGTTATCGCGGAATGATGATATATGTATCTACGGGGGCTGGGGCTGGGCGG	180
Query	181	GCTCCTGCTTCTGGCAGTGGTCCTTCTGTCCGCCTGCCTGTGTTGGCTGCATCGAAGAGT	240
Sbjct	181	GCTCCTGCTTCTGGCAGTGGTCCTTCTGTCCGCCTGCCTGTGTTGGCTGCATCGAAGAGT	240
Query	241	AAAGAGGCTGGAGAGGAGCTGGGCCCAGGGCTCCTCAGAGCAGGAACTCCACTATGCATC	300
Sbjct	241	AAAGAGGCTGGAGAGGAGCTGGGCCCAGGGCTCCTCAGAGCAGGAACTCCACTATGCATC	300
Query	301	TCTGCAGAGGCTGCCAGTGCCAGCAGTGAGGGACCTGACCTCAGGGGCAGAGACAAGAG	360
Sbjct	301	TCTGCAGAGGCTGCCAGTGCCAGCAGTGAGGGACCTGACCTCAGGGGCAGAGACAAGAG	360
Query	361	AGGCACCAAGGAGGATCCAAGAGCTGACTATGCCTGCATTGCTGAGAACAAACCCACCTG	420
Sbjct	361	AGGCACCAAGGAGGATCCAAGAGCTGACTATGCCTGCATTGCTGAGAACAAACCCACCTG	420
Query	421	AGCACCCAGACACCTTCCTCAACCCAGGCGGGTGGACAGGGTCCCCCTGTGGTCCAGCC	480
Sbjct	421	AGCACCCAGACACCTTCCTCAACCCAGGCGGGTGGACAGGGTCCCCCTGTGGTCCAGCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGTAAAAACCATGGTCCCCCACTTCTGTGTCTCAGTCCTCTCAGTCATCTCGAGCCTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGTAAAAACCATGGTCCCCCACTTCTGTGTCTCAGTCCTCTCAGTCATCTCGAGCCTCC  540

Query  541  GTTCAAAATGATCATCATCAAACTTATGTGGCTTTTGGACCTTTGAATAGGGAAttttt  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GTTCAAAATGATCATCATCAAACTTATGTGGCTTTTGGACCTTTGAATAGGGAATTTTT  600

Query  601  taaaattttttAAAAATT  618
          ||||||||||||||||
Sbjct   601  TAAAATTTTTTAAAAATT  618
```

Sequence 768 matched with Sequence 321

Query= Sequence ID 768
Length=596

SEQ ID NO: 321

ALIGNMENTS

Identities = 596/596 (100%), Gaps = 0/596 (0%)

Query	1	CCAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGttt	60
Sbjct	1	CCAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTT	60
Query	61	ttttCTCTTTGAAAGATAGAGATTAATACAACACTTAAAAAATATAGTCAATAGGTTAC	120
Sbjct	61	TTTTCTCTTTGAAAGATAGAGATTAATACAACACTTAAAAAATATAGTCAATAGGTTAC	120
Query	121	TAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGA	180
Sbjct	121	TAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGA	180
Query	181	AAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAACAT	240
Sbjct	181	AAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAACAT	240
Query	241	GACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAATTGAG	300
Sbjct	241	GACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAGAAAATTGAG	300
Query	301	AGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA	360
Sbjct	301	AGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA	360
Query	361	TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTT	420
Sbjct	361	TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTT	420
Query	421	GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAGACCTTGAAATCCATG	480
Sbjct	421	GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAGACCTTGAAATCCATG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA  540
          |||
Sbjct  481  ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA  540

Query  541  ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTT  596
          |||
Sbjct  541  ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTT  596
```

Sequence 773 matched with Sequence 322

Query= Sequence ID 773
Length=534

SEQ ID NO: 322

ALIGNMENTS

Identities = 534/534 (100%), Gaps = 0/534 (0%)

Query	1	GAGGAAAGGGGAGTTAATATTTAGTGGACAGAATTTTCAGTTTTACAGATGAAAAGAGTTC	60
Sbjct	1	GAGGAAAGGGGAGTTAATATTTAGTGGACAGAATTTTCAGTTTTACAGATGAAAAGAGTTC	60
Query	61	TGGAGATAGACGGTGTGATAGTTGCACAGCAGTGTGAATGTGCTCATTGTTACCGAACT	120
Sbjct	61	TGGAGATAGACGGTGTGATAGTTGCACAGCAGTGTGAATGTGCTCATTGTTACCGAACT	120
Query	121	TAAAAATGTTTAAACATAGTATTATGTGATTTTTATTTTGCCACTTaaaaaaaaGAATGA	180
Sbjct	121	TAAAAATGTTTAAACATAGTATTATGTGATTTTTATTTTGCCACTTAAAAAAAAAGAATGA	180
Query	181	AGTACTGATACATGCTACAACATGGGTGAGCTTTAAATACATTCTGCTCAGTGAAATAAG	240
Sbjct	181	AGTACTGATACATGCTACAACATGGGTGAGCTTTAAATACATTCTGCTCAGTGAAATAAG	240
Query	241	CCAGATGCAAAAGATCACATATTATATAATCCACTTATACGAGATACCTAGAATAGGCAA	300
Sbjct	241	CCAGATGCAAAAGATCACATATTATATAATCCACTTATACGAGATACCTAGAATAGGCAA	300
Query	301	ATTCATAGAGACAGAAAGTAGAATAGTGGTTCCCAGGGGCTGGGGACAAGGGGGCAGTGA	360
Sbjct	301	ATTCATAGAGACAGAAAGTAGAATAGTGGTTCCCAGGGGCTGGGGACAAGGGGGCAGTGA	360
Query	361	GAGATTGAGAGTTATTATTAATGCGTACAGAGTTTCAGTTTGGGCTGATAAAAAAGTTCT	420
Sbjct	361	GAGATTGAGAGTTATTATTAATGCGTACAGAGTTTCAGTTTGGGCTGATAAAAAAGTTCT	420
Query	421	GAAGATGGATGGTGTATGATGGTTGTACATCAATGTGAGTGTAATTACCGCCACTGAACTG	480
Sbjct	421	GAAGATGGATGGTGTATGATGGTTGTACATCAATGTGAGTGTAATTACCGCCACTGAACTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCCTTAAAAACGTTTAAAAAGAGTAAATTTTATGTTGNGTATATTTTACCATAAT	534
Sbjct	481	CCCTTAAAAACGTTTAAAAAGAGTAAATTTTATGTTGNGTATATTTTACCATAAT	534

Sequence 776 matched with Sequence 323

Query= Sequence ID 776
Length=556

SEQ ID NO: 323

ALIGNMENTS

Identities = 556/556 (100%), Gaps = 0/556 (0%)

Query	1	tttttttttCATAAGAGGCAAGTACAAGAAAAAGCTTAATTACTTTAACTTCTAAGTAGT	60
Sbjct	1	TTTTTTTTTCATAAGAGGCAAGTACAAGAAAAAGCTTAATTACTTTAACTTCTAAGTAGT	60
Query	61	TTGGAATCTAAATAAATAGGAGTTACCAAATATATGCGCTTCTGTGAATAGTTTTCCCCC	120
Sbjct	61	TTGGAATCTAAATAAATAGGAGTTACCAAATATATGCGCTTCTGTGAATAGTTTTCCCCC	120
Query	121	ACATGTTTATTTATATTTTTGCATCTCATCAAACCTAACAGATTCTAAAGTCTCTGGTGA	180
Sbjct	121	ACATGTTTATTTATATTTTTGCATCTCATCAAACCTAACAGATTCTAAAGTCTCTGGTGA	180
Query	181	TAATGACAATATCTGCTACGGAGAGACTAGCCTGGGGGAAGAGGATCTCCCTGAACAAGG	240
Sbjct	181	TAATGACAATATCTGCTACGGAGAGACTAGCCTGGGGGAAGAGGATCTCCCTGAACAAGG	240
Query	241	ATAGCGGAGTTGCTGCAGCTTTCAAATGAAGCTGGACATTTAGCTGCGGGGGTAGCACCC	300
Sbjct	241	ATAGCGGAGTTGCTGCAGCTTTCAAATGAAGCTGGACATTTAGCTGCGGGGGTAGCACCC	300
Query	301	TTTGATCAAGGCAGCCCAAAGATGAGTTTCAGGGATGGGACTGACAGAAGAGAAAAGTTC	360
Sbjct	301	TTTGATCAAGGCAGCCCAAAGATGAGTTTCAGGGATGGGACTGACAGAAGAGAAAAGTTC	360
Query	361	TTCCCAGCCCTTTCTACTTTTTCTCTTTGTTTCTCAGGCTTCTGGCCGTCTTCAGTTTTTC	420
Sbjct	361	TTCCCAGCCCTTTCTACTTTTTCTCTTTGTTTCTCAGGCTTCTGGCCGTCTTCAGTTTTTC	420
Query	421	ACAAGTTTCACTCTCAACCCTAAACAGTACTTCTGTGAAGTACCCTTTGGCCCCTCGTTT	480
Sbjct	421	ACAAGTTTCACTCTCAACCCTAAACAGTACTTCTGTGAAGTACCCTTTGGCCCCTCGTTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TCAGCTCCTAAACTCACCTGGAAATAGATGTCAATCTAATTTTGGGTCTGACTAGTGCAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TCAGCTCCTAAACTCACCTGGAAATAGATGTCAATCTAATTTTGGGTCTGACTAGTGCAG  540

Query  541  TAGGCATTTTGGTGA  556
          ||||||||||||
Sbjct   541  TAGGCATTTTGGTGA  556
```

Sequence 782 matched with Sequence 324

Query= Sequence ID 782
Length=382

SEQ ID NO: 324

ALIGNMENTS

Identities = 382/382 (100%), Gaps = 0/382 (0%)

Query	1	CTCACACAGAACAAAAATGAATGAGTGTGGCTGTGTGCCACTATCACTGTGTCTACAAAA	60
Sbjct	1	CTCACACAGAACAAAAATGAATGAGTGTGGCTGTGTGCCACTATCACTGTGTCTACAAAA	60
Query	61	ACAGCCAGTGGGCCTGATTTGGCCCTTGGCTGCAGTGCGCCCGTCTCTGTTTTGAGGAA	120
Sbjct	61	ACAGCCAGTGGGCCTGATTTGGCCCTTGGCTGCAGTGCGCCCGTCTCTGTTTTGAGGAA	120
Query	121	TAAAATCGCATCATTTTCATATGGCTAATGCAAttttttCCCATCTGGAAGCAACATCTG	180
Sbjct	121	TAAAATCGCATCATTTTCATATGGCTAATGCAATTTTTTCCCATCTGGAAGCAACATCTG	180
Query	181	ATTGGACTCATCTTGTATGGTGCTTGTTACAGTCTCTGTAAATGGGAGAGGGTCCGAGAA	240
Sbjct	181	ATTGGACTCATCTTGTATGGTGCTTGTTACAGTCTCTGTAAATGGGAGAGGGTCCGAGAA	240
Query	241	TAGCTCTTCCTGTTTTTCATCAGGACTGTTTTTAGGGATGGCAAAGAAGTCAGTGTGTCCA	300
Sbjct	241	TAGCTCTTCCTGTTTTTCATCAGGACTGTTTTTAGGGATGGCAAAGAAGTCAGTGTGTCCA	300
Query	301	GCCTGTGTCCTCCTCACCACGTGGCTGATTCTGAATCTGCATGTGCANCACTGCCGTT	360
Sbjct	301	GCCTGTGTCCTCCTCACCACGTGGCTGATTCTGAATCTGCATGTGCANCACTGCCGTT	360
Query	361	GTCTGGGGCATGATCTGTGTGA	382
Sbjct	361	GTCTGGGGCATGATCTGTGTGA	382

Sequence 785 matched with Sequence 325

Query= Sequence ID - 785 nt: 556
Length=556

SEQ ID NO: 325 nt: 556

ALIGNMENTS

Identities = 556/556 (100%), Gaps = 0/556 (0%)

Query	1	CTTTTCTCTGGGTATAGATTACCTAGCACCTATCTCATTATATTGAATTTTCCAGCAT	60
Sbjct	1	CTTTTCTCTGGGTATAGATTACCTAGCACCTATCTCATTATATTGAATTTTCCAGCAT	60
Query	61	ATTTAAATAAACTATTAATTAGTCACACTATTTCTTAAAAGTCACACTATCAACTAATCG	120
Sbjct	61	ATTTAAATAAACTATTAATTAGTCACACTATTTCTTAAAAGTCACACTATCAACTAATCG	120
Query	121	TGACCGCAATTATCTAGGGGTGATAATCTGCTGAGTCTACTCTTTAAATACACTGGGACC	180
Sbjct	121	TGACCGCAATTATCTAGGGGTGATAATCTGCTGAGTCTACTCTTTAAATACACTGGGACC	180
Query	181	CAGCATATTGAGTTATATTGGCACAGAACTTCACTCTGGGTATAGATTACCTAGTAC	240
Sbjct	181	CAGCATATTGAGTTATATTGGCACAGAACTTCACTCTGGGTATAGATTACCTAGTAC	240
Query	241	CTTGCCGGCAGGATCCTATTATTCATGGTTGTACAAGCAAGGTTCAAGGAAGAGGCTGGC	300
Sbjct	241	CTTGCCGGCAGGATCCTATTATTCATGGTTGTACAAGCAAGGTTCAAGGAAGAGGCTGGC	300
Query	301	ACAGAGAAGGTACCTGGTAACTGTTGTTTGAGGCTGAATTCAGCTCAACTCAGCTCCAGT	360
Sbjct	301	ACAGAGAAGGTACCTGGTAACTGTTGTTTGAGGCTGAATTCAGCTCAACTCAGCTCCAGT	360
Query	361	AGAGATGGTGTCCCTTCTCTACCGTGGTGAGATAGTGTGCAGTCCCTTCCTAAGGGCTG	420
Sbjct	361	AGAGATGGTGTCCCTTCTCTACCGTGGTGAGATAGTGTGCAGTCCCTTCCTAAGGGCTG	420
Query	421	TTACCCACCGCAATAGGACTTGTGAGCTTCAACTTTTAAATTTCTCTGCTCCCGCTGGGA	480
Sbjct	421	TTACCCACCGCAATAGGACTTGTGAGCTTCAACTTTTAAATTTCTCTGCTCCCGCTGGGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCCACCCGCTTCAAAAATCATCATGGNGGNTTTAGCACCAATTTAGTAAACACAAACTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCCACCCGCTTCAAAAATCATCATGGNGGNTTTAGCACCAATTTAGTAAACACAAACTGT  540

Query  541  CTGAAATATTTTGGAT  556
          ||||||||||||
Sbjct  541  CTGAAATATTTTGGAT  556
```

Sequence 796 matched with Sequence 326

Query= Sequence ID 796
Length=716

SEQ ID NO: 326

ALIGNMENTS

Identities = 716/716 (100%), Gaps = 0/716 (0%)

Query	1	GAACATTCAAGATAGTGAGAGGAAGAAAAAGATATGGCTGTACGGGACCGAGGTCTCTTC	60
Sbjct	1	GAACATTCAAGATAGTGAGAGGAAGAAAAAGATATGGCTGTACGGGACCGAGGTCTCTTC	60
Query	61	TATTATCGCCTCCTCTTAGTTGGCATTGATGAAGTTAAGCGGATTCTGTGTAGCCCTAAA	120
Sbjct	61	TATTATCGCCTCCTCTTAGTTGGCATTGATGAAGTTAAGCGGATTCTGTGTAGCCCTAAA	120
Query	121	TCTGACCCTACTCTTGGACTTTTGGAGGATCCGGCAGAAAGACCTGTGAATAGCTGGGCC	180
Sbjct	121	TCTGACCCTACTCTTGGACTTTTGGAGGATCCGGCAGAAAGACCTGTGAATAGCTGGGCC	180
Query	181	TCAGACTTCAACACACTGGTGCCAGTGTATGGCAAAGCCCACTGGGCAACTATCTCTAAA	240
Sbjct	181	TCAGACTTCAACACACTGGTGCCAGTGTATGGCAAAGCCCACTGGGCAACTATCTCTAAA	240
Query	241	TGCCAGGGGGCAGAGCGTTGTGACCCAGAGCTTCCTAAAACTTCATCCTTTGCCGCATCA	300
Sbjct	241	TGCCAGGGGGCAGAGCGTTGTGACCCAGAGCTTCCTAAAACTTCATCCTTTGCCGCATCA	300
Query	301	GGACCCTTGATTCTGAAGAGAACAAGGAGAGGGTACAAGAACTCCCTGATTCTGGAGCC	360
Sbjct	301	GGACCCTTGATTCTGAAGAGAACAAGGAGAGGGTACAAGAACTCCCTGATTCTGGAGCC	360
Query	361	CTCATGCTAGTCCCCAATCGCCAGCTTACTGCTGATTATTTTGAGAAAACTTGGCTTAGC	420
Sbjct	361	CTCATGCTAGTCCCCAATCGCCAGCTTACTGCTGATTATTTTGAGAAAACTTGGCTTAGC	420
Query	421	CTTAAAGTTGCTCATCAGCAAGTGTTGCCTTGGCGGGGAGAATTCCATCCTGACACCCTC	480
Sbjct	421	CTTAAAGTTGCTCATCAGCAAGTGTTGCCTTGGCGGGGAGAATTCCATCCTGACACCCTC	480

PATENT SEQUENCE ALIGNMENT

Query	481	CAGATGGCTCTTCAAGTAGTGAACATCCAGACCATCGCAATGAGTAGGGCTGGGTCTCGG	540
Sbjct	481	CAGATGGCTCTTCAAGTAGTGAACATCCAGACCATCGCAATGAGTAGGGCTGGGTCTCGG	540
Query	541	CCATGGAAAGCATACCTCAGTGCTCANGATGATACTGGCTGTCTGTTCTTAACAGAACTG	600
Sbjct	541	CCATGGAAAGCATACCTCAGTGCTCANGATGATACTGGCTGTCTGTTCTTAACAGAACTG	600
Query	601	CTATTGGAGCCTGGAAACTCAGAATGCAGATCTTTTGTGAACAAAATGAAGCAAGAACCG	660
Sbjct	601	CTATTGGAGCCTGGAAACTCAGAATGCAGATCTTTTGTGAACAAAATGAAGCAAGAACCG	660
Query	661	GAGACNCTGAATAGTTTTATTCTGTATTAAAAACTGNGATTGGAACAATTGAAGA	716
Sbjct	661	GAGACNCTGAATAGTTTTATTCTGTATTAAAAACTGNGATTGGAACAATTGAAGA	716

Sequence 801 matched with Sequence 327

Query= Sequence ID 801
Length=664

SEQ ID NO: 327

ALIGNMENTS

Identities = 664/664 (100%), Gaps = 0/664 (0%)

Query	1	CCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGC	60
Sbjct	1	CCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGC	60
Query	61	GATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTAT	120
Sbjct	61	GATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTAT	120
Query	121	AACCAAGCATAATATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAGA	180
Sbjct	121	AACCAAGCATAATATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAGA	180
Query	181	AATGAGGATTCTGACCTTGACTTTGATATCAGCAAATTGGAACAGCAGAGCAAGGTGCAA	240
Sbjct	181	AATGAGGATTCTGACCTTGACTTTGATATCAGCAAATTGGAACAGCAGAGCAAGGTGCAA	240
Query	241	AACACAGGACATGGAAAACCAAGAGAAAAGTCCATAATAGACGAGAAATTCTTCCAAGTC	300
Sbjct	241	AACACAGGACATGGAAAACCAAGAGAAAAGTCCATAATAGACGAGAAATTCTTCCAAGTC	300
Query	301	TCTGAAATGGAGGCTTATTTAGAAAACAGAGAAAAGAAGAGGAACGAAAAGATGATAAT	360
Sbjct	301	TCTGAAATGGAGGCTTATTTAGAAAACAGAGAAAAGAAGAGGAACGAAAAGATGATAAT	360
Query	361	GATGATGAGTCAGGTAAAAGTTCCAGAAATGTGAACAACAAAGAttttttGATCCAGTT	420
Sbjct	361	GATGATGAGTCAGGTAAAAGTTCCAGAAATGTGAACAACAAAGATTTTTTGGATCCAGTT	420
Query	421	GAAAGTGATGAAGACATAGCAAGTGATCATGATGATGAGCTGGGTTCAAACAAGATGATG	480
Sbjct	421	GAAAGTGATGAAGACATAGCAAGTGATCATGATGATGAGCTGGGTTCAAACAAGATGATG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAATTGCTGAAGAAGAAGCAGAAGAAGGAAGCATTCTGAAATATGAATGaaaaaaTTA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AAATTGCTGAAGAAGAAGCAGAAGAAGGAAGCATTCTGAAATATGAATGAAAAAAATTA  540

Query  541  CATCTTTAGAAAAAGAGTTATTAGAAAAAAGCCTTGGCAGCCGTCNGGGGAAGTGACGC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CATCTTTAGAAAAAGAGTTATTAGAAAAAAGCCTTGGCAGCCGTCNGGGGAAGTGACGC  600

Query  601  ACAGAAGAGACCAGAGAATAGCTTCCTGGANGAGACCCTGCACTTTACCCATGCTGCTGG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  ACAGAAGAGACCAGAGAATAGCTTCCTGGANGAGACCCTGCACTTTACCCATGCTGCTGG  660

Query  661  ATGG  664
          ||||
Sbjct   661  ATGG  664
```

Sequence 808 matched with Sequence 328

Query= Sequence ID - 808 nt: 641
Length=641

SEQ ID NO: 328 nt: 641

ALIGNMENTS

Identities = 641/641 (100%), Gaps = 0/641 (0%)

Query	1	CCGGGTTTTAGTATTTAACCAAGAGCCTTTTAAATATTGAAAACCCATAGTTCAGAAAAT	60
Sbjct	1	CCGGGTTTTAGTATTTAACCAAGAGCCTTTTAAATATTGAAAACCCATAGTTCAGAAAAT	60
Query	61	GTTAGTATTGCTGCCCTTCTTCACATAAAAttttttttAAATTATACTATTATTTTGCTT	120
Sbjct	61	GTTAGTATTGCTGCCCTTCTTCACATAAAATTTTTTTTTTAAATTATACTATTATTTTGCTT	120
Query	121	AATTTTATATTGGGTAAAAACAACCTTCAAGAAGGTAACTAGGAAAGAAGACctttttg	180
Sbjct	121	AATTTTATATTGGGTAAAAACAACCTTCAAGAAGGTAACTAGGAAAGAAGACCTTTTTG	180
Query	181	ttttatttttACTATTTATATATAGAAGACAAATCAGCATTTGGTGATAGTTTACATGA	240
Sbjct	181	TTTTATTTTACTATTTATATATAGAAGACAAATCAGCATTTGGTGATAGTTTACATGA	240
Query	241	CCAGTTATCAAACGGTCATAGTATGAAGTGTGCAGTTGTTCAATTATTAGTAAATTATGTT	300
Sbjct	241	CCAGTTATCAAACGGTCATAGTATGAAGTGTGCAGTTGTTCAATTATTAGTAAATTATGTT	300
Query	301	TGATTTTTAACTATTTAGTACTAATAGTTGAGATGAAAACCTGAAGAAAAATGCCAATGT	360
Sbjct	301	TGATTTTTAACTATTTAGTACTAATAGTTGAGATGAAAACCTGAAGAAAAATGCCAATGT	360
Query	361	GACGTTTGTGTATAGCTAGCCTTAAAAAACTTCCCATGTTTTTAGGTGACTTTTTTCCCC	420
Sbjct	361	GACGTTTGTGTATAGCTAGCCTTAAAAAACTTCCCATGTTTTTAGGTGACTTTTTTCCCC	420
Query	421	CTCTTAGTACTCTGGAGAAACAATGAAGATGGGCCATCTCAATTCCAGATGTAAACAAAA	480
Sbjct	421	CTCTTAGTACTCTGGAGAAACAATGAAGATGGGCCATCTCAATTCCAGATGTAAACAAAA	480

.....

Sequence 814 matched with Sequence 329

Query= Sequence ID - 814 nt: 132
Length=132

SEQ ID NO: 329 nt: 132

ALIGNMENTS

Identities = 132/132 (100%), Gaps = 0/132 (0%)

Query	1	GTAAAGTGATACATTTTATACCAAATGTGTTTAttttttGTGCAAGTAATCCTTAAA	60
Sbjct	1	GTAAAGTGATACATTTTATACCAAATGTGTTTATTTTGTGCAAGTAATCCTTAAA	60
Query	61	ATTGCAATTGTATTAGGTGTtaaaataaagtttttaaaaaattaaaaaaaaaaaaaaaa	120
Sbjct	61	ATTGCAATTGTATTAGGTGTAAAAATAAAGTTTTTAAAAATTAAAAAAAAAAAAAAAA	120
Query	121	aaaaaaaaaaaa 132	
Sbjct	121	AAAAAAAAAAAA 132	

Sequence 817 matched with Sequence 330

Query= Sequence ID 817
Length=666

SEQ ID NO: 330

ALIGNMENTS

Identities = 666/666 (100%), Gaps = 0/666 (0%)

Query	1	GACAACCTTAGCCAAACCATTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGG	60
Sbjct	1	GACAACCTTAGCCAAACCATTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGG	60
Query	61	CGCAATAGATATAGTACCGTAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCA	120
Sbjct	61	CGCAATAGATATAGTACCGTAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCA	120
Query	121	AGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAACTAGAAATAAAGTAACTTTGCAAGGAGAG	180
Sbjct	121	AGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAACTAGAAATAAAGTAACTTTGCAAGGAGAG	180
Query	181	CCAAAGCTAAGACCCCGAAACAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCC	240
Sbjct	181	CCAAAGCTAAGACCCCGAAACAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCC	240
Query	241	GTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTG	300
Sbjct	241	GTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTG	300
Query	301	GTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCC	360
Sbjct	301	GTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCC	360
Query	361	TCTAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAG	420
Sbjct	361	TCTAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAG	420
Query	421	GAAAAACCTTGTAAGAGAGTAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCA	480
Sbjct	421	GAAAAACCTTGTAAGAGAGTAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTaaaaaaaTCCCAAACATATAAC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAAATCCCAAACATATAAC  540

Query  541  TGAACCTCTCACACCCAATTGGACCAATCTATCACCTATAGAAGACTAATGTTAGTATA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TGAACCTCTCACACCCAATTGGACCAATCTATCACCTATAGAAGACTAATGTTAGTATA  600

Query  601  AGTAACATGAAAACATTCTTCTNCGCATAAGCCTGCGTCAGATTA AAAACACTGAACTGAC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  AGTAACATGAAAACATTCTTCTNCGCATAAGCCTGCGTCAGATTA AAAACACTGAACTGAC  660

Query  661  AATTAA  666
          |||||
Sbjct   661  AATTAA  666
```

Sequence 821 matched with Sequence 331

Query= Sequence ID - 821 nt: 370
Length=370

SEQ ID NO: 331 nt: 370

ALIGNMENTS

Identities = 370/370 (100%), Gaps = 0/370 (0%)

Query	1	AAAGAGCTCCCAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAATGGAATATCATCCT	60
Sbjct	1	AAAGAGCTCCCAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAATGGAATATCATCCT	60
Query	61	GATTTANAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAAT	120
Sbjct	61	GATTTANAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAAT	120
Query	121	ACCAGGATAGCTGTTGTTTCANAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTC	180
Sbjct	121	ACCAGGATAGCTGTTGTTTCANAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTC	180
Query	181	ATTGCTGTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGT	240
Sbjct	181	ATTGCTGTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGT	240
Query	241	ACCATGGCTGGTTTCAAAGCTGTGGAATTCAAAGGATAAATTAATGAAGAAAACAAGCGG	300
Sbjct	241	ACCATGGCTGGTTTCAAAGCTGTGGAATTCAAAGGATAAATTAATGAAGAAAACAAGCGG	300
Query	301	AGCTGAAGAAGAAAGTACAATATGGTGCTGTCTTCCTAATGAAATAAATTCACTAAATGG	360
Sbjct	301	AGCTGAAGAAGAAAGTACAATATGGTGCTGTCTTCCTAATGAAATAAATTCACTAAATGG	360
Query	361	ACATTAAAAA 370	
Sbjct	361	ACATTAAAAA 370	

Sequence 825 matched with Sequence 332

Query= Sequence ID 825
Length=741

SEQ ID NO: 332

ALIGNMENTS

Identities = 741/741 (100%), Gaps = 0/741 (0%)

Query	1	AGACTCGAGCAAGCTTATGCATGCATGCGGCCGCAATTCGAGCTCGGCCACTTGGCCAAT	60
Sbjct	1	AGACTCGAGCAAGCTTATGCATGCATGCGGCCGCAATTCGAGCTCGGCCACTTGGCCAAT	60
Query	61	TCGCCCTATAGTGAGTCGTATTACAATTCAGTGGCCGTCGTTTTACAACGTCGTGACTGG	120
Sbjct	61	TCGCCCTATAGTGAGTCGTATTACAATTCAGTGGCCGTCGTTTTACAACGTCGTGACTGG	120
Query	121	GAAAACCCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTCGCCAGCTGG	180
Sbjct	121	GAAAACCCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTCGCCAGCTGG	180
Query	181	CGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGC	240
Sbjct	181	CGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGC	240
Query	241	GAATGGAAATTGTAAGCGTTAATATTTTGTAAAATTTCGCGTTAAATTTTGTAAATCA	300
Sbjct	241	GAATGGAAATTGTAAGCGTTAATATTTTGTAAAATTTCGCGTTAAATTTTGTAAATCA	300
Query	301	GCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGA	360
Sbjct	301	GCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGA	360
Query	361	CCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGG	420
Sbjct	361	CCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGG	420
Query	421	ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCAT	480
Sbjct	421	ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAG  540

Query  541  GGAGCCCCCGATTTTAAAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GGAGCCCCCGATTTTAAAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGA  600

Query  601  AAAAAGCCAAANGGAGCCGGCGCTAGGGCCTGGCAAGTGTACGGGCACGCTGCGCGTAAC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  AAAAAGCCAAANGGAGCCGGCGCTAGGGCCTGGCAAGTGTACGGGCACGCTGCGCGTAAC  660

Query  661  CACCCACACCCCGCCGNGCTTAATGCCCCNTTCAGGGCGCGTNCTGATGCCGNATTTTNT  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  CACCCACACCCCGCCGNGCTTAATGCCCCNTTCAGGGCGCGTNCTGATGCCGNATTTTNT  720

Query  721  CTTACNCATNTGTGCNGGNTT  741
          ||||||||||||||||
Sbjct   721  CTTACNCATNTGTGCNGGNTT  741
```

Blast comparison trimmed “NGGNTT” from the 3’ end of both sequences and reported 735 identities. The report has been manually corrected for this. “NGGNTT” has been appended to both sequences and identity count has been increased to 741.

Sequence 833 matched with Sequence 333

Query= Sequence ID 833
Length=719

SEQ ID NO: 333

ALIGNMENTS

Identities = 719/719 (100%), Gaps = 0/719 (0%)

Query	1	TAAAATAATGGCaaaaaacaacaaaaaaCAAGTTCTCTAAACAGAAAGGAAATTACTAA	60
Sbjct	1	TAAAATAATGGCAAAAAACAAACAAAAACAAGTTCTCTAAACAGAAAGGAAATTACTAA	60
Query	61	AGAAGGAATCTTGAAATAACAGGAAAGAGGAAATACCACAGTAGGCAACATTATGGGTAA	120
Sbjct	61	AGAAGGAATCTTGAAATAACAGGAAAGAGGAAATACCACAGTAGGCAACATTATGGGTAA	120
Query	121	ATAAACAGACTTTCCTTCTTTAGTTTCCTAAATATGTTTGATGATTAATGCAAAAATT	180
Sbjct	121	ATAAACAGACTTTCCTTCTTTAGTTTCCTAAATATGTTTGATGATTAATGCAAAAATT	180
Query	181	ACAATATTTTCTTATGTAGCACTAAAGGTATGTAGAGAAAATATTTAAGATAATTGTACT	240
Sbjct	181	ACAATATTTTCTTATGTAGCACTAAAGGTATGTAGAGAAAATATTTAAGATAATTGTACT	240
Query	241	GTAAGCGGGAGATGACAGTGACATAAAGGCAACGTTTTTATACTTCACTCAAACTTTATG	300
Sbjct	241	GTAAGCGGGAGATGACAGTGACATAAAGGCAACGTTTTTATACTTCACTCAAACTTTATG	300
Query	301	TATTAATGTAATCCATAAAGCAACCAAAAAAGCTATACTAAGTACATTCAAAAACACAAT	360
Sbjct	301	TATTAATGTAATCCATAAAGCAACCAAAAAAGCTATACTAAGTACATTCAAAAACACAAT	360
Query	361	AGATAAACCAAACAAAATTCTAAAGGATGTACAAGTAACCCACTGGAAGCTGCaaaaaat	420
Sbjct	361	AGATAAACCAAACAAAATTCTAAAGGATGTACAAGTAACCCACTGGAAGCTGCAAAAAAT	420
Query	421	gtaaacagaaactaaaaacagagaataaatgaaaaattaaaaacgaaatGGCAGACTTAG	480
Sbjct	421	GTAAACAGAACTAAAAACAGAGAATAAATGAAAAATTAAAAACGAAATGGCAGACTTAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCCCTAATATACAAATTATCACATTAAATATAAATGGTCTAAATACACCAACTGTAAGAC	540
Sbjct	481	GCCCTAATATACAAATTATCACATTAAATATAAATGGTCTAAATACACCAACTGTAAGAC	540
Query	541	AGAGATTAGCAAAGTCGATTTAAAAACATGACTCAACTACGTGCTGTCTACAAGAAACTC	600
Sbjct	541	AGAGATTAGCAAAGTCGATTTAAAAACATGACTCAACTACGTGCTGTCTACAAGAAACTC	600
Query	601	ACTTCAAATATACCAAGATAGGAAGGTTGAAAGTAAAACGATGGAAAAAGATGTATCATG	660
Sbjct	601	ACTTCAAATATACCAAGATAGGAAGGTTGAAAGTAAAACGATGGAAAAAGATGTATCATG	660
Query	661	TGAACATTAATCAAAGGAAAGCAGGGGTGGCTATATTAACATCAGGTAAAAATAAACTTT	719
Sbjct	661	TGAACATTAATCAAAGGAAAGCAGGGGTGGCTATATTAACATCAGGTAAAAATAAACTTT	719

Sequence 837 matched with Sequence 334

Query= Sequence ID - 837 nt: 603
Length=603

SEQ ID NO: 334 nt: 603

ALIGNMENTS

Identities = 603/603 (100%), Gaps = 0/603 (0%)

Query	1	TGAGGNTGGTCATGATGCANAAGCTACTCAAATGCAGTCGGCTTGTCTGGCTCTTGCCC	60
Sbjct	1	TGAGGNTGGTCATGATGCANAAGCTACTCAAATGCAGTCGGCTTGTCTGGCTCTTGCCC	60
Query	61	TCATCCTGGTTCTGGAATCCTCAGTTCAAGGTTATCCTACGCGGAGAGCCAGGTACCAAT	120
Sbjct	61	TCATCCTGGTTCTGGAATCCTCAGTTCAAGGTTATCCTACGCGGAGAGCCAGGTACCAAT	120
Query	121	GGGTGCGCTGCAATCCAGACAGTAATTCTGCAAAGTGCCTTGAAGAAAAAGGACCAATGT	180
Sbjct	121	GGGTGCGCTGCAATCCAGACAGTAATTCTGCAAAGTGCCTTGAAGAAAAAGGACCAATGT	180
Query	181	TCGAACTACTTCCAGGTGAATCCAACAAGATCCCCGTCTGAGGACTGACCTTTTTTCCAA	240
Sbjct	181	TCGAACTACTTCCAGGTGAATCCAACAAGATCCCCGTCTGAGGACTGACCTTTTTTCCAA	240
Query	241	AGACGAGAATCCAGGACTTGAATCGTATCTTCCCACTTTCTGAGGACTACTCTGGATCAG	300
Sbjct	241	AGACGAGAATCCAGGACTTGAATCGTATCTTCCCACTTTCTGAGGACTACTCTGGATCAG	300
Query	301	GCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTGGGAGTGGCTTCCTAACGGAAATGG	360
Sbjct	301	GCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTGGGAGTGGCTTCCTAACGGAAATGG	360
Query	361	AACAGGATTACCAACTAGTAGACGAAAGTGATGCTTTCCATGACAACCTTAGGTCTCTTG	420
Sbjct	361	AACAGGATTACCAACTAGTAGACGAAAGTGATGCTTTCCATGACAACCTTAGGTCTCTTG	420
Query	421	ACAGGAATCTGCCCTCAGACAGCCAGGACTTGGGTCAACATGGATTAGAAGAGGATTTTA	480
Sbjct	421	ACAGGAATCTGCCCTCAGACAGCCAGGACTTGGGTCAACATGGATTAGAAGAGGATTTTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TGTTATAAAAGAGGATTTTCCACCTTGACACCAGGCAATGTAGTTAGCATATTTTATGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TGTTATAAAAGAGGATTTTCCACCTTGACACCAGGCAATGTAGTTAGCATATTTTATGT  540

Query  541  ACCATGGNTATATGATTAATCTTGGGACAAAGAATTTTATAGAAATTTTAAACATCTGA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ACCATGGNTATATGATTAATCTTGGGACAAAGAATTTTATAGAAATTTTAAACATCTGA  600

Query  601  AAA  603
          |||
Sbjct   601  AAA  603
```

Sequence 839 matched with Sequence 335

Query= Sequence ID - 839 nt: 71
Length=71

SEQ ID NO: 335 nt: 71

ALIGNMENTS

Identities = 71/71 (100%), Gaps = 0/71 (0%)

```
Query 1  ATTTATCTAATATTTGGTTTAATAAAATGTGAATAATGaaaaaaaaaaaaaaaaaaaaa 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  ATTTATCTAATATTTGGTTTAATAAAATGTGAATAATGAAAAAAAAAAAAAAAAAAAAA 60

Query 61  aaaaaaaaaa 71
          |||||||||
Sbjct 61  AAAAAAAAAA 71
```

Sequence 849 matched with Sequence 336

Query= Sequence ID - 849 nt: 622
Length=622

SEQ ID NO: 336 nt: 622

ALIGNMENTS

Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query	1	ttttttttttattttttGAGAATGGAGTCTTGCTCTGCCGTCCAGGCTAGAGTTCAGTGGT	60
Sbjct	1	TTTTTTTTTATTTTTTGAGAATGGAGTCTTGCTCTGCCGTCCAGGCTAGAGTTCAGTGGT	60
Query	61	GCGATCTCAGCTCACTGCCACCTCACCTCCTAGGTTCCAGAGATTCTTGCTTCAGCCT	120
Sbjct	61	GCGATCTCAGCTCACTGCCACCTCACCTCCTAGGTTCCAGAGATTCTTGCTTCAGCCT	120
Query	121	CCTCAGTAGTTGAGAATACAGGAACACGCCACCACGCCTAGCTAATTTTGTATTTT	180
Sbjct	121	CCTCAGTAGTTGAGAATACAGGAACACGCCACCACGCCTAGCTAATTTTGTATTTT	180
Query	181	TAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACCTCGGCCTAAGTGACCC	240
Sbjct	181	TAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACCTCGGCCTAAGTGACCC	240
Query	241	ACCTGCCTCAGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGTCATTGTCCCCAGCCGGA	300
Sbjct	241	ACCTGCCTCAGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGTCATTGTCCCCAGCCGGA	300
Query	301	TGTTTTTCATCTTGATTTGCCTTAGTTTCTAAATCTCATCCTCTCCATTTTCTCCTGTTAG	360
Sbjct	301	TGTTTTTCATCTTGATTTGCCTTAGTTTCTAAATCTCATCCTCTCCATTTTCTCCTGTTAG	360
Query	361	TAGTCACAGAGAACCAAATTCTGTCAAGTTATGAACTAAAGTCTCTCTCCACAAGTCT	420
Sbjct	361	TAGTCACAGAGAACCAAATTCTGTCAAGTTATGAACTAAAGTCTCTCTCCACAAGTCT	420
Query	421	TCCTGTGTTCTGCCTCAAGTGAACCTGAAAGAACATCAGTTTGTGGGAAGGTTGAAGACC	480
Sbjct	421	TCCTGTGTTCTGCCTCAAGTGAACCTGAAAGAACATCAGTTTGTGGGAAGGTTGAAGACC	480

PATENT SEQUENCE ALIGNMENT

Query	481	GAATGATCTGCTGGGAAATCACTGAGGCATTGCCATTCTCTTGAGGAATTCATTTTCAT	540
Sbjct	481	GAATGATCTGCTGGGAAATCACTGAGGCATTGCCATTCTCTTGAGGAATTCATTTTCAT	540
Query	541	CGAAGTTTCGGTTTATATCCCTTTCTTGGTGAGTACTATTGCTGTTATGTAAATTAAATG	600
Sbjct	541	CGAAGTTTCGGTTTATATCCCTTTCTTGGTGAGTACTATTGCTGTTATGTAAATTAAATG	600
Query	601	AGTCGTCATCCTTCTTNTGAGC	622
Sbjct	601	AGTCGTCATCCTTCTTNTGAGC	622

Sequence 860 matched with Sequence 337

Query= Sequence ID - 860 nt: 501
Length=501

SEQ ID NO: 337 nt: 501

ALIGNMENTS

Identities = 501/501 (100%), Gaps = 0/501 (0%)

Query	1	GTGAAATCACTTTCATGGATTATTAATGGATTTAAGAGGGCATCAATCAGCTCAACTCAA	60
Sbjct	1	GTGAAATCACTTTCATGGATTATTAATGGATTTAAGAGGGCATCAATCAGCTCAACTCAA	60
Query	61	GATTTTCATAATCATTTTTAGTATTTAGATTGTGCCTCAAAGTTGTAGTACCTCACAATAC	120
Sbjct	61	GATTTTCATAATCATTTTTAGTATTTAGATTGTGCCTCAAAGTTGTAGTACCTCACAATAC	120
Query	121	CTCCACTGGTTTCCTGTTGTAAAAACCTTCAGTGAGTTTGACCATTGTGCTCTTGGCTCT	180
Sbjct	121	CTCCACTGGTTTCCTGTTGTAAAAACCTTCAGTGAGTTTGACCATTGTGCTCTTGGCTCT	180
Query	181	TGGGCTGGAGTACCGTGGTGAGGGAGTAAACACTAGAAAGTCTTTAGTACAAAACTGCTCT	240
Sbjct	181	TGGGCTGGAGTACCGTGGTGAGGGAGTAAACACTAGAAAGTCTTTAGTACAAAACTGCTCT	240
Query	241	AGGGACACCTGGTGATTCCCTACACAAGTGATGTTTATATTTCTCATAAAGAGTCTTCCCT	300
Sbjct	241	AGGGACACCTGGTGATTCCCTACACAAGTGATGTTTATATTTCTCATAAAGAGTCTTCCCT	300
Query	301	ATCCCAAGGTCTTCATGATGCCAGTAGCCATATATGATAAATTATGTTTCAGTGATAACTT	360
Sbjct	301	ATCCCAAGGTCTTCATGATGCCAGTAGCCATATATGATAAATTATGTTTCAGTGATAACTT	360
Query	361	AGTTATCAGAAATCAGCTCAGTGGTCTTCCCCGCCATGATTCACATTTGATGAGTTTTTA	420
Sbjct	361	AGTTATCAGAAATCAGCTCAGTGGTCTTCCCCGCCATGATTCACATTTGATGAGTTTTTA	420
Query	421	AAAATCAAAGTGATTTTGAAAAATCTCTAATGGCTCAGAAAATAAAAAACATCCAGTTTGTG	480
Sbjct	421	AAAATCAAAGTGATTTTGAAAAATCTCTAATGGCTCAGAAAATAAAAAACATCCAGTTTGTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GATGACTATATTTAGATTCT	501
Sbjct	481	GATGACTATATTTAGATTCT	501

Sequence 864 matched with Sequence 338

Query= Sequence ID 864
Length=630

SEQ ID NO: 338

ALIGNMENTS

Identities = 630/630 (100%), Gaps = 0/630 (0%)

Query	1	TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC	60
Sbjct	1	TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC	60
Query	61	ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG	120
Sbjct	61	ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG	120
Query	121	ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC	180
Sbjct	121	ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC	180
Query	181	ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA	240
Sbjct	181	ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA	240
Query	241	TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAATGCATACTAATATTTTC	300
Sbjct	241	TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAATGCATACTAATATTTTC	300
Query	301	AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG	360
Sbjct	301	AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG	360
Query	361	AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTCAAGCAATGCATAAGCA	420
Sbjct	361	AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTCAAGCAATGCATAAGCA	420
Query	421	AGAGAGAATATGACATAAGAGGACCATTCTACATTAGCCAttttttttCACAAAGATACC	480
Sbjct	421	AGAGAGAATATGACATAAGAGGACCATTCTACATTAGCCATTTTTTTTTCACAAAGATACC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TATGTGAATACAGGGCACCTGGGAGGGTAAGTGGAGGACTATTTCTAACTATATTTATAA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TATGTGAATACAGGGCACCTGGGAGGGTAAGTGGAGGACTATTTCTAACTATATTTATAA  540

Query  541  GCACATACTGATATTGGTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GCACATACTGATATTGGTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA  600

Query  601  CAATGTGTAAGGAGATCAGGAATTCATTAG  630
          |||||||||||||||||||||||||
Sbjct   601  CAATGTGTAAGGAGATCAGGAATTCATTAG  630
```

Sequence 865 matched with Sequence 339

Query= Sequence ID - 865 nt: 122
Length=122

SEQ ID NO: 339 nt: 122

ALIGNMENTS

Identities = 122/122 (100%), Gaps = 0/122 (0%)

```
Query 1 CCANAATCCACTCTCCAGTCTCCCTCCCCTGACTCCCTCTGCTGTCCTCCCCTCTCACGA 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 CCANAATCCACTCTCCAGTCTCCCTCCCCTGACTCCCTCTGCTGTCCTCCCCTCTCACGA 60

Query 61 GAATAAAGTGTCAAGCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAATAAAGTGTCAAGCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 120

Query 121 aa 122
      ||
Sbjct 121 AA 122
```

Sequence 867 matched with Sequence 340

Query= Sequence ID 867
Length=640

SEQ ID NO: 340

ALIGNMENTS

Identities = 640/640 (100%), Gaps = 0/640 (0%)

```
Query 1      tttttttttttttttttttttCAGAGTCACAGATATTGTATAGCTGAGGTAAGCATTTTACA 60
              |||
Sbjct 1      TTTTTTTCAGAGTCACAGATATTGTATAGCTGAGGTAAGCATTTTACA 60

Query 61     ACTTTTCAGACACAAGTAAGTACATAAAATATTATTTTACAACCAACAATNTTTAATATTT 120
              |||
Sbjct 61     ACTTTTCAGACACAAGTAAGTACATAAAATATTATTTTACAACCAACAATNTTTAATATTT 120

Query 121    CCACATTGAANAATAGATGTGATAATTAATCTTTTATAAGGTTTTAAAAAGACATGAAA 180
              |||
Sbjct 121    CCACATTGAANAATAGATGTGATAATTAATCTTTTATAAGGTTTTAAAAAGACATGAAA 180

Query 181    CATAAACCTAATTATACATAAAAAGAAAAGAATTTTAAACAAGAGCTTATTGNGATGACAT 240
              |||
Sbjct 181    CATAAACCTAATTATACATAAAAAGAAAAGAATTTTAAACAAGAGCTTATTGNGATGACAT 240

Query 241    TACTCATAACTTTTACCTTTAAACCTTTTCTTGGGTAGCTATTCAAAAAGTAAAGACCAC 300
              |||
Sbjct 241    TACTCATAACTTTTACCTTTAAACCTTTTCTTGGGTAGCTATTCAAAAAGTAAAGACCAC 300

Query 301    AAGTTTGTGGCCANATTTCTTATGTTTNGTATATTTAAGCTCTTTATTTATTGAACAG 360
              |||
Sbjct 301    AAGTTTGTGGCCANATTTCTTATGTTTNGTATATTTAAGCTCTTTATTTATTGAACAG 360

Query 361    ATGNGTCATTAATTCATTNGGAGCATTACTATTATCAGTAAAATTTGAttttttttCCC 420
              |||
Sbjct 361    ATGNGTCATTAATTCATTNGGAGCATTACTATTATCAGTAAAATTTGATTTTTTTTCCC 420

Query 421    CTCAGTCATAGGTAAATCAGCTCCACCTGGAATTTCTAAGGACCCAGTTTGTAGCAATAT 480
              |||
Sbjct 421    CTCAGTCATAGGTAAATCAGCTCCACCTGGAATTTCTAAGGACCCAGTTTGTAGCAATAT 480
```

PATENT SEQUENCE ALIGNMENT

Query	481	TTTCAAGTAATCATGACCTCAGAAATAGTCTTAATTAAGATAACAAATATTAGCCATCAA	540
Sbjct	481	TTTCAAGTAATCATGACCTCAGAAATAGTCTTAATTAAGATAACAAATATTAGCCATCAA	540
Query	541	AATGGAACCAAGACAAGATTCTAATGTTTGTAACAGTCAATCCATATTTATGAATATTA	600
Sbjct	541	AATGGAACCAAGACAAGATTCTAATGTTTGTAACAGTCAATCCATATTTATGAATATTA	600
Query	601	GCATATATTGGNGAATAGTTAAGGCAAAAGGGTCTAGCAG	640
Sbjct	601	GCATATATTGGNGAATAGTTAAGGCAAAAGGGTCTAGCAG	640

Sequence 869 matched with Sequence 341

Query= Sequence ID - 869 nt: 667
Length=667

SEQ ID NO: 341 nt: 667

ALIGNMENTS

Identities = 667/667 (100%), Gaps = 0/667 (0%)

Query	1	TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC	60
Sbjct	1	TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC	60
Query	61	ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG	120
Sbjct	61	ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG	120
Query	121	ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC	180
Sbjct	121	ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC	180
Query	181	ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA	240
Sbjct	181	ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA	240
Query	241	TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAATGCATACTAATATTTTC	300
Sbjct	241	TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAATGCATACTAATATTTTC	300
Query	301	AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG	360
Sbjct	301	AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG	360
Query	361	AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTTCAGCAATGCATAAGCA	420
Sbjct	361	AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTTCAGCAATGCATAAGCA	420
Query	421	AGAGAGAATATGACATAAGAGGACCATTTCTACATTAGCCAttttttttCACAAAGATACC	480
Sbjct	421	AGAGAGAATATGACATAAGAGGACCATTTCTACATTAGCCATTTTTTTTTCACAAAGATACC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TATGTGAATACAGGGCACCTGGGANGGTAAGTGGAGGACTATTTCTAACTATATTTATAA	540
Sbjct	481	TATGTGAATACAGGGCACCTGGGANGGTAAGTGGAGGACTATTTCTAACTATATTTATAA	540
Query	541	GCACATACTGATATTGNTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA	600
Sbjct	541	GCACATACTGATATTGNTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA	600
Query	601	CAATGTGTAAGGAGATCAGGAATTCATTAGTCACCTTTCAGATGGTTTAATGCATACAGC	660
Sbjct	601	CAATGTGTAAGGAGATCAGGAATTCATTAGTCACCTTTCAGATGGTTTAATGCATACAGC	660
Query	661	TGTACCG	667
Sbjct	661	TGTACCG	667

Sequence 870 matched with Sequence 342

Query= Sequence ID 870
Length=591

SEQ ID NO: 342

ALIGNMENTS

Identities = 591/591 (100%), Gaps = 0/591 (0%)

Query	1	GGAGTTTGAGCAGATCCTTCAGGAGCGGAATGAACTCAAAGCCAAAGTGTTCCTGCTCAA	60
Sbjct	1	GGAGTTTGAGCAGATCCTTCAGGAGCGGAATGAACTCAAAGCCAAAGTGTTCCTGCTCAA	60
Query	61	GGAGGAACTGGCCTACTTCCAGCGGGAGCTGCTCACAGACCACCGGGTCCCCGGCCTTCT	120
Sbjct	61	GGAGGAACTGGCCTACTTCCAGCGGGAGCTGCTCACAGACCACCGGGTCCCCGGCCTTCT	120
Query	121	GCTCGAGGCCATGAAGGTGGCTGTCCGGAAGCAGCGGAAGAAGATCAAGGCCAAGATGTT	180
Sbjct	121	GCTCGAGGCCATGAAGGTGGCTGTCCGGAAGCAGCGGAAGAAGATCAAGGCCAAGATGTT	180
Query	181	AGGGACACCAGAGGAAGCAGAGAGCAGTGAGGATGAGGCTGGCCCATGGATCCTGCTCTC	240
Sbjct	181	AGGGACACCAGAGGAAGCAGAGAGCAGTGAGGATGAGGCTGGCCCATGGATCCTGCTCTC	240
Query	241	CGATGACAAGGGAGACCATCCCCACCCCGGAGTCCAAAATACAGAGTTTCTTTGGCCT	300
Sbjct	241	CGATGACAAGGGAGACCATCCCCACCCCGGAGTCCAAAATACAGAGTTTCTTTGGCCT	300
Query	301	ATGGTATCGGGGTAAAGCTGAATCCTCTGAGGATGAGACCAGCAGCCCTGCACCCAGCAA	360
Sbjct	301	ATGGTATCGGGGTAAAGCTGAATCCTCTGAGGATGAGACCAGCAGCCCTGCACCCAGCAA	360
Query	361	GCTAGGGGGAGAAGAGGAGGCCCAACCACAGTCTCCAGCTCCTGATCCGCCCTGTTCTGC	420
Sbjct	361	GCTAGGGGGAGAAGAGGAGGCCCAACCACAGTCTCCAGCTCCTGATCCGCCCTGTTCTGC	420
Query	421	CCTCCACGAACACCTTTGTCTGGGGGCCTCAGCCGCCCCAGAGGCCTGACTTAGGGGTCT	480
Sbjct	421	CCTCCACGAACACCTTTGTCTGGGGGCCTCAGCCGCCCCAGAGGCCTGACTTAGGGGTCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGCTGTGGAAGGATGTGTGGCCTCAAATGAGGACAGGGCTCCCGCCTTCACAGCCCTCGC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGCTGTGGAAGGATGTGTGGCCTCAAATGAGGACAGGGCTCCCGCCTTCACAGCCCTCGC  540

Query  541  CAGGGGTCTGCCCCAATCCTGGCCTGCATCAGGCAAGGACGGGGTCTCAGC  591
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAGGGGTCTGCCCCAATCCTGGCCTGCATCAGGCAAGGACGGGGTCTCAGC  591
```

Sequence 871 matched with Sequence 343

Query= Sequence ID - 871 nt: 642
Length=642

SEQ ID NO: 343 nt: 642

ALIGNMENTS

Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query	1	GCAAGTCTTCAGTATGTACATTTATCCCCTAGAAGAAGAAAAATTAGTTGTGCATGAAAA	60
Sbjct	1	GCAAGTCTTCAGTATGTACATTTATCCCCTAGAAGAAGAAAAATTAGTTGTGCATGAAAA	60
Query	61	AGAAACATTAAGTCAAAGCTAAATGCTCACACTCTAAATCAGTGCTCTCCAAAGTACAG	120
Sbjct	61	AGAAACATTAAGTCAAAGCTAAATGCTCACACTCTAAATCAGTGCTCTCCAAAGTACAG	120
Query	121	CAGGCGGGAAAAGAAAATGGTAGATtttttttCTTCCAATTACTTTAACTTATTCTTTTTTA	180
Sbjct	121	CAGGCGGGAAAAGAAAATGGTAGATTTTTTTCTTCCAATTACTTTAACTTATTCTTTTTTA	180
Query	181	ATGGACACTTcatacataaatatattcacatatattaatatatacataaatgtataagca	240
Sbjct	181	ATGGACACTTCATACATAAAATATATTCACAATATATTAATATATACATAATGTATAAGCA	240
Query	241	tacatatTGAATGTGCAGTCAAAAAATGTACTAATGGAATGCTCTACCAAAACAAGTTCA	300
Sbjct	241	TACATATTGAATGTGCAGTCAAAAAATGTACTAATGGAATGCTCTACCAAAACAAGTTCA	300
Query	301	CGTTCATCTGTAAAATGGGAATAATATTTTTTAAAAGGCATACAGTCTGAACATTTTTAGA	360
Sbjct	301	CGTTCATCTGTAAAATGGGAATAATATTTTTTAAAAGGCATACAGTCTGAACATTTTTAGA	360
Query	361	TTATTCATAAAATCTATTTCAGAAAGTTAAACTAAAAAATTTAACGTATGCCTATAACAAA	420
Sbjct	361	TTATTCATAAAATCTATTTCAGAAAGTTAAACTAAAAAATTTAACGTATGCCTATAACAAA	420
Query	421	TTTTGTACTTAATGTAATTGNTTTTCATCCTGAGATCTAATATCCTCGTTTTTAAGTAGA	480
Sbjct	421	TTTTGTACTTAATGTAATTGNTTTTCATCCTGAGATCTAATATCCTCGTTTTTAAGTAGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCCACTTGTTTGCTACAGTTTAGTCAAAACGTTAACATTAGATGGGTAAAGTAATATGAA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCCACTTGTTTGCTACAGTTTAGTCAAAACGTTAACATTAGATGGGTAAAGTAATATGAA  540

Query  541  ATCTTTCTACTACTCCAAAATAGAAAACAGAACATTAAAAAGATAAAAAATTCAAACATAC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATCTTTCTACTACTCCAAAATAGAAAACAGAACATTAAAAAGATAAAAAATTCAAACATAC  600

Query  601  TTACCAGTAGATTTTCAACTGNGCAAAAGCTCATTGCATGGG  642
          |||||||||||||||||||||||||||||||||||
Sbjct   601  TTACCAGTAGATTTTCAACTGNGCAAAAGCTCATTGCATGGG  642
```

Sequence 873 matched with Sequence 344

Query= Sequence ID 873
Length=661

SEQ ID NO: 344

ALIGNMENTS

Identities = 661/661 (100%), Gaps = 0/661 (0%)

Query	1	GTTTTCCACCGTGAAGAGAACATTTCTCTGGGAATGACAAAGCCCTCAGGAACNGCTTT	60
Sbjct	1	GTTTTCCACCGTGAAGAGAACATTTCTCTGGGAATGACAAAGCCCTCAGGAACNGCTTT	60
Query	61	TATTTCTATTGGAAGATGCCCATCATACTTCTGGCAGGATAAAATGATAAATTTATTTAT	120
Sbjct	61	TATTTCTATTGGAAGATGCCCATCATACTTCTGGCAGGATAAAATGATAAATTTATTTAT	120
Query	121	TCAACAGATGATACTCAATTCCCTGCTGTTTTACTAAAGGTTCTTTACGTTTTATAGAAG	180
Sbjct	121	TCAACAGATGATACTCAATTCCCTGCTGTTTTACTAAAGGTTCTTTACGTTTTATAGAAG	180
Query	181	CTAAATTTACTGTCATAGAAATTGCAATTGTAGATGTTACTGTAATCTAGTCAGAATATC	240
Sbjct	181	CTAAATTTACTGTCATAGAAATTGCAATTGTAGATGTTACTGTAATCTAGTCAGAATATC	240
Query	241	CTTATCCTTCTAAAATAAACTAGTTAAAATTATTAACATACGTACTGATATTAATTTTT	300
Sbjct	241	CTTATCCTTCTAAAATAAACTAGTTAAAATTATTAACATACGTACTGATATTAATTTTT	300
Query	301	AAGTTTAATGCTGCCACGTGCTTCTGCTAAGAACATTTATCACTACAAGTGGCAGAAAAT	360
Sbjct	301	AAGTTTAATGCTGCCACGTGCTTCTGCTAAGAACATTTATCACTACAAGTGGCAGAAAAT	360
Query	361	TCCAAACTCATCAAAACCAAAGTGTGCTTCTTCCCTGCTTTTTCAGAAAATGAGAAAGG	420
Sbjct	361	TCCAAACTCATCAAAACCAAAGTGTGCTTCTTCCCTGCTTTTTCAGAAAATGAGAAAGG	420
Query	421	ATGACTTTATTCCAACATATTCTAAAAGTATTCCAAGAACACTACCTTTATTCTAAATTC	480
Sbjct	421	ATGACTTTATTCCAACATATTCTAAAAGTATTCCAAGAACACTACCTTTATTCTAAATTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTATTTTCACAAAATAAAGGCTGCAGATTGAAAGATAAAGGATTGCTATTAAAGAACAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTTATTTTCACAAAATAAAGGCTGCAGATTGAAAGATAAAGGATTGCTATTAAAGAACAA  540

Query  541  AAGAAAACAAAACCGAGAGAGAAGGAGAGCTAGGGAAATCCCTGCanaanaaCCGAATAN  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AAGAAAACAAAACCGAGAGAGAAGGAGAGCTAGGGAAATCCCTGCANAANAACCGAATAN  600

Query  601  GGTCCCTCTATTCTGGGCCGGGGCCTGAAACTATGAAACAGGCCAACACAGAATCTTGGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GGTCCCTCTATTCTGGGCCGGGGCCTGAAACTATGAAACAGGCCAACACAGAATCTTGGC  660

Query  661  A   661
          |
Sbjct   661  A   661
```

Sequence 875 matched with Sequence 345

Query= Sequence ID 875
Length=661

SEQ ID NO: 345

ALIGNMENTS

Identities = 661/661 (100%), Gaps = 0/661 (0%)

Query	1	CCTCTGACTCGCTCAGCTCACCCACGCTGCTGGCCCTGTGAGGGGGCAGGGAAGGGGAGG	60
Sbjct	1	CCTCTGACTCGCTCAGCTCACCCACGCTGCTGGCCCTGTGAGGGGGCAGGGAAGGGGAGG	60
Query	61	CAGCCGGCACCCACAAGTGCCACTGCCCCGAGCTGGTGCATTACAGAGAGGAGAAACACAT	120
Sbjct	61	CAGCCGGCACCCACAAGTGCCACTGCCCCGAGCTGGTGCATTACAGAGAGGAGAAACACAT	120
Query	121	CTTCCCTAGAGGGTTCCTGTANACCTAGGGAGGACCTTATCTGTGCGTGAAACACACCAG	180
Sbjct	121	CTTCCCTAGAGGGTTCCTGTANACCTAGGGAGGACCTTATCTGTGCGTGAAACACACCAG	180
Query	181	GCTGTGGGCCTCAAGGACTTGAAAGCATCCATGTGTGGACTCAAGTCCTTACCTCTTCCG	240
Sbjct	181	GCTGTGGGCCTCAAGGACTTGAAAGCATCCATGTGTGGACTCAAGTCCTTACCTCTTCCG	240
Query	241	GAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCCAGTGACACTTCANAGAGCTGGTA	300
Sbjct	241	GAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCCAGTGACACTTCANAGAGCTGGTA	300
Query	301	GTTAGTAGCATGTTGAGCCAGGCCTGGGTCTGTGTCTCTTTTCTCTTTCTCCTTAGTCTT	360
Sbjct	301	GTTAGTAGCATGTTGAGCCAGGCCTGGGTCTGTGTCTCTTTTCTCTTTCTCCTTAGTCTT	360
Query	361	CTCATAGCATTAACTAATCTATTGGGTTTATTGGAATTAACCTGGTGCTGGATATTT	420
Sbjct	361	CTCATAGCATTAACTAATCTATTGGGTTTATTGGAATTAACCTGGTGCTGGATATTT	420
Query	421	TCAAATTGTATCTAGTGCAGCTGATTTTAACAATAACTACTGTGTTCCTGGCAATAGTGT	480
Sbjct	421	TCAAATTGTATCTAGTGCAGCTGATTTTAACAATAACTACTGTGTTCCTGGCAATAGTGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GTTCTGATTAGAAATGACCAATATTATACTAAGAAAAGATACGACTTTATTTTCTGGTAG	540
Sbjct	481	GTTCTGATTAGAAATGACCAATATTATACTAAGAAAAGATACGACTTTATTTTCTGGTAG	540
Query	541	ATAGAAATAAATAGCTATATCCATGTACTGNAGTTTTTCTTCAACATCAATGGTCATTGN	600
Sbjct	541	ATAGAAATAAATAGCTATATCCATGTACTGNAGTTTTTCTTCAACATCAATGGTCATTGN	600
Query	601	AATGTTACTGATCATGCATTGGTGAGGNGGTCTGAATGTTCTGACATTAACAATTTTCCA	660
Sbjct	601	AATGTTACTGATCATGCATTGGTGAGGNGGTCTGAATGTTCTGACATTAACAATTTTCCA	660
Query	661	T	661
Sbjct	661	T	661

Sequence 876 matched with Sequence 346

Query= Sequence ID - 876 nt: 115
Length=115

SEQ ID NO: 346 nt: 115

ALIGNMENTS

Identities = 115/115 (100%), Gaps = 0/115 (0%)

Query	1	AAACTTTTGTGGCAACAGTGCACTAATTTGGATAATGTTTGTCCCAATAAATTAAGAGC	60
Sbjct	1	AAACTTTTGTGGCAACAGTGCACTAATTTGGATAATGTTTGTCCCAATAAATTAAGAGC	60
Query	61	CAAATTGTaaa	115
Sbjct	61	CAAATTGTAA	115

Sequence 878 matched with Sequence 347

Query= Sequence ID - 878 nt: 634
Length=634

SEQ ID NO: 347 nt: 634

ALIGNMENTS

Identities = 634/634 (100%), Gaps = 0/634 (0%)

Query	1	GCCAGGCTTTGTGAATTACAGGACATTTGAGACAATCGTGAAACAGCAAATCAAGGCACT	60
Sbjct	1	GCCAGGCTTTGTGAATTACAGGACATTTGAGACAATCGTGAAACAGCAAATCAAGGCACT	60
Query	61	GGAAGAGCCGGCTGTGGATATGCTACACACCGTGACGGATATGGTCCGGCTTGCTTTTCACT	120
Sbjct	61	GGAAGAGCCGGCTGTGGATATGCTACACACCGTGACGGATATGGTCCGGCTTGCTTTTCACT	120
Query	121	AGATGTTTCGATAAAAAATTTGAAGAGTTTTTTAACTCCACAGAACCGCCAAGTCCAA	180
Sbjct	121	AGATGTTTCGATAAAAAATTTGAAGAGTTTTTTAACTCCACAGAACCGCCAAGTCCAA	180
Query	181	AATTGAAGACATTAGAGCAGAACAAGAGAGAGAAGGTGAGAAGCTGATCCGCCTCCACTT	240
Sbjct	181	AATTGAAGACATTAGAGCAGAACAAGAGAGAGAAGGTGAGAAGCTGATCCGCCTCCACTT	240
Query	241	CCAGATGGAACAGATTGTCTACTGCCAGGACCAGGTATACAGGGGTGCATTGCagaaggt	300
Sbjct	241	CCAGATGGAACAGATTGTCTACTGCCAGGACCAGGTATACAGGGGTGCATTGCAGAAGGT	300
Query	301	cagagagaaggagctggaagaagaaaagaagaagaaATCCTGGGATTTTGGGGCTTTCCA	360
Sbjct	301	CAGAGAGAAGGAGCTGGAAGAAGAAAAGAAGAAGAAATCCTGGGATTTTGGGGCTTTCCA	360
Query	361	ATCCAGCTCGGCAACAGACTCTTCCATGGAGGAGATCTTTCAGCACCTGATGGCCTATCA	420
Sbjct	361	ATCCAGCTCGGCAACAGACTCTTCCATGGAGGAGATCTTTCAGCACCTGATGGCCTATCA	420
Query	421	CCAGGAGGCCAGCAAGCGCATCTCCAGCCACATCCCTTTGATCATCCAGTTCTTCATGCT	480
Sbjct	421	CCAGGAGGCCAGCAAGCGCATCTCCAGCCACATCCCTTTGATCATCCAGTTCTTCATGCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCAGACGTACGGCCAGCAGCTTCAAAAGGCCATGCTGCAGCTCCTGCAGGGACAAGGACA  540
          |||
Sbjct  481  CCAGACGTACGGCCAGCAGCTTCAAAAGGCCATGCTGCAGCTCCTGCAGGGACAAGGACA  540

Query  541  CCTACAGCTGGCTCCTGAAGGAGCGGAGCGACACCAGCGACAAGCGGAAGTTNCTGAAGG  600
          |||
Sbjct  541  CCTACAGCTGGCTCCTGAAGGAGCGGAGCGACACCAGCGACAAGCGGAAGTTNCTGAAGG  600

Query  601  AGCGGCTTGCACGGCTGACGCAGGCTCGGCGCCG  634
          |||
Sbjct  601  AGCGGCTTGCACGGCTGACGCAGGCTCGGCGCCG  634
```

Sequence 879 matched with Sequence 348

Query= Sequence ID 879
Length=528

SEQ ID NO: 348

ALIGNMENTS

Identities = 528/528 (100%), Gaps = 0/528 (0%)

Query	1	GTTGCCGGGTCCTGTGATAACTCTGTTTAAACATTTTGAGGAACTGTTGAATGGTTTTTCA	60
Sbjct	1	GTTGCCGGGTCCTGTGATAACTCTGTTTAAACATTTTGAGGAACTGTTGAATGGTTTTTCA	60
Query	61	CAGCAGCTGCCTCATTTTTTATTCCCATCAGCAGTACTTCTTGGTTCTAATACCTCCACG	120
Sbjct	61	CAGCAGCTGCCTCATTTTTTATTCCCATCAGCAGTACTTCTTGGTTCTAATACCTCCACG	120
Query	121	TTCTCGCCAACACTTGTTGTTGTCTGTAATTCGTTGTTAGCCATCCCAGTGGGGATGAA	180
Sbjct	121	TTCTCGCCAACACTTGTTGTTGTCTGTAATTCGTTGTTAGCCATCCCAGTGGGGATGAA	180
Query	181	GTAGTATCTTACTGTGGTTTTTCAGTTGCGTTTCCCTGATAATTAATGATGGTGAACATCT	240
Sbjct	181	GTAGTATCTTACTGTGGTTTTTCAGTTGCGTTTCCCTGATAATTAATGATGGTGAACATCT	240
Query	241	TTTCATGTTCTTGTTGGCCATTTGTATGTCTTCTTGGGaaaaaaaaaTGCTGTTCAAA	300
Sbjct	241	TTTCATGTTCTTGTTGGCCATTTGTATGTCTTCTTGGGAAAAAAAAAATGTCTGTTCAAA	300
Query	301	TCCTTTACAAAGTATTTATTTTTTATGTCAACAATATAACCACTCAGTACACTGCTTTTT	360
Sbjct	301	TCCTTTACAAAGTATTTATTTTTTATGTCAACAATATAACCACTCAGTACACTGCTTTTT	360
Query	361	ANACAATGATCTTTTAAAGGTTTGTTTACAACATTTAGCACTTGAAATTTAAGGTTATG	420
Sbjct	361	ANACAATGATCTTTTAAAGGTTTGTTTACAACATTTAGCACTTGAAATTTAAGGTTATG	420
Query	421	CCCTCaaaaaaATTGCTGAGGGAGCTAAGCTATGAAGATGCAAAGGCATAANAATTATAC	480
Sbjct	421	CCCTCAAAAAAATTGCTGAGGGAGCTAAGCTATGAAGATGCAAAGGCATAANAATTATAC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AATGGACTTTGGGGGAATCCAGGGAAAGGGTGGGAGGGGGGTGANGGA	528
Sbjct	481	AATGGACTTTGGGGGAATCCAGGGAAAGGGTGGGAGGGGGGTGANGGA	528

Sequence 881 matched with Sequence 349

Query= Sequence ID 881
Length=573

SEQ ID NO: 349

ALIGNMENTS

Identities = 573/573 (100%), Gaps = 0/573 (0%)

Query	1	TCGACTCTGAttttttttCTCCTTCCTCGCAGCCGCGCCAGGGAGCTCGCGNGCGCGG	60
Sbjct	1	TCGACTCTGATTTTTTTTCTCCTTCCTCGCAGCCGCGCCAGGGAGCTCGCGNGCGCGG	60
Query	61	CCCCTGTCTCCGGCCCCGAGATGAATCCTGCGGCAGAAGCCGAGTTCAACATCCTCCTGG	120
Sbjct	61	CCCCTGTCTCCGGCCCCGAGATGAATCCTGCGGCAGAAGCCGAGTTCAACATCCTCCTGG	120
Query	121	CCACCGACTCCTACAAGTTACTCACTATAAAACAATATCCACCCAACACAAGCAAAGTTT	180
Sbjct	121	CCACCGACTCCTACAAGTTACTCACTATAAAACAATATCCACCCAACACAAGCAAAGTTT	180
Query	181	ATTCTACTTTGAATGCCGTGAAAAGAAGACAGAAAACCTCAAATTAAGGAAGGTGAAAT	240
Sbjct	181	ATTCTACTTTGAATGCCGTGAAAAGAAGACAGAAAACCTCAAATTAAGGAAGGTGAAAT	240
Query	241	ATGAGGAAACAGTATTTTATGGGTTGCAGTACATTCTTAATAAGTACTTAAAAGGTAAAG	300
Sbjct	241	ATGAGGAAACAGTATTTTATGGGTTGCAGTACATTCTTAATAAGTACTTAAAAGGTAAAG	300
Query	301	TAGTAACCAAAGAGAAAAATCCAGGAAGCCAAAGATGTCTACAAAGAACATTTCCAAGATG	360
Sbjct	301	TAGTAACCAAAGAGAAAAATCCAGGAAGCCAAAGATGTCTACAAAGAACATTTCCAAGATG	360
Query	361	ATGTCTTTAATGAAAAGGGATGGAACCTACATTCTTGAGAAGTATGATGGGCATCTTCCAA	420
Sbjct	361	ATGTCTTTAATGAAAAGGGATGGAACCTACATTCTTGAGAAGTATGATGGGCATCTTCCAA	420
Query	421	TANAAATAAAAGCTGTTCTGAGGGCTTTGTCATTCCCAGAGGAAATGTTCTCTTCACGG	480
Sbjct	421	TANAAATAAAAGCTGTTCTGAGGGCTTTGTCATTCCCAGAGGAAATGTTCTCTTCACGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TGGAAAACACAGATCCAGAGTGTTACTGGCTTACAAATTGGATTGAGACTATTCTTGTTTC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TGGAAAACACAGATCCAGAGTGTTACTGGCTTACAAATTGGATTGAGACTATTCTTGTTTC  540

Query  541  AGTCCTGGTATCCAATCACAGTGGCCACAAATT  573
          ||||||||||||||||||||||||||||
Sbjct   541  AGTCCTGGTATCCAATCACAGTGGCCACAAATT  573
```


Sequence 883 matched with Sequence 350

Query= Sequence ID 883
Length=659

SEQ ID NO: 350

ALIGNMENTS

Identities = 659/659 (100%), Gaps = 0/659 (0%)

Query	1	TCATTTACATTAATACTCAAAACTGCTCGATTAAGCAGGTGCTGTTCTTATCGCCATTTT	60
Sbjct	1	TCATTTACATTAATACTCAAAACTGCTCGATTAAGCAGGTGCTGTTCTTATCGCCATTTT	60
Query	61	GCATATGATGAGAAAGGGTAAGGTCACCCAGCTAGTATTTGGCTCACAGCAGGCCTTAAG	120
Sbjct	61	GCATATGATGAGAAAGGGTAAGGTCACCCAGCTAGTATTTGGCTCACAGCAGGCCTTAAG	120
Query	121	ACTTGGTTTGTGTGACTCATCAGTCCACGCTCCTAAAACCACTAAGTTGTTCTACCCTTT	180
Sbjct	121	ACTTGGTTTGTGTGACTCATCAGTCCACGCTCCTAAAACCACTAAGTTGTTCTACCCTTT	180
Query	181	AATGTTGAATTAACATTGGATAGTGTTCAAGTTTANATGGGTGGGTGAGGGCCCAAGGAC	240
Sbjct	181	AATGTTGAATTAACATTGGATAGTGTTCAAGTTTANATGGGTGGGTGAGGGCCCAAGGAC	240
Query	241	CTTTCAAACCTCAGATCTCTTATTTAATAACCTGGTCCCAGATCCATTCTCTGTGCAAGA	300
Sbjct	241	CTTTCAAACCTCAGATCTCTTATTTAATAACCTGGTCCCAGATCCATTCTCTGTGCAAGA	300
Query	301	GGAAGTCATCCTTCAGTGGCTATTCATTGTGGGGTTAAGAGCGCAGACTATGAATTCAGT	360
Sbjct	301	GGAAGTCATCCTTCAGTGGCTATTCATTGTGGGGTTAAGAGCGCAGACTATGAATTCAGT	360
Query	361	CTTTTGGGTCCCAGTTTGCCAGACCTTGAGTGAGTGCCCCGAGTTTACTTACTTGTAAG	420
Sbjct	361	CTTTTGGGTCCCAGTTTGCCAGACCTTGAGTGAGTGCCCCGAGTTTACTTACTTGTAAG	420
Query	421	GGTAGGTGGAGGtaatatataattaaataaaacttaaaaaactaattaaaaacaaaacaaatG	480
Sbjct	421	GGTAGGTGGAGGTAATATAATTAAATAAACTTAAAAAACTAATTAAAAACAAAACAAATG	480

PATENT SEQUENCE ALIGNMENT

Query	481	AACTAAGGTCTTAGGATATCTGGCGTCTATTTTGCGCCAAATCACATAATGTCTATTGTT	540
Sbjct	481	AACTAAGGTCTTAGGATATCTGGCGTCTATTTTGCGCCAAATCACATAATGTCTATTGTT	540
Query	541	GTGTGTTGGACTATAGGATTGTCCTTTAACAGGGAAGGGTTTATTTCTGTAATCAAGTCT	600
Sbjct	541	GTGTGTTGGACTATAGGATTGTCCTTTAACAGGGAAGGGTTTATTTCTGTAATCAAGTCT	600
Query	601	GTCAATATTATGACCATGTTGATAATAGCTACCTTTAATTGAGGGCTTCCATGTGCCAA	659
Sbjct	601	GTCAATATTATGACCATGTTGATAATAGCTACCTTTAATTGAGGGCTTCCATGTGCCAA	659

Sequence 885 matched with Sequence 351

Query= Sequence ID 885
Length=517

SEQ ID NO: 351

ALIGNMENTS

Identities = 517/517 (100%), Gaps = 0/517 (0%)

Query	1	TCAGTGAAAAGGGCAGGTTGAATCAAGGTGAATCAATCTGAAATTGAGCACACCTGCCT	60
Sbjct	1	TCAGTGAAAAGGGCAGGTTGAATCAAGGTGAATCAATCTGAAATTGAGCACACCTGCCT	60
Query	61	GCCATCGCTGTTTCCTTCAACTGAGTGCTGCACATCATGGGCTCTGTCTGTGAGAGAAAAA	120
Sbjct	61	GCCATCGCTGTTTCCTTCAACTGAGTGCTGCACATCATGGGCTCTGTCTGTGAGAGAAAAA	120
Query	121	TCCCGGTGCTTGGTGTCTTGCATGACATGGAGTTTTGCATGTAGATCAATTTAAATGT	180
Sbjct	121	TCCCGGTGCTTGGTGTCTTGCATGACATGGAGTTTTGCATGTAGATCAATTTAAATGT	180
Query	181	ACCTCTTGTTTACATAATTTGCATAATTTTAAAAGATAATGTTGCCAAACTTTGGAAATG	240
Sbjct	181	ACCTCTTGTTTACATAATTTGCATAATTTTAAAAGATAATGTTGCCAAACTTTGGAAATG	240
Query	241	TTAATGTTCANACTGAAAATCTCCACTACATGTAACCTTCTTCCTCTGGATCAGTGGCAT	300
Sbjct	241	TTAATGTTCANACTGAAAATCTCCACTACATGTAACCTTCTTCCTCTGGATCAGTGGCAT	300
Query	301	GGCTTATAATCCCAGCCAGTGGTTGAACTGTTCCAGTGTCAACTGCCATGTGCTCTGCT	360
Sbjct	301	GGCTTATAATCCCAGCCAGTGGTTGAACTGTTCCAGTGTCAACTGCCATGTGCTCTGCT	360
Query	361	TCAAGGGGGAAGTAGCCTTTTGTGAATTTTTGTACATAAGTATTTGTTACAAATATTTT	420
Sbjct	361	TCAAGGGGGAAGTAGCCTTTTGTGAATTTTTGTACATAAGTATTTGTTACAAATATTTT	420
Query	421	AGCAAATGCTTTCTATTTCTCTTGCTTGTGCATATCTTGGCTGGCGTTACAGAAAAATAG	480
Sbjct	421	AGCAAATGCTTTCTATTTCTCTTGCTTGTGCATATCTTGGCTGGCGTTACAGAAAAATAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGTAAACATTATTTTCCTTACCGGGGAATGAGGGTTTT	517
Sbjct	481	TGTAAACATTATTTTCCTTACCGGGGAATGAGGGTTTT	517

Sequence 887 matched with Sequence 352

Query= Sequence ID 887
Length=174

SEQ ID NO: 352

ALIGNMENTS

Identities = 174/174 (100%), Gaps = 0/174 (0%)

Query	1	AGCACCTGGCACAGAGTAGTAGCTAACACAGATGTTAATTTTGCTGCGTCAAATGTTTTTC	60
Sbjct	1	AGCACCTGGCACAGAGTAGTAGCTAACACAGATGTTAATTTTGCTGCGTCAAATGTTTTTC	60
Query	61	ACTTTGAATCTCTCTTGAGTATTGTTCTCCTTATTGATTACATGATGACATCCTGTTTTTC	120
Sbjct	61	ACTTTGAATCTCTCTTGAGTATTGTTCTCCTTATTGATTACATGATGACATCCTGTTTTTC	120
Query	121	TCTCCCTGACCTTTACTGTTTGTGTTAGaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	174
Sbjct	121	TCTCCCTGACCTTTACTGTTTGTGTTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	174

Sequence 889 matched with Sequence 353

Query= Sequence ID 889
Length=664

SEQ ID NO: 353

ALIGNMENTS

Identities = 664/664 (100%), Gaps = 0/664 (0%)

Query	1	CAGAGAGCTTGTTCCTCCCTCCCTGTGCATGCAAACAAGAGGGCATGGGAGCACACAGA	60
Sbjct	1	CAGAGAGCTTGTTCCTCCCTCCCTGTGCATGCAAACAAGAGGGCATGGGAGCACACAGA	60
Query	61	GAGATGGCAGCCACCTACAAGCCAAGAGGAGAAGCCTCACAATCAAACCTCTCGCTGCTGG	120
Sbjct	61	GAGATGGCAGCCACCTACAAGCCAAGAGGAGAAGCCTCACAATCAAACCTCTCGCTGCTGG	120
Query	121	CGAGAGTCTTGGACTCTGTCTTGGACTTCCAGCCTCCAGACTGTGAGAAACAAATTTCTG	180
Sbjct	121	CGAGAGTCTTGGACTCTGTCTTGGACTTCCAGCCTCCAGACTGTGAGAAACAAATTTCTG	180
Query	181	TTGTTTCAGCTTCTCAGTCTCTGGTGTTTTGTTATTGCAGCCTGAGAACACAGCTGTACN	240
Sbjct	181	TTGTTTCAGCTTCTCAGTCTCTGGTGTTTTGTTATTGCAGCCTGAGAACACAGCTGTACN	240
Query	241	ATTATNAGGGAAACAGAAAACACTGATACTTAACAATGCTAATGCAATTATTTATTTGCT	300
Sbjct	241	ATTATNAGGGAAACAGAAAACACTGATACTTAACAATGCTAATGCAATTATTTATTTGCT	300
Query	301	TTTCAGTCTCTACAAAACGTTCTAAAACACTAATCTAAATATTAACAGTAAAAATTTTGC	360
Sbjct	301	TTTCAGTCTCTACAAAACGTTCTAAAACACTAATCTAAATATTAACAGTAAAAATTTTGC	360
Query	361	ATAACTAATGGAACTAAGAAATCATATGACCAATATTTCACTTATTGGTAATCTTACTC	420
Sbjct	361	ATAACTAATGGAACTAAGAAATCATATGACCAATATTTCACTTATTGGTAATCTTACTC	420
Query	421	TACTGATTTCCCCCAGACTGTGATTTTTGAACTTCCTTGCCTTTCTCCTGTCTTTCTGN	480
Sbjct	421	TACTGATTTCCCCCAGACTGTGATTTTTGAACTTCCTTGCCTTTCTCCTGTCTTTCTGN	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTTATTCATGGAATTCAGTTATCTGGGCTTGAAATTGCAGGCTCTCCTAACTTAAGCA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTTTATTCATGGAATTCAGTTATCTGGGCTTGAAATTGCAGGCTCTCCTAACTTAAGCA  540

Query  541  AAATCTGACAGATCAGCAAAATGAGATAAATGTTTCTTTTTCTTTCTGACTGCATTAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AAATCTGACAGATCAGCAAAATGAGATAAATGTTTCTTTTTCTTTCTGACTGCATTAAA  600

Query  601  TCAGATACAACCTCAGCATTAAAAAGCTATCTTTGNAAAATGNTGGTACTAATAAATTAGT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TCAGATACAACCTCAGCATTAAAAAGCTATCTTTGNAAAATGNTGGTACTAATAAATTAGT  660

Query  661  CTTA  664
          ||||
Sbjct   661  CTTA  664
```

Sequence 890 matched with Sequence 354

Query= Sequence ID 890
Length=661

SEQ ID NO: 354

ALIGNMENTS

Identities = 661/661 (100%), Gaps = 0/661 (0%)

Query	1	CCAGTTCCACATTCAAGTCATGAAGTGGCCATGATCAAAAAGTATTTAA	60
Sbjct	1	CCAGTTCCACATTCAAGTCATGAAGTGGCCATGATCAAAAAGTATTTAA	60
Query	61	ATCACAGAAGTTGCAAATGCCACAAATCAAGGTCTTTTCTCTTGGAGAACCTGTAAAC	120
Sbjct	61	ATCACAGAAGTTGCAAATGCCACAAATCAAGGTCTTTTCTCTTGGAGAACCTGTAAAC	120
Query	121	ATTTACCAACTCACGACCGCCATGCACCCAATACTGCAATAGGTCTATAGATGCAGATAC	180
Sbjct	121	ATTTACCAACTCACGACCGCCATGCACCCAATACTGCAATAGGTCTATAGATGCAGATAC	180
Query	181	TGTCTCCATGAATCTTATAGGCTAGAAAGGAAATAGATAAGTAGTCCTACCAGAAGAACA	240
Sbjct	181	TGTCTCCATGAATCTTATAGGCTAGAAAGGAAATAGATAAGTAGTCCTACCAGAAGAACA	240
Query	241	TGATGAAGGCATTTGTGGTAAACAGAATGATGGCCCCCAAAGATGTCCACATCCTAATC	300
Sbjct	241	TGATGAAGGCATTTGTGGTAAACAGAATGATGGCCCCCAAAGATGTCCACATCCTAATC	300
Query	301	CCTGAAGCCTATGAATATACTACTTTACTTGGCAAAGGGACTTTGCCACAGGTTTTTAA	360
Sbjct	301	CCTGAAGCCTATGAATATACTACTTTACTTGGCAAAGGGACTTTGCCACAGGTTTTTAA	360
Query	361	TTAAGGACCTTGAAATAGAGAGATTATCCTGGATAATCCAGATGGCCCCAGTGTAATCCC	420
Sbjct	361	TTAAGGACCTTGAAATAGAGAGATTATCCTGGATAATCCAGATGGCCCCAGTGTAATCCC	420
Query	421	AAGGGTCCTCACAAGGGTAGGAAGGAGAGCCAGAGTCAGAGAAGGAGACGTAGCAATGG	480
Sbjct	421	AAGGGTCCTCACAAGGGTAGGAAGGAGAGCCAGAGTCAGAGAAGGAGACGTAGCAATGG	480

PATENT SEQUENCE ALIGNMENT

Query 481 AGGCAGAGGTCANAGAGAGATCTGCAGATGCTGCTGTGTTGGCTTTGAAAATGAGGAATG 540
|||||
Sbjct 481 AGGCAGAGGTCANAGAGAGATCTGCAGATGCTGCTGTGTTGGCTTTGAAAATGAGGAATG 540

Query 541 CAGGTGACCTCAANGNGCTAGATGATGCAAGGAAACAAATAATCTCCTATGAACCCTAGG 600
|||||
Sbjct 541 CAGGTGACCTCAANGNGCTAGATGATGCAAGGAAACAAATAATCTCCTATGAACCCTAGG 600

Query 601 ATGGGCATTATTATGAGTCCTATTTTATAAACAAGGAACTGACNTCCAGAAAGATAAATG 660
|||||
Sbjct 601 ATGGGCATTATTATGAGTCCTATTTTATAAACAAGGAACTGACNTCCAGAAAGATAAATG 660

Query 661 C 661
|
Sbjct 661 C 661

Sequence 891 matched with Sequence 355

Query= Sequence ID - 891 nt: 626
Length=626

SEQ ID NO: 355 nt: 626

ALIGNMENTS

Identities = 626/626 (100%), Gaps = 0/626 (0%)

Query	1	GGCAGAGGTTGCAGTGAAGTGAATCATGCCATTGCAATCCAGCCTGGGCAACANGAGTG	60
Sbjct	1	GGCAGAGGTTGCAGTGAAGTGAATCATGCCATTGCAATCCAGCCTGGGCAACANGAGTG	60
Query	61	AGACTCCATCTCaaaaaaaaaaaaaaGACAAGAGTNTCCACTCTAAACACTTNTATT	120
Sbjct	61	AGACTCCATCTCAAAAAAAAAAAAAAAAAAGACAAGAGTNTCCACTCTAAACACTTNTATT	120
Query	121	CAACATAGTCCTGAAAGTCGTAGCCACAGCAATTTAACAAGATAAAGCAATAAAATGTAT	180
Sbjct	121	CAACATAGTCCTGAAAGTCGTAGCCACAGCAATTTAACAAGATAAAGCAATAAAATGTAT	180
Query	181	TCAAATAGAAAAAGAGGAAGTCAAATTATCTTCACTGGNGATATAATTCTCTACCTGGGA	240
Sbjct	181	TCAAATAGAAAAAGAGGAAGTCAAATTATCTTCACTGGNGATATAATTCTCTACCTGGGA	240
Query	241	AACTTCACCGAAAAAGATTTACCAAAAAGATTTCTAAGCCTAAATAATGACTTCAGCAAA	300
Sbjct	241	AACTTCACCGAAAAAGATTTACCAAAAAGATTTCTAAGCCTAAATAATGACTTCAGCAAA	300
Query	301	GTCTCACCATACAAAATCAACATACACAAATGAGTAGCATTCTGTGCACCAATAATATT	360
Sbjct	301	GTCTCACCATACAAAATCAACATACACAAATGAGTAGCATTCTGTGCACCAATAATATT	360
Query	361	CAAGCTGAGaaaaaaGAACATGGTTCTATTTACAATAGCTACAAACaaaaaaTATGTA	420
Sbjct	361	CAAGCTGAGAAAAAAGAACATGGTTCTATTTACAATAGCTACAAACAAAAAATATGTA	420
Query	421	CCTAGTAATACATTAAATCAAGGNGGTAAAATATCTNTACAACAAGAACTACAAAACCTGC	480
Sbjct	421	CCTAGTAATACATTAAATCAAGGNGGTAAAATATCTNTACAACAAGAACTACAAAACCTGC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGaaaaaaaaTAGAGACACGCAAATAAGTAAAAAGGCACTCCATGCTCATGAATTTAAAG	540
Sbjct	481	TGAAAAAAAAATAGAGACACGCAAATAAGTAAAAAGGCACTCCATGCTCATGAATTTAAAG	540
Query	541	AATCAATATAATTAAAAATGTCCGNGCTGCCTAAAGCAACTTACAGATTAAAGGCTATTTTC	600
Sbjct	541	AATCAATATAATTAAAAATGTCCGNGCTGCCTAAAGCAACTTACAGATTAAAGGCTATTTTC	600
Query	601	TCTCAAACCTATAAATGCACCTTTTTA	626
Sbjct	601	TCTCAAACCTATAAATGCACCTTTTTA	626

Sequence 893 matched with Sequence 356

Query= Sequence ID - 893 nt: 585
Length=585

SEQ ID NO: 356 nt: 585

ALIGNMENTS

Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query	1	GTCATTGCTGGGTGGCGCCAGCCCTCAGACTTGCCTCTTTGCAGTAGGAAGAAGGCCTCC	60
Sbjct	1	GTCATTGCTGGGTGGCGCCAGCCCTCAGACTTGCCTCTTTGCAGTAGGAAGAAGGCCTCC	60
Query	61	CCACATACCTTCCCACACTCATCACCTTAAGCCAGACTCGGTGTCCAGTGAATATGACCA	120
Sbjct	61	CCACATACCTTCCCACACTCATCACCTTAAGCCAGACTCGGTGTCCAGTGAATATGACCA	120
Query	121	TCTCTTGCCCATTTTCTAATGAGTGTTTTTCATTAATGAGTTATAAGAATGTGGTGGGTAA	180
Sbjct	121	TCTCTTGCCCATTTTCTAATGAGTGTTTTTCATTAATGAGTTATAAGAATGTGGTGGGTAA	180
Query	181	ATCTATGGGCTTTGAACTAGTGAATCAACTTGGTTTTCAGAATCTGGCACTGCTACTTACT	240
Sbjct	181	ATCTATGGGCTTTGAACTAGTGAATCAACTTGGTTTTCAGAATCTGGCACTGCTACTTACT	240
Query	241	AGTGAATTTAAGCAAGTTATTTACCTTTTCAGAGTGTGAGTTCCCTCATGCATACAAGGA	300
Sbjct	241	AGTGAATTTAAGCAAGTTATTTACCTTTTCAGAGTGTGAGTTCCCTCATGCATACAAGGA	300
Query	301	AGATAAAAAATAATGTNTACNAAAGTATTGGAGTAATTAATACATGGGAGAACTACATGTA	360
Sbjct	301	AGATAAAAAATAATGTNTACNAAAGTATTGGAGTAATTAATACATGGGAGAACTACATGTA	360
Query	361	AAGCGTTTAGCATGATGTCTGACATATTAAGCATCCAATATTAGTNGCTTGCAGAATTAT	420
Sbjct	361	AAGCGTTTAGCATGATGTCTGACATATTAAGCATCCAATATTAGTNGCTTGCAGAATTAT	420
Query	421	TAGTAAAAGAGATTGCTTCTGAAAGCCATTCCAATTCTTAAATTTTATAATGCCACATTT	480
Sbjct	421	TAGTAAAAGAGATTGCTTCTGAAAGCCATTCCAATTCTTAAATTTTATAATGCCACATTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAGGTCACCTGAAGTCGTGTATAACATGTGTACATTTTGGCGATTATTTTTTCAATTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAGGTCACCTGAAGTCGTGTATAACATGTGTACATTTTGGCGATTATTTTTTCAATTCC  540

Query  541  CANATTAAAGGCATAGAGATATCCTAGCNANGGACTCCAAGTGTG  585
          ||||||||||||||||||||||||||||||||||||
Sbjct  541  CANATTAAAGGCATAGAGATATCCTAGCNANGGACTCCAAGTGTG  585
```

Sequence 895 matched with Sequence 357

Query= Sequence ID - 895 nt: 560
Length=560

SEQ ID NO: 357 nt: 560

ALIGNMENTS

Identities = 560/560 (100%), Gaps = 0/560 (0%)

Query	1	GTAATTGCAGCCTGGGCAACGGAGTGAGAGACTGTCTCAGG	60
Sbjct	1	GTAATTGCAGCCTGGGCAACGGAGTGAGAGACTGTCTCAGG	60
		AAAAAAAAAAGAAAAAAAAA	
Query	61	CTACTGAGGTAGTTGAATATATCCTCCATTCCCATT	120
Sbjct	61	CTACTGAGGTAGTTGAATATATCCTCCATTCCCATT	120
Query	121	CATCTTAGGGTTTAAATATGTCCAGGGTCACTGAGGATCAGATCCTAGGGTTCCTTTGAC	180
Sbjct	121	CATCTTAGGGTTTAAATATGTCCAGGGTCACTGAGGATCAGATCCTAGGGTTCCTTTGAC	180
Query	181	TCAAGGCTTTTGTCTCAGCAAAACGTCACCTTCCAGCAGGAAGGCTTCTCAGGCAAGTA	240
Sbjct	181	TCAAGGCTTTTGTCTCAGCAAAACGTCACCTTCCAGCAGGAAGGCTTCTCAGGCAAGTA	240
Query	241	GCAGGGTGGCTACTATGTATCGCTTCTTTA	300
Sbjct	241	GCAGGGTGGCTACTATGTATCGCTTCTTTA	300
Query	301	GTGCGCATAATTTAAAAAATCAGTGCTAAAACCTT	360
Sbjct	301	GTGCGCATAATTTAAAAAATCAGTGCTAAAACCTT	360
Query	361	CCTGTCtttctttttttttctttttat	420
Sbjct	361	CCTGTCtttctttttttttctttttat	420
Query	421	ttagggtacatgtgcacaacgtgcaggtttgttacat	480
Sbjct	421	ttagggtacatgtgcacaacgtgcaggtttgttacat	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAGCTGCACCCATTAACTCGTCATTTAGCATTAGGTATATCTCCTAATGCTATccctccc  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GAGCTGCACCCATTAACTCGTCATTTAGCATTAGGTATATCTCCTAATGCTATCCCTCCC  540

Query  541  ccctccccccctttttttttt  560
          ||||||||||||||||
Sbjct   541  CCCTCCCCCCTTTTTTTTTTT  560
```

Sequence 896 matched with Sequence 358

Query= Sequence ID 896
Length=645

SEQ ID NO: 358

ALIGNMENTS

Identities = 645/645 (100%), Gaps = 0/645 (0%)

Query	1	GGGAATGTCTTAGGCACTGGGACTGTAAGTGCAAAGACCCTGTGGCACAAGGGAATGTTA	60
Sbjct	1	GGGAATGTCTTAGGCACTGGGACTGTAAGTGCAAAGACCCTGTGGCACAAGGGAATGTTA	60
Query	61	ATTATCTACCTTTCANAACTGGAANAAGGCCTAGCCTAGAGCATTGAAAAACAATAAGGG	120
Sbjct	61	ATTATCTACCTTTCANAACTGGAANAAGGCCTAGCCTAGAGCATTGAAAAACAATAAGGG	120
Query	121	AAAGGAGGAGTAAGGCTGGANAGATAGGAATGGTTTAAAGTCTTTGTTAAAAAAtttttt	180
Sbjct	121	AAAGGAGGAGTAAGGCTGGANAGATAGGAATGGTTTAAAGTCTTTGTTAAAAATTTTTT	180
Query	181	aaaaaaaTCTTTATCACAAGAAGAGGATTGGCNTGATCAAATTTGACTTTTaaaaanaTT	240
Sbjct	181	AAAAAATCTTTATCACAAGAAGAGGATTGGCNTGATCAAATTTGACTTTTAAAAANATT	240
Query	241	ACTTGGGTTGGGCATGATCAAATACTACTTAGGGAGATTAGTTTANATGATAATGGCATT	300
Sbjct	241	ACTTGGGTTGGGCATGATCAAATACTACTTAGGGAGATTAGTTTANATGATAATGGCATT	300
Query	301	CTGGACCANAGTGGAGTCAGAGGTGAAAAGAGGTAGATATTCCANAATTGAGGGATTTGT	360
Sbjct	301	CTGGACCANAGTGGAGTCAGAGGTGAAAAGAGGTAGATATTCCANAATTGAGGGATTTGT	360
Query	361	GAGGTGAAATCATTTGTTACAGATATTAAGGATAAGGAGCTTTGTCAAAGGGGATCTTA	420
Sbjct	361	GAGGTGAAATCATTTGTTACAGATATTAAGGATAAGGAGCTTTGTCAAAGGGGATCTTA	420
Query	421	AGTTTCTGGTATGGTAACTGGGTTAGAGAGCCCTGGAACATGACCAGCTTTAAGGGAAGA	480
Sbjct	421	AGTTTCTGGTATGGTAACTGGGTTAGAGAGCCCTGGAACATGACCAGCTTTAAGGGAAGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAGCTTGAGCTCTGTTCTTGTTAAGCTCAGTTTGAGATCTTTGTGGAATCAAGTGGAGAG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GAGCTTGAGCTCTGTTCTTGTTAAGCTCAGTTTGAGATCTTTGTGGAATCAAGTGGAGAG  540

Query  541  GTCTAAGCAGGGAAGCTGGCTTAGGCTGTAAAGATGAATCTGAGAGTCCCAAGAATA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GTCTAAGCAGGGAAGCTGGCTTAGGCTGTAAAGATGAATCTGAGAGTCCCAAGAATA  600

Query  601  TGGTAATTATTAATAAAAAGCCTTAGGTANATGAAATTGTTTTGGG  645
          |||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TGGTAATTATTAATAAAAAGCCTTAGGTANATGAAATTGTTTTGGG  645
```

Sequence 897 matched with Sequence 359

Query= Sequence ID - 897 nt: 509
Length=509

SEQ ID NO: 359 nt: 509

ALIGNMENTS

Identities = 509/509 (100%), Gaps = 0/509 (0%)

Query	1	GCAAATCTACACATTTGATTAAATGATAGGGAACATGCACACACATAATACATATAATG	60
Sbjct	1	GCAAATCTACACATTTGATTAAATGATAGGGAACATGCACACACATAATACATATAATG	60
Query	61	CTAGTTTCTTGGTTTTGATATTGTACCATAGTTATGTAAGATGTAACCATTGGGGGAAAC	120
Sbjct	61	CTAGTTTCTTGGTTTTGATATTGTACCATAGTTATGTAAGATGTAACCATTGGGGGAAAC	120
Query	121	TGGGTGAAGGCTACATGAGACCTCTCTGTAATCTTTGCAACTTATGTGAATCTATA	180
Sbjct	121	TGGGTGAAGGCTACATGAGACCTCTCTGTAATCTTTGCAACTTATGTGAATCTATA	180
Query	181	ATTATTCCAAAATAAAAAAGTTTAAAGAACCTAAGTATCCTTATTACTGAGGGTCATCGT	240
Sbjct	181	ATTATTCCAAAATAAAAAAGTTTAAAGAACCTAAGTATCCTTATTACTGAGGGTCATCGT	240
Query	241	GCTAGACAGCAAGGTTGGGCCAGAGCTTCTAGTTATTTAAATACTAAATACCAGCCTGG	300
Sbjct	241	GCTAGACAGCAAGGTTGGGCCAGAGCTTCTAGTTATTTAAATACTAAATACCAGCCTGG	300
Query	301	GCAACATAGCAAGACCCTGCCTCTACaaaaagcaaaaaaTTAGCTGGGCATGGTGGTAC	360
Sbjct	301	GCAACATAGCAAGACCCTGCCTCTACAAAAAGCAAAAAAATTAGCTGGGCATGGTGGTAC	360
Query	361	ATGCCTGTGGTCCTAGTTACTCTTGGAGGAGTCTGAGGTGGGGAGCTTGAGCCTAGGAGT	420
Sbjct	361	ATGCCTGTGGTCCTAGTTACTCTTGGAGGAGTCTGAGGTGGGGAGCTTGAGCCTAGGAGT	420
Query	421	TTGAGGCCGCAGTGAGCCTTGATTGTGTCTCTGTACTCCAGTCTGGGCCACAGAGCAAGA	480
Sbjct	421	TTGAGGCCGCAGTGAGCCTTGATTGTGTCTCTGTACTCCAGTCTGGGCCACAGAGCAAGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCCGGTCTCTAAAAATAAATAAATAAATA	509
Sbjct	481	CCCGGTCTCTAAAAATAAATAAATAAATA	509

Sequence 898 matched with Sequence 360

Query= Sequence ID 898
Length=511

SEQ ID NO: 360

ALIGNMENTS

Identities = 511/511 (100%), Gaps = 0/511 (0%)

Query	1	ANTGCACTCCAGCTTGGTGACAGAGGGAGACTCCATNTTaaaaaaaaaaaaaaaaaaaaa	62
Sbjct	1	ANTGCACTCCAGCTTGGTGACAGAGGGAGACTCCATNTTAAAAAAAAAAAAAAAAAAAAA	62
Query	63	aGGGAGTAGCTTGAAGCCACATAGTAGTTAGTGGTAAAGGCCACCCCTTTCCCACT	122
Sbjct	63	AGGGAGTAGCTTGAAGCCACATAGTAGTTAGTGGTAAAGGCCACCCCTTTCCCACT	122
Query	123	CACACCAGCACCACAAGCTAGCCTTTNTAATTTCCAAGCCAGTGCCCTTTCAACGCACAC	182
Sbjct	123	CACACCAGCACCACAAGCTAGCCTTTNTAATTTCCAAGCCAGTGCCCTTTCAACGCACAC	182
Query	183	ACCCCTGTGTCAGTTCCTTTCTGCTGCAAGCTCTCTGGAGGCAGATACTGTTGAGTCCC	242
Sbjct	183	ACCCCTGTGTCAGTTCCTTTCTGCTGCAAGCTCTCTGGAGGCAGATACTGTTGAGTCCC	242
Query	243	TGGCCTGCCTATGAGAACGGCTCATGATCTCTATTTCTTCTGCTTAATGACCATCTCGAA	302
Sbjct	243	TGGCCTGCCTATGAGAACGGCTCATGATCTCTATTTCTTCTGCTTAATGACCATCTCGAA	302
Query	303	GTAACAAGTTTAGCCTAAAATAAACTTGCTAAGTTAGCAAAGGAAGTCCTTAGCAGCCAC	362
Sbjct	303	GTAACAAGTTTAGCCTAAAATAAACTTGCTAAGTTAGCAAAGGAAGTCCTTAGCAGCCAC	362
Query	363	CATTTCTCGATTCTCCATCACCTCCCCTGCCCCTCAACTCCCTCATTTCTCCCAAGATA	422
Sbjct	363	CATTTCTCGATTCTCCATCACCTCCCCTGCCCCTCAACTCCCTCATTTCTCCCAAGATA	422
Query	423	TGGGCTCCAGGCTGGGCGCGGTGGCTCACGCCTATAATCCTAGCACTTTGGGAGGCTGAG	482
Sbjct	423	TGGGCTCCAGGCTGGGCGCGGTGGCTCACGCCTATAATCCTAGCACTTTGGGAGGCTGAG	482

PATENT SEQUENCE ALIGNMENT

```
Query  483  GTGAGCAGATCACTGAGGTCAGGAGTTCG  511
          |||||||||||||||||||||||||
Sbjct  483  GTGAGCAGATCACTGAGGTCAGGAGTTCG  511
```

Blast comparison trimmed “AN” from the 5’ end of both sequences and reported 509 identities. The report has been manually corrected for this. “AN” has been prepended to both sequences and identity count has been increased to 511.

Sequence 899 matched with Sequence 361

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 899
Length=16

SEQ ID NO: 361	26.3	2e-06
----------------	------	-------

ALIGNMENTS

Identities = 16/16 (100%), Gaps = 0/16 (0%)

Query	1	TCNTTCGGAACGCGCC	16
Sbjct	1	TCNTTCGGAACGCGCC	16

Blast comparison trimmed "TCN" from the 5' end of both sequences and reported 13 identities. The report has been manually corrected for this. "TCN" has been prepended to both sequences and identity count has been increased to 16.

Sequence 900 matched with Sequence 362

Query= Sequence ID 900
Length=579

SEQ ID NO: 362

ALIGNMENTS

Identities = 579/579 (100%), Gaps = 0/579 (0%)

Query	1	CTGGAGGGATGGGTAGGATTTTGACAAGAGTGGTTGAAGGTATTCTAATTCACCTTAGTAC	60
Sbjct	1	CTGGAGGGATGGGTAGGATTTTGACAAGAGTGGTTGAAGGTATTCTAATTCACCTTAGTAC	60
Query	61	CTACATGTGCGAGGCAGCATGAAGGCCAAAAAGCCTGGGGCATGTTGAGAGAATAGCAAG	120
Sbjct	61	CTACATGTGCGAGGCAGCATGAAGGCCAAAAAGCCTGGGGCATGTTGAGAGAATAGCAAG	120
Query	121	TATTCTAGTTTGAGTGGCACCTGGTACGTATATAAGGGAATAGTAAAAGATCTGGCTGGA	180
Sbjct	121	TATTCTAGTTTGAGTGGCACCTGGTACGTATATAAGGGAATAGTAAAAGATCTGGCTGGA	180
Query	181	AAGGAAAAGTAGGGGCAGGTTACGAAGGACCTCTGAAAGTCAGACTGTGGAAGTGGAACT	240
Sbjct	181	AAGGAAAAGTAGGGGCAGGTTACGAAGGACCTCTGAAAGTCAGACTGTGGAAGTGGAACT	240
Query	241	TTTATCAGGAAGCAGTAGTTAGTTTTTTCAAGCAAAAGCTAATTAGAGTTGATATTTAGG	300
Sbjct	241	TTTATCAGGAAGCAGTAGTTAGTTTTTTCAAGCAAAAGCTAATTAGAGTTGATATTTAGG	300
Query	301	AGGATGAATCTAACAGTTGTGTGCAAGGATGCCTTCAAAGTGAAGTGAAGTGAAGTGAAGT	360
Sbjct	301	AGGATGAATCTAACAGTTGTGTGCAAGGATGCCTTCAAAGTGAAGTGAAGTGAAGTGAAGT	360
Query	361	GACTGGTTAAGAGACTACAACAATAACCTGAGTAAGAATTAATACAGGCCTGACCTAGTT	420
Sbjct	361	GACTGGTTAAGAGACTACAACAATAACCTGAGTAAGAATTAATACAGGCCTGACCTAGTT	420
Query	421	TTGAGTGAGTAGGATTGGAAACAAGAGTTTTAGGTATTATAGGATTTATGCATATAAAAT	480
Sbjct	421	TTGAGTGAGTAGGATTGGAAACAAGAGTTTTAGGTATTATAGGATTTATGCATATAAAAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGACTTGACAGAACTTGAAGAAAGAGAAAGTGTCAAAGGACACAGAAAGTGAGGCAGGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGACTTGACAGAACTTGAAGAAAGAGAAAGTGTCAAAGGACACAGAAAGTGAGGCAGGA  540

Query  541  TATCTTACAATGTTAAAGGAAAGGAATAATAGAAGTTAC  579
          ||||||||||||||||||||||||||||
Sbjct   541  TATCTTACAATGTTAAAGGAAAGGAATAATAGAAGTTAC  579
```


Sequence 903 matched with Sequence 363

Query= Sequence ID 903
Length=185

SEQ ID NO: 363

ALIGNMENTS

Identities = 185/185 (100%), Gaps = 0/185 (0%)

```
Query   1      GGAAACATAAGCTTGTTTCAGTACACTCACGCTGTAGATTAATTCTGATATTACATATCT   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1      GGAAACATAAGCTTGTTTCAGTACACTCACGCTGTAGATTAATTCTGATATTACATATCT   60

Query   61     CCATCAGACTTTGTACCCTCTCTCTTCCATCCCTTACCCTTACCGATTAGGTTGGTATTA   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61     CCATCAGACTTTGTACCCTCTCTCTTCCATCCCTTACCCTTACCGATTAGGTTGGTATTA   120

Query   121    CCTAAAAATCCATAGAAAATGTCCAGGTGAATTGCCTTATGCTTTCTACCCCATAGGTA   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121    CCTAAAAATCCATAGAAAATGTCCAGGTGAATTGCCTTATGCTTTCTACCCCATAGGTA   180

Query   181     TAATT   185
          ||||
Sbjct   181     TAATT   185
```

Sequence 904 matched with Sequence 364

Query= Sequence ID 904
Length=649

SEQ ID NO: 364

ALIGNMENTS

Identities = 649/649 (100%), Gaps = 0/649 (0%)

Query	1	CTCTGTGGTGTGAGAACACAGTGGGTGACCAAGGCTTTCAGATGAACCCAAGGAAAGTG	60
Sbjct	1	CTCTGTGGTGTGAGAACACAGTGGGTGACCAAGGCTTTCAGATGAACCCAAGGAAAGTG	60
Query	61	AAAAAGCTGATGCTAATAACCAGACAACAGAACCTCAGCTTAAGAAAGGCAGCCAAGTGG	120
Sbjct	61	AAAAAGCTGATGCTAATAACCAGACAACAGAACCTCAGCTTAAGAAAGGCAGCCAAGTGG	120
Query	121	AGGCACTCTTCAGTTATGAGGCTACCCAACCAGAGGACCTGGAGTTTCAGGAAGGGGATA	180
Sbjct	121	AGGCACTCTTCAGTTATGAGGCTACCCAACCAGAGGACCTGGAGTTTCAGGAAGGGGATA	180
Query	181	TAATCCTGGTGTTATCAAAGGTGAATGAAGAATGGCTGGAAGGGGAGTGCAAAGGGAAGG	240
Sbjct	181	TAATCCTGGTGTTATCAAAGGTGAATGAAGAATGGCTGGAAGGGGAGTGCAAAGGGAAGG	240
Query	241	TGGGCATTTTCCCCAAAGTTTTTGTGTAAGACTGCGCAACTACAGATTGGAAGCACTC	300
Sbjct	241	TGGGCATTTTCCCCAAAGTTTTTGTGTAAGACTGCGCAACTACAGATTGGAAGCACTC	300
Query	301	GGAGAGAAGTCTAGGATGTTTCACAAACTACAAAGCTGAAGAAAATGAAGCCCTATTACT	360
Sbjct	301	GGAGAGAAGTCTAGGATGTTTCACAAACTACAAAGCTGAAGAAAATGAAGCCCTATTACT	360
Query	361	TGTTTGTAAGATTTAGCACCCCTCTGCTGTATACTGTACTGAGACATTACAGTTTGAAG	420
Sbjct	361	TGTTTGTAAGATTTAGCACCCCTCTGCTGTATACTGTACTGAGACATTACAGTTTGAAG	420
Query	421	TGTAACTATTTATTCCTGTAAAAATTTAACCTACTAGACAATGATGTGAGTACCCAGG	480
Sbjct	421	TGTAACTATTTATTCCTGTAAAAATTTAACCTACTAGACAATGATGTGAGTACCCAGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATGATTTCTGGGGCACAGTGGGTGAGGAGATGGGGACAGGTGAATGGAGGAGTTAGGGG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATGATTTCTGGGGCACAGTGGGTGAGGAGATGGGGACAGGTGAATGGAGGAGTTAGGGG  540

Query  541  AGAGGAAAAGTGGATGGAAGTGTCTGGAAAGGGCACCAAAAAGTCTTCCAGGTCTGATC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AGAGGAAAAGTGGATGGAAGTGTCTGGAAAGGGCACCAAAAAGTCTTCCAGGTCTGATC  600

Query  601  CTGTTTCTTGCTCTGAGTGCTAGCTACCACTGTGTCACACTGTAACATN   649
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  CTGTTTCTTGCTCTGAGTGCTAGCTACCACTGTGTCACACTGTAACATN   649
```

Blast comparison trimmed “N” from the 3’ end of both sequences and reported 648 identities. The report has been manually corrected for this. “N” has been appended to both sequences and identity count has been increased to 649.

Sequence 905 matched with Sequence 365

Query= Sequence ID - 905 nt: 655
Length=655

SEQ ID NO: 365 nt: 655

ALIGNMENTS

Identities = 655/655 (100%), Gaps = 0/655 (0%)

Query	1	CTCAGCTCTTGCCTGGTCACCTTGTGGCTTTTACCATCCTCATCCCCTGTGCCACCCACA	60
Sbjct	1	CTCAGCTCTTGCCTGGTCACCTTGTGGCTTTTACCATCCTCATCCCCTGTGCCACCCACA	60
Query	61	TCCTGCCACTTCTGCATGGAGTTGGGGTGGGGCCATTGGAGAAAAGAGGTTAAACAAGCA	120
Sbjct	61	TCCTGCCACTTCTGCATGGAGTTGGGGTGGGGCCATTGGAGAAAAGAGGTTAAACAAGCA	120
Query	121	GTAATTTACTTGAGTACAGTCTTTGAGCCAATGAAATGCCAGTCATCATTTCCCAGGGGT	180
Sbjct	121	GTAATTTACTTGAGTACAGTCTTTGAGCCAATGAAATGCCAGTCATCATTTCCCAGGGGT	180
Query	181	ACTTGTTCATCTTGTCAACAACCCGCTGATAATGCTCCTTCAATGTGAATAGCAAAAGTAG	240
Sbjct	181	ACTTGTTCATCTTGTCAACAACCCGCTGATAATGCTCCTTCAATGTGAATAGCAAAAGTAG	240
Query	241	GGAGAGACGCTGAATGAAGAAGATGCCTACCCCTCAGGAAGACTGCTGTCCGCCTCCAGG	300
Sbjct	241	GGAGAGACGCTGAATGAAGAAGATGCCTACCCCTCAGGAAGACTGCTGTCCGCCTCCAGG	300
Query	301	CCtgcatgcacacacccatgcccacctgcacccccagcaccacgcccacactcactcgca	360
Sbjct	301	CCTGCATGCACACACCCATGCCACCTGCACCCCCAGCACCCACGCCCACTCACTCGCA	360
Query	361	cacacccacatgccaGTGTTTTGGGGTTGGCAGCCTGGACACTGCTGAGGCAAAACACAAG	420
Sbjct	361	CACACCCACATGCCAGTGTGTTTTGGGGTTGGCAGCCTGGACACTGCTGAGGCAAAACACAAG	420
Query	421	TCATCAAGCATAATTCTCATTCTCTCCTTCTGTCTCTGTTTTAGTTACAGGAATTTGGTC	480
Sbjct	421	TCATCAAGCATAATTCTCATTCTCTCCTTCTGTCTCTGTTTTAGTTACAGGAATTTGGTC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGTTTAGAGGATTTAATAAGTCCGTGGAAAATTTGTTTCTGTCTCTTGCTACCCACGTGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGTTTAGAGGATTTAATAAGTCCGTGGAAAATTTGTTTCTGTCTCTTGCTACCCACGTGA  540

Query  541  AAAGTAAGTGCATGCTTCATGATGTGTTTTCCCACTACCTTCCAGGCCAGCCGAGCCCAC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AAAGTAAGTGCATGCTTCATGATGTGTTTTCCCACTACCTTCCAGGCCAGCCGAGCCCAC  600

Query  601  TGGCCANGGCCTGGCCCGGTGACCTCGGTTGACACTGTCCTCANGCCACTCACTT  655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TGGCCANGGCCTGGCCCGGTGACCTCGGTTGACACTGTCCTCANGCCACTCACTT  655
```

Sequence 906 matched with Sequence 366

Query= Sequence ID 906
Length=334

SEQ ID NO: 366

ALIGNMENTS

Identities = 334/334 (100%), Gaps = 0/334 (0%)

Query	1	CAGAATTTTCATGTTTATGCTGCACAAGGCCTGTATTTTATAATGGTGGCTCTTTTGGACG	60
Sbjct	1	CAGAATTTTCATGTTTATGCTGCACAAGGCCTGTATTTTATAATGGTGGCTCTTTTGGACG	60
Query	61	ATGACTTCCTCGATGGTGAAACTTCCAGTAATCTCCCTCATCATACTGAAATGATATCAG	120
Sbjct	61	ATGACTTCCTCGATGGTGAAACTTCCAGTAATCTCCCTCATCATACTGAAATGATATCAG	120
Query	121	TATATCATCAGAACACCATGGAGCTTGTCATTTGAGGGACACAGCTTGCTTGTGTGCTTG	180
Sbjct	121	TATATCATCAGAACACCATGGAGCTTGTCATTTGAGGGACACAGCTTGCTTGTGTGCTTG	180
Query	181	GGAAAGAAGAGGTTTAGCATGGTTTCAGGTCAGTGATGAGTCCAATGATCTCTGCAAGTT	240
Sbjct	181	GGAAAGAAGAGGTTTAGCATGGTTTCAGGTCAGTGATGAGTCCAATGATCTCTGCAAGTT	240
Query	241	CCCTTAGCTCTGANAATTCTGATGTCATATGCACTTCTGCCGCCAGAGTTGCTGCTTACT	300
Sbjct	241	CCCTTAGCTCTGANAATTCTGATGTCATATGCACTTCTGCCGCCAGAGTTGCTGCTTACT	300
Query	301	GGATGCGTAAGAAGAAAAAGaaaaaaaaaaaaaaaaa	334
Sbjct	301	GGATGCGTAAGAAGAAAAAGAAAAAAAAAAAAAAAAA	334

Sequence 907 matched with Sequence 367

Query= Sequence ID - 907 nt: 582
Length=582

SEQ ID NO: 367 nt: 582

ALIGNMENTS

Identities = 582/582 (100%), Gaps = 0/582 (0%)

Query	1	CTTCCATTGGGGTAAAGATCAAACCTTTAGGCGAGCCAGGTCTGTATCTCCATTCCTGTC	60
Sbjct	1	CTTCCATTGGGGTAAAGATCAAACCTTTAGGCGAGCCAGGTCTGTATCTCCATTCCTGTC	60
Query	61	TCTGACTGCTTCCCTGTAGGGATTGTCTGCAAGCGCACACCTGCATTTTCTTGTCACAA	120
Sbjct	61	TCTGACTGCTTCCCTGTAGGGATTGTCTGCAAGCGCACACCTGCATTTTCTTGTCACAA	120
Query	121	GTCTATGCTCTAACTCTGTACCTGCATGGCTGCAAATTAGCTTCCTTCTTCTGCCCCTC	180
Sbjct	121	GTCTATGCTCTAACTCTGTACCTGCATGGCTGCAAATTAGCTTCCTTCTTCTGCCCCTC	180
Query	181	TTCTCTCTAGCTTGGATTTTGAATTTGAATGGCAGGCATGGGATGTCCGTGTGTGTAC	240
Sbjct	181	TTCTCTCTAGCTTGGATTTTGAATTTGAATGGCAGGCATGGGATGTCCGTGTGTGTAC	240
Query	241	TGCTGATGTGTACAGCCGCTTGTTAGCGCTCTCATTGTCTTCAAATGTAAGTCATTTTGG	300
Sbjct	241	TGCTGATGTGTACAGCCGCTTGTTAGCGCTCTCATTGTCTTCAAATGTAAGTCATTTTGG	300
Query	301	CTGGGTGCGGTGGCTCATGCGTATAATCCCACGCTTTGGGAGGCTGAGGTGAGCTGATCA	360
Sbjct	301	CTGGGTGCGGTGGCTCATGCGTATAATCCCACGCTTTGGGAGGCTGAGGTGAGCTGATCA	360
Query	361	TTTGAGGTAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAACTCCATCTCTACCAAA	420
Sbjct	361	TTTGAGGTAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAACTCCATCTCTACCAAA	420
Query	421	AATACAAAAATTAGCTGGGTATGGTAGTGCACGCCTGTAATCCCAGCTACTTGGAATGCT	480
Sbjct	421	AATACAAAAATTAGCTGGGTATGGTAGTGCACGCCTGTAATCCCAGCTACTTGGAATGCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GAAGCAGGAGAATTGCCTGAACCCANGAGGCGGAGGTTGCGGTGAGCCAAGATCACGCCA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GAAGCAGGAGAATTGCCTGAACCCANGAGGCGGAGGTTGCGGTGAGCCAAGATCACGCCA  540

Query  541  CTGCACTCCAACCTGGGTGACAGAGCAAGGCTGTGTCTCAA  582
          ||||||||||||||||||||||||||||
Sbjct   541  CTGCACTCCAACCTGGGTGACAGAGCAAGGCTGTGTCTCAA  582
```


Sequence 908 matched with Sequence 368

Query= Sequence ID 908
Length=530

SEQ ID NO: 368

ALIGNMENTS

Identities = 530/530 (100%), Gaps = 0/530 (0%)

Query	1	ACCTGACTTCAAAC TACTACGAGGCTACAGTAATCAAACAGCATGGTACTAGTACAA	60
Sbjct	1	ACCTGACTTCAAAC TACTACGAGGCTACAGTAATCAAACAGCATGGTACTAGTACAA	60
Query	61	AAACAGACCAATGGAACAGAATAGAGATCTCAGAAATAAACTGCACATCTACAACCATC	120
Sbjct	61	AAACAGACCAATGGAACAGAATAGAGATCTCAGAAATAAACTGCACATCTACAACCATC	120
Query	121	TGATCTTCAACAAACCTGACAAAACGAGCAATGGGGAAAGGATTCCCTATTTAATAAATG	180
Sbjct	121	TGATCTTCAACAAACCTGACAAAACGAGCAATGGGGAAAGGATTCCCTATTTAATAAATG	180
Query	181	GTGCTGGGAGAACTGGCTAGCCATGTGCAGAAAATTGAACTGGACCCCTTCCTTACACC	240
Sbjct	181	GTGCTGGGAGAACTGGCTAGCCATGTGCAGAAAATTGAACTGGACCCCTTCCTTACACC	240
Query	241	TTATACAAAAATTAAC TCAAGATGGATTAAAGACTTAAATGTAGAACCCAAAACGATAAA	300
Sbjct	241	TTATACAAAAATTAAC TCAAGATGGATTAAAGACTTAAATGTAGAACCCAAAACGATAAA	300
Query	301	AACCCTAGAAGAAAATCTAGGCAATATCATTAAGGACATAGACATGGGCAAAAATTTTCAT	360
Sbjct	301	AACCCTAGAAGAAAATCTAGGCAATATCATTAAGGACATAGACATGGGCAAAAATTTTCAT	360
Query	361	GATGAAAACATCAAAGCAATGGCAACAAAAGCAGAACTGACAAATGGGCTTCTGCACA	420
Sbjct	361	GATGAAAACATCAAAGCAATGGCAACAAAAGCAGAACTGACAAATGGGCTTCTGCACA	420
Query	421	GCAAAAGAACTATCGTCAGAGTGAACAGACAACCTACAGAATGGGAGACAGTTTTTGCA	480
Sbjct	421	GCAAAAGAACTATCGTCAGAGTGAACAGACAACCTACAGAATGGGAGACAGTTTTTGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATCTATCCATCTGACAAAAGTCTAATATCCAGAATCTACAAGGAATTAA	530
Sbjct	481	ATCTATCCATCTGACAAAAGTCTAATATCCAGAATCTACAAGGAATTAA	530

Sequence 910 matched with Sequence 369

Query= Sequence ID 910
Length=653

SEQ ID NO: 369

ALIGNMENTS

Identities = 653/653 (100%), Gaps = 0/653 (0%)

Query	1	CAAAAAACAAGAATTACCCGGGCTTGGTGGTGCATGTCTGTAGTCCTATCTACTCAGGAG	60
Sbjct	1	CAAAAAACAAGAATTACCCGGGCTTGGTGGTGCATGTCTGTAGTCCTATCTACTCAGGAG	60
Query	61	GCTGAGGCTGAAGGATCACTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGTGAGCCATGAT	120
Sbjct	61	GCTGAGGCTGAAGGATCACTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGTGAGCCATGAT	120
Query	121	CATGCCAGTGTACTCCAGCCTTGGCAGACTGAGCAAACTTGGTCCCTCGCAAAATGTTG	180
Sbjct	121	CATGCCAGTGTACTCCAGCCTTGGCAGACTGAGCAAACTTGGTCCCTCGCAAAATGTTG	180
Query	181	AAGCCCAGTTTTCACTATTAACCTGTATTTTCAGTTTCCCATGCTAACTTTGAAACACTG	240
Sbjct	181	AAGCCCAGTTTTCACTATTAACCTGTATTTTCAGTTTCCCATGCTAACTTTGAAACACTG	240
Query	241	GGGCTGGCCTGAGGGTATAAAGGCTTATTCAAACCTCAGTAATTTAAACTTAAATCCTAA	300
Sbjct	241	GGGCTGGCCTGAGGGTATAAAGGCTTATTCAAACCTCAGTAATTTAAACTTAAATCCTAA	300
Query	301	GGAACCTCAAAAAGTGAATCTAGTCCAAATGGGGCATCAATTCTAAAGCATTTGCTTGT	360
Sbjct	301	GGAACCTCAAAAAGTGAATCTAGTCCAAATGGGGCATCAATTCTAAAGCATTTGCTTGT	360
Query	361	TTGAGCAGATTTTCTGTGTCTGAGGTATATAGATAACTTATCTTTTTATGACTAAATCCA	420
Sbjct	361	TTGAGCAGATTTTCTGTGTCTGAGGTATATAGATAACTTATCTTTTTATGACTAAATCCA	420
Query	421	AGTCCTTAGTTCCTGTTGGAATTCAAAATCATATTTAAAAATTGATGCTTTGTTCTATAA	480
Sbjct	421	AGTCCTTAGTTCCTGTTGGAATTCAAAATCATATTTAAAAATTGATGCTTTGTTCTATAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTAATGCTTTGATTGTATAAAATAATAAGTATTCTTCCAAATCCCTTTTACAGATGATGA	540
Sbjct	481	TTAATGCTTTGATTGTATAAAATAATAAGTATTCTTCCAAATCCCTTTTACAGATGATGA	540
Query	541	TTCTGATACCGAGACGTCAAATGACTTGCCAAAATTTGCAGATGGAATCAAGGCCNGAAA	600
Sbjct	541	TTCTGATACCGAGACGTCAAATGACTTGCCAAAATTTGCAGATGGAATCAAGGCCNGAAA	600
Query	601	CAGAAATCAGAACTACCTGGNTCCCAGTCCTGTNCTTAAAATTCTAACTCGAC	653
Sbjct	601	CAGAAATCAGAACTACCTGGNTCCCAGTCCTGTNCTTAAAATTCTAACTCGAC	653

Sequence 911 matched with Sequence 370

Query= Sequence ID - 911 nt: 595
Length=595

SEQ ID NO: 370 nt: 595

ALIGNMENTS

Identities = 595/595 (100%), Gaps = 0/595 (0%)

Query	1	GAGGGTGTAGAAGAGAAGAAGAAGGAGGTTCTGCTGTGCCANAAACCCCTTAAGAAAAAG	60
Sbjct	1	GAGGGTGTAGAAGAGAAGAAGAAGGAGGTTCTGCTGTGCCANAAACCCCTTAAGAAAAAG	60
Query	61	CGAAGGAATTTTCGCAGAGCTGAAGATCAAGCGCCTGAGAAAGAAGTTTGCCCAAAGATG	120
Sbjct	61	CGAAGGAATTTTCGCAGAGCTGAAGATCAAGCGCCTGAGAAAGAAGTTTGCCCAAAGATG	120
Query	121	CTTCGAAAGGCAAGGAGGAAGCTTATCTATGAAAAANCAAAGCACTATCACAAGGAATAT	180
Sbjct	121	CTTCGAAAGGCAAGGAGGAAGCTTATCTATGAAAAANCAAAGCACTATCACAAGGAATAT	180
Query	181	AGGCAGATGTACAAANCTGAAATTCGAATGGCGAGGATGGCAAGAAAAGCTGGCAACTTC	240
Sbjct	181	AGGCAGATGTACAAANCTGAAATTCGAATGGCGAGGATGGCAAGAAAAGCTGGCAACTTC	240
Query	241	TATGTACCTGCAGAACCCAAATTGGCGTTTGTTCATCAGAATCAGAGGTATCAATGGAGTG	300
Sbjct	241	TATGTACCTGCAGAACCCAAATTGGCGTTTGTTCATCAGAATCAGAGGTATCAATGGAGTG	300
Query	301	AGCCCAAAGGTTTCGAAAGGTGTTGCAGCTTCTTCGCCTTCGTCAAATCTTCAATGGAACC	360
Sbjct	301	AGCCCAAAGGTTTCGAAAGGTGTTGCAGCTTCTTCGCCTTCGTCAAATCTTCAATGGAACC	360
Query	361	TTTGTGAAGCTCAACAAGGCTTCGATTAACATGCTGAGGATTGTAGAGCCATATATTGCA	420
Sbjct	361	TTTGTGAAGCTCAACAAGGCTTCGATTAACATGCTGAGGATTGTAGAGCCATATATTGCA	420
Query	421	TGGGGGTACCCCAATCTGAAGTCAGTAAATGAACTAATCTACAAGCGTGGTTATGGCAAA	480
Sbjct	421	TGGGGGTACCCCAATCTGAAGTCAGTAAATGAACTAATCTACAAGCGTGGTTATGGCAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATCAATAAGAAGCGAATTGCTTTGACAGATAACGCTTTGATTGCTCGATCTCTTGGTAAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATCAATAAGAAGCGAATTGCTTTGACAGATAACGCTTTGATTGCTCGATCTCTTGGTAAA  540

Query  541  TACNGCATCATCTGCATGGAGGATTTGATTCATGAGATCTATACTGTTGGAAAAC  595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TACNGCATCATCTGCATGGAGGATTTGATTCATGAGATCTATACTGTTGGAAAAC  595
```

Sequence 912 matched with Sequence 371

Query= Sequence ID - 912 nt: 651
Length=651

SEQ ID NO: 371 nt: 651

ALIGNMENTS

Identities = 651/651 (100%), Gaps = 0/651 (0%)

Query	1	CATTTCCAGAGTTTATGTGAATTGAATTGAACTATGGTTTTATGTTACTGTCAGTAGAAT	60
Sbjct	1	CATTTCCAGAGTTTATGTGAATTGAATTGAACTATGGTTTTATGTTACTGTCAGTAGAAT	60
Query	61	GAAGTACGAATATTTGAAAAATACACCTTCAACTTCAAAGTGATTCTTGACAAAAATTAT	120
Sbjct	61	GAAGTACGAATATTTGAAAAATACACCTTCAACTTCAAAGTGATTCTTGACAAAAATTAT	120
Query	121	AAGGAATCATTTTGGACACATTTTCTGGTAGAGCCTTGTA AAAATTAA AACCAAGTGTTG	180
Sbjct	121	AAGGAATCATTTTGGACACATTTTCTGGTAGAGCCTTGTA AAAATTAA AACCAAGTGTTG	180
Query	181	TTTTCAAGAAGAACTGTAATACATAATCAGGAATTTGAGTAGGGAGATTATTTTGTTATT	240
Sbjct	181	TTTTCAAGAAGAACTGTAATACATAATCAGGAATTTGAGTAGGGAGATTATTTTGTTATT	240
Query	241	TAA AATTAAAGTGGCTGTGTAGTTTAACTTTAGTATTGCAGGTAGAGTAAGCTTACATG	300
Sbjct	241	TAA AATTAAAGTGGCTGTGTAGTTTAACTTTAGTATTGCAGGTAGAGTAAGCTTACATG	300
Query	301	ATAACAAAAATCTTGGTCTTAGTGACTTAATGATTCTGATATTTATTGATTGATTGGTTA	360
Sbjct	301	ATAACAAAAATCTTGGTCTTAGTGACTTAATGATTCTGATATTTATTGATTGATTGGTTA	360
Query	361	TCATTCCAAATATTTTAAAAGATAATAGCTGGCTGGGTGCGGTGGCTCATGCCTGTAATC	420
Sbjct	361	TCATTCCAAATATTTTAAAAGATAATAGCTGGCTGGGTGCGGTGGCTCATGCCTGTAATC	420
Query	421	CCAGCACTTTGGGAGGCCAGGACGGGCGGATCACGAGGTCAGGAGATCAAGACCATCCTG	480
Sbjct	421	CCAGCACTTTGGGAGGCCAGGACGGGCGGATCACGAGGTCAGGAGATCAAGACCATCCTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCTAACACGGTGAAACCCCGTCTCTACTaaaaatcaaaaaaTTAGCCGGGTGTAGTGGCG	540
Sbjct	481	GCTAACACGGTGAAACCCCGTCTCTACTAAAAATCAAAAAATTAGCCGGGTGTAGTGGCG	540
Query	541	GGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAG	600
Sbjct	541	GGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAG	600
Query	601	GCGGAGCTTGCAGTGAGCTGAAATCGTGCCACTGCCTCCACCTGGCGACAA	651
Sbjct	601	GCGGAGCTTGCAGTGAGCTGAAATCGTGCCACTGCCTCCACCTGGCGACAA	651

Sequence 913 matched with Sequence 372

Query= Sequence ID 913
Length=531

SEQ ID NO: 372

ALIGNMENTS

Identities = 531/531 (100%), Gaps = 0/531 (0%)

Query	1	GTGAGGTGGGACTTCATTCA	TTCCTATTTCTATCTCCACTTTGTGCCTGGAGAGCTT	60
Sbjct	1	GTGAGGTGGGACTTCATTCA	TTCCTATTTCTATCTCCACTTTGTGCCTGGAGAGCTT	60
Query	61	TCAGGGGAGGTGGAGGAGGAGGGTCTGCCAAGCTACTGCAACATCTGTCACCCACTATAC	120	
Sbjct	61	TCAGGGGAGGTGGAGGAGGAGGGTCTGCCAAGCTACTGCAACATCTGTCACCCACTATAC	120	
Query	121	CCAGTTACTTGGGGGAGGACAGACACTGTGGTGTCA	TAAAGTTGTTTGAACCAAAGTGG	180
Sbjct	121	CCAGTTACTTGGGGGAGGACAGACACTGTGGTGTCA	TAAAGTTGTTTGAACCAAAGTGG	180
Query	181	CGGCTGCATCTTTGTCCCGATGCTAGCCGTGCCGGTCTCCCATCATCCGCTCGCCCTCCT	240	
Sbjct	181	CGGCTGCATCTTTGTCCCGATGCTAGCCGTGCCGGTCTCCCATCATCCGCTCGCCCTCCT	240	
Query	241	TTNCCCTGGGCTGCGCCCACTTGTCTTCCTGGATATTTGGGGGTGACTCGCCATGCTTGG	300	
Sbjct	241	TTNCCCTGGGCTGCGCCCACTTGTCTTCCTGGATATTTGGGGGTGACTCGCCATGCTTGG	300	
Query	301	CACCCTCTGCTTCCTGGTGTGCTCTGACTCGAAGACGGGACAGTCCCTGGTGCACATCC	360	
Sbjct	301	CACCCTCTGCTTCCTGGTGTGCTCTGACTCGAAGACGGGACAGTCCCTGGTGCACATCC	360	
Query	361	AGGGAAGAGGAGTGTCTCGGTAGTTCTTGCAGTAGGCACTTTATCAGGACCTGACCTGTTGC	420	
Sbjct	361	AGGGAAGAGGAGTGTCTCGGTAGTTCTTGCAGTAGGCACTTTATCAGGACCTGACCTGTTGC	420	
Query	421	TGGGTGATTTTAGTCTCTACAAACAGAAAGCGTTTCAAAGCGTCAGCTGTGGGAGCAGAG	480	
Sbjct	421	TGGGTGATTTTAGTCTCTACAAACAGAAAGCGTTTCAAAGCGTCAGCTGTGGGAGCAGAG	480	

PATENT SEQUENCE ALIGNMENT

Query	481	TGACCCTTTGCTGATGCTGGGGGGAGGGGATCTAAATCCTCATTATCTCT	531
Sbjct	481	TGACCCTTTGCTGATGCTGGGGGGAGGGGATCTAAATCCTCATTATCTCT	531

Sequence 914 matched with Sequence 373

Query= Sequence ID 914
Length=602

SEQ ID NO: 373

ALIGNMENTS

Identities = 602/602 (100%), Gaps = 0/602 (0%)

Query	1	GGCGCCTGCTGGAGGAGGAGAGCTCTGCTGGCATGAGCCACAGTTTCTTGA	60
Sbjct	1	GGCGCCTGCTGGAGGAGGAGAGCTCTGCTGGCATGAGCCACAGTTTCTTGA	60
Query	61	CCATCAACCCTCTTGGTTGAGGCCTTGTCTGAGCCCTGACATGTGCTTGGG	120
Sbjct	61	CCATCAACCCTCTTGGTTGAGGCCTTGTCTGAGCCCTGACATGTGCTTGGG	120
Query	121	GGCCTGGGCTTCTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCCG	180
Sbjct	121	GGCCTGGGCTTCTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCCG	180
Query	181	CTCTCAGTTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGAAAGATT	240
Sbjct	181	CTCTCAGTTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGAAAGATT	240
Query	241	AATAATCAGGCTTTTTAAATGATGTAATCCCACTGTAATAGCATAGGGAT	300
Sbjct	241	AATAATCAGGCTTTTTAAATGATGTAATCCCACTGTAATAGCATAGGGAT	300
Query	301	AGCTGCTGGTGGCTTGGGACATCAGTGGGGCCAAGGGTTCTCTGTCCCT	360
Sbjct	301	AGCTGCTGGTGGCTTGGGACATCAGTGGGGCCAAGGGTTCTCTGTCCCT	360
Query	361	GATTTGGCTTTCCCGTGTCTTTCCTGGTGATGCCTTGTTTGGGGTTCTG	420
Sbjct	361	GATTTGGCTTTCCCGTGTCTTTCCTGGTGATGCCTTGTTTGGGGTTCTG	420
Query	421	GGGAAGAGGGCCATCTGCCTGAATGTAACCTGCTAGCTCTCCGAAGCC	480
Sbjct	421	GGGAAGAGGGCCATCTGCCTGAATGTAACCTGCTAGCTCTCCGAAGCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTGTGTGAACCGTGTGGACAGTGGTGGCCGCGCTGTGCCTGCTCGTGTGCCTACATGTC	540
Sbjct	481	TTGTGTGAACCGTGTGGACAGTGGTGGCCGCGCTGTGCCTGCTCGTGTGCCTACATGTC	540
Query	541	CCTGGCTGTTGAGGCGCTGCTTTAACCTGCACCCCTNCCTTGCTCATANATGCTCCTTTT	600
Sbjct	541	CCTGGCTGTTGAGGCGCTGCTTTAACCTGCACCCCTNCCTTGCTCATANATGCTCCTTTT	600
Query	601	GA	602
Sbjct	601	GA	602

Sequence 915 matched with Sequence 374

Query= Sequence ID - 915 nt: 230
Length=230

SEQ ID NO: 374 nt: 230

ALIGNMENTS

Identities = 230/230 (100%), Gaps = 0/230 (0%)

Query	1	TTTGAGACCAGCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAG	60
Sbjct	1	TTTGAGACCAGCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAG	60
Query	61	CCGGGCGTGGCGGCACATGCCTATAATCCCACTTACTTGGGAGGCTGANGTAGGAGAATC	120
Sbjct	61	CCGGGCGTGGCGGCACATGCCTATAATCCCACTTACTTGGGAGGCTGANGTAGGAGAATC	120
Query	121	GCTTGAACCCANANAGGCAGAGTTTGCAGTGAGCCGAGATTGTGCCATTGCACTCCAGCC	180
Sbjct	121	GCTTGAACCCANANAGGCAGAGTTTGCAGTGAGCCGAGATTGTGCCATTGCACTCCAGCC	180
Query	181	TGGGCGACAGAGCGAGACTCCATCTaaaaaTAAATGAATAAAATAA	230
Sbjct	181	TGGGCGACAGAGCGAGACTCCATCTAAAAAATAAATGAATAAAATAA	230

Sequence 917 matched with Sequence 375

Query= Sequence ID 917
Length=483

SEQ ID NO: 375

ALIGNMENTS

Identities = 483/483 (100%), Gaps = 0/483 (0%)

```
Query 1  NNCAGAtttttttttttttttCAGNGTTAGACCATCTTTCAATTCCTGGAACAAACTTAACT 62
          |||
Sbjct 1  NNCAGATTTTTTTTTTTTTTTTCAGNGTTAGACCATCTTTCAATTCCTGGAACAAACTTAACT 62

Query 63  TTCCATGATATGtattttttatacattgctggattttatttgctaataattttacttagga 122
          |||
Sbjct 63  TTCCATGATATGTATTTTTTATACATTGCTGGATTTTATTGCTAATATTTTACTTAGGA 122

Query 123  ttttaattttCTAAGTNGACCTATAATTNTCCTGTATAAAATTGCATTTGTCACATTTTAG 182
          |||
Sbjct 123  TTTAATTTTCTAAGTNGACCTATAATTNTCCTGTATAAAATTGCATTTGTCACATTTTAG 182

Query 183  TATCAAGGTTGTCCTANCNCCATGAAATGGATTTANAATGGTTTATGTAANATAAAGTAC 242
          |||
Sbjct 183  TATCAAGGTTGTCCTANCNCCATGAAATGGATTTANAATGGTTTATGTAANATAAAGTAC 242

Query 243  ATTTCTTCTAAAGGTTTGN GTGGATTAAC TTTCAAATCTGCCANAGNGNGtttttttcct 302
          |||
Sbjct 243  ATTTCTTCTAAAGGTTTGN GTGGATTAAC TTTCAAATCTGCCANAGNGNGTTTTTTTCCT 302

Query 303  tttttttttttttttCATTNNAAGGGAGNGCAAGTANCttttcaaatnctgatttaatttt 362
          |||
Sbjct 303  TTTTTTTTTTTTTTTCATTNNAAGGGAGNGCAAGTANC TTTTCAAATNCTGATTTAATTTT 362

Query 363  taaaatatttncaagtntntttanagtttttattntntntngaangttaacatttttata 422
          |||
Sbjct 363  TAAATATTTNCAAGTNTNTTANAGTTTTTATTTNTTNTNGAANGTTAACATTTTATA 422

Query 423  naaaanGGTNTTATCTTTTTAAATTCTTTGACATCAGTTTCTTCANAATTCCTTCTTTTA 482
          |||
Sbjct 423  NAAAANGGTNTTATCTTTTTAAATTCTTTGACATCAGTTTCTTCANAATTCCTTCTTTTA 482
```

Query 483 A 483
|
Sbjct 483 A 483

Blast comparison trimmed “NN” from the 5’ end of both sequences and reported 481 identities. The report has been manually corrected for this. “NN” has been prepended to both sequences and identity count has been increased to 483.

Sequence 926 matched with Sequence 376

Query= Sequence ID 926
Length=538

SEQ ID NO: 376

ALIGNMENTS

Identities = 538/538 (100%), Gaps = 0/538 (0%)

Query	1	GTCATATCTCTTCCCAGGGAAAGCAGGAGCCCTTCTGGAGCCCTTCAGCAGGGTCAGGGC	60
Sbjct	1	GTCATATCTCTTCCCAGGGAAAGCAGGAGCCCTTCTGGAGCCCTTCAGCAGGGTCAGGGC	60
Query	61	CCCTCGTCTTCCCCTCCTTTCCCAGAGCCATCTTCCCAGTCCACCATCCCCATCGTGGGC	120
Sbjct	61	CCCTCGTCTTCCCCTCCTTTCCCAGAGCCATCTTCCCAGTCCACCATCCCCATCGTGGGC	120
Query	121	ATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTACTGTG	180
Sbjct	121	ATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTACTGTG	180
Query	181	ATGTGTAGGAGGAAGAGCTCAGGTAGGGAAGGGGTGAGGGGTGGGGTCTGGGTTTTCTTG	240
Sbjct	181	ATGTGTAGGAGGAAGAGCTCAGGTAGGGAAGGGGTGAGGGGTGGGGTCTGGGTTTTCTTG	240
Query	241	TCCCACTGGGGGTTTCAAGCCCCAGGTAGAAGTGTTCCCTGCCTCATTACTGGGAAGCAG	300
Sbjct	241	TCCCACTGGGGGTTTCAAGCCCCAGGTAGAAGTGTTCCCTGCCTCATTACTGGGAAGCAG	300
Query	301	CATCCACACAGGGGCTAACGCAGCCTGGGACCCTGTGTGCCAGCACTTACTCTTTTGTGC	360
Sbjct	301	CATCCACACAGGGGCTAACGCAGCCTGGGACCCTGTGTGCCAGCACTTACTCTTTTGTGC	360
Query	361	AGCACATGTGACAATGAAGGACGGATGTATCACCTTGATGGTTGTGGTGTGGGGTCCTG	420
Sbjct	361	AGCACATGTGACAATGAAGGACGGATGTATCACCTTGATGGTTGTGGTGTGGGGTCCTG	420
Query	421	ATTTTCAGCATTTCATGAGTCAGGGGAAGGTCCCTGCTAAGGACAGACCTTAGGAGGGCAGT	480
Sbjct	421	ATTTTCAGCATTTCATGAGTCAGGGGAAGGTCCCTGCTAAGGACAGACCTTAGGAGGGCAGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGGTCCAGGACCCACACTTGCTTTCCTCGTGTTTCCTGATCCTGCCTTGGGTCTGTAG	538
Sbjct	481	TGGTCCAGGACCCACACTTGCTTTCCTCGTGTTTCCTGATCCTGCCTTGGGTCTGTAG	538

Sequence 938 matched with Sequence 377

Query= Sequence ID 938
Length=440

SEQ ID NO: 377

ALIGNMENTS

Identities = 440/440 (100%), Gaps = 0/440 (0%)

Query	1	TGGCCATCCTTTTCCCCCAAACACACCCCCTTAACCTATCTCTTGGGACTTAGCCCGAC	60
Sbjct	1	TGGCCATCCTTTTCCCCCAAACACACCCCCTTAACCTATCTCTTGGGACTTAGCCCGAC	60
Query	61	CCTCCCTCTCATTTCCCATTAAGTCTGAGAGGCAAGAGCTAGGTTAGGCAAGGAGGTGGT	120
Sbjct	61	CCTCCCTCTCATTTCCCATTAAGTCTGAGAGGCAAGAGCTAGGTTAGGCAAGGAGGTGGT	120
Query	121	TGGCCAGAGATGGGGAACAGCCAGGTGCCCCAGTCCTCTGATTTTTCCTCCATCCTGCTT	180
Sbjct	121	TGGCCAGAGATGGGGAACAGCCAGGTGCCCCAGTCCTCTGATTTTTCCTCCATCCTGCTT	180
Query	181	ACCACCTCCCTGGGTACTTACAGCCTTCTCTTGGGAACAGCCGGGGCCAGGACTGGGTCA	240
Sbjct	181	ACCACCTCCCTGGGTACTTACAGCCTTCTCTTGGGAACAGCCGGGGCCAGGACTGGGTCA	240
Query	241	CCTATGAGCTGAATCAGCATCTCCTCCTGAGTCCCAGGGCCCCTGCAGTTCCCAGTCTCT	300
Sbjct	241	CCTATGAGCTGAATCAGCATCTCCTCCTGAGTCCCAGGGCCCCTGCAGTTCCCAGTCTCT	300
Query	301	TCTGTCCTGCAGCCCTTGCCTCTTTCCACAGGTTCCACTTTATATCCACCTttttccttt	360
Sbjct	301	TCTGTCCTGCAGCCCTTGCCTCTTTCCACAGGTTCCACTTTATATCCACCTTTTCCTTT	360
Query	361	tgttcaatttttatttttatttttttttATTATTAAATGATGTGGTCTATGGaaaaaaa	420
Sbjct	361	TGTTCAATTTTATTTTATTTTATTATTAAATGATGTGGTCTATGGAAAAAAAAA	420
Query	421	taaaaTCTGACTTAGTTTT	440
Sbjct	421	TAAAAATCTGACTTAGTTTT	440

Sequence 939 matched with Sequence 378

Query= Sequence ID - 939 nt: 513
Length=513

SEQ ID NO: 378 nt: 513

ALIGNMENTS

Identities = 513/513 (100%), Gaps = 0/513 (0%)

Query	1	GGAACCCAGTGTATTACCTGCTGGAACCAAGGAACTAACAATGTAGGTTACTAGTGAAT	60
Sbjct	1	GGAACCCAGTGTATTACCTGCTGGAACCAAGGAACTAACAATGTAGGTTACTAGTGAAT	60
Query	61	ACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAAAATTCTCTAA	120
Sbjct	61	ACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAAAATTCTCTAA	120
Query	121	CACTGCAAAGAGTGAGCCATGCCTGTAACTGTAAAGAATGTAACATGTGGGGGACAC	180
Sbjct	121	CACTGCAAAGAGTGAGCCATGCCTGTAACTGTAAAGAATGTAACATGTGGGGGACAC	180
Query	181	ACAGGGGCAGATGGGATGGTTTAGTTTAGGATTTTATTAGTGCATGCCCTACCCTCTGGG	240
Sbjct	181	ACAGGGGCAGATGGGATGGTTTAGTTTAGGATTTTATTAGTGCATGCCCTACCCTCTGGG	240
Query	241	GGAACGTCCCATCTGAGGTTTCTTCTCGGTGGGGGATTTAACTTCTGTCCTAGGGAAA	300
Sbjct	241	GGAACGTCCCATCTGAGGTTTCTTCTCGGTGGGGGATTTAACTTCTGTCCTAGGGAAA	300
Query	301	ACAGTGTCTGATGAGGAGTGTTCACACAGGCTACATGAATCCCCTATACCAGTGCG	360
Sbjct	301	ACAGTGTCTGATGAGGAGTGTTCACACAGGCTACATGAATCCCCTATACCAGTGCG	360
Query	361	AAAGCAGCCAGGAGTCCCCGTTGAAAAGAACAATGCCACTCTCTTTTATGTATCTTGGT	420
Sbjct	361	AAAGCAGCCAGGAGTCCCCGTTGAAAAGAACAATGCCACTCTCTTTTATGTATCTTGGT	420
Query	421	TCTGCAACTCATTGTGTAAGTAGGGTTAATCGAGTATCAGGTTACAGTATCCTGCCC	480
Sbjct	421	TCTGCAACTCATTGTGTAAGTAGGGTTAATCGAGTATCAGGTTACAGTATCCTGCCC	480

PATENT SEQUENCE ALIGNMENT

Query 481 TTATTATTTTATGATTCACTGACTCAAGTTCCA 513
|||||
Sbjct 481 TTATTATTTTATGATTCACTGACTCAAGTTCCA 513

Sequence 947 matched with Sequence 379

Query= Sequence ID 947
Length=646

SEQ ID NO: 379

ALIGNMENTS

Identities = 646/646 (100%), Gaps = 0/646 (0%)

Query	1	GAGAGTGAAAAAATTCTGGTACAAATTGGGAAATTAGTATATAACAACATAGTGTTAAAT	60
Sbjct	1	GAGAGTGAAAAAATTCTGGTACAAATTGGGAAATTAGTATATAACAACATAGTGTTAAAT	60
Query	61	TCAATGGGAAAAGTTTAATAAGAGGATTTGGTATCAACTGGCTGTCCAAAGATAAAAAATG	120
Sbjct	61	TCAATGGGAAAAGTTTAATAAGAGGATTTGGTATCAACTGGCTGTCCAAAGATAAAAAATG	120
Query	121	GACCGTCCTATCACATACAAAATTGTTTTTTAGATAAAGATTTAAATACAGGCACTCCTT	180
Sbjct	121	GACCGTCCTATCACATACAAAATTGTTTTTTAGATAAAGATTTAAATACAGGCACTCCTT	180
Query	181	CATTTGCGTGGTGACCTTGAGGTGTTGCAGAAATGATGAGAGCTGAAACTGCAAAGCAA	240
Sbjct	181	CATTTGCGTGGTGACCTTGAGGTGTTGCAGAAATGATGAGAGCTGAAACTGCAAAGCAA	240
Query	241	TTTTAATACTTTATCTGTTGGAAATCTTATAGTTTTCTGTGACCGTTAAAATTTTCATT	300
Sbjct	241	TTTTAATACTTTATCTGTTGGAAATCTTATAGTTTTCTGTGACCGTTAAAATTTTCATT	300
Query	301	AAACTATTAAAAACACCCATGACTGGTCACaaatgtattgggaaatggaaaagaattaat	360
Sbjct	301	AAACTATTAAAAACACCCATGACTGGTCACAAATGTATTGGGAAATGGAAAAGAATTAAT	360
Query	361	acactaaaaatacaaaaaatagaaaatatataaaattatctaaaaatttgaaacattaga	420
Sbjct	361	ACACTAAAAATACAAAAATAGAAAATATTTAAAATTATCTAAAAATTTGAAACATTAGA	420
Query	421	aaaattGAGAACTAGGCAGGGCGTGGTGGCTCACATCTGTAATTTTAGCCCTTTGGGAGG	480
Sbjct	421	AAAATTGAGAACTAGGCAGGGCGTGGTGGCTCACATCTGTAATTTTAGCCCTTTGGGAGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTGANGCAGGTGGATCACCTGANGTCAGGAGTTCGAGACCAGCCTGCCAACGTGGGGAAA  540
          |||
Sbjct  481  CTGANGCAGGTGGATCACCTGANGTCAGGAGTTCGAGACCAGCCTGCCAACGTGGGGAAA  540

Query  541  CCCC GTCTCTACTGAAAATACAAAAATTANCCGGGCATGGTGGCACAAGCCTGTAATNCT  600
          |||
Sbjct  541  CCCC GTCTCTACTGAAAATACAAAAATTANCCGGGCATGGTGGCACAAGCCTGTAATNCT  600

Query  601  TGCTNACCAGGANGCTGAGGCAGGAGAATCACTTGAACCCANGANG  646
          |||
Sbjct  601  TGCTNACCAGGANGCTGAGGCAGGAGAATCACTTGAACCCANGANG  646
```

Blast comparison trimmed “NGANG” from the 3’ end of both sequences and reported 641 identities. The report has been manually corrected for this. “NGANG” has been appended to both sequences and identity count has been increased to 646.

Sequence 949 matched with Sequence 380

Query= Sequence ID 949
Length=362

SEQ ID NO: 380

ALIGNMENTS

Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query	1	GTTTCACATGAGAAGGTAGTATTATGTACAGTGACCTTGTTTAAAGTGTCNGTTTAATGT	60
Sbjct	1	GTTTCACATGAGAAGGTAGTATTATGTACAGTGACCTTGTTTAAAGTGTCNGTTTAATGT	60
Query	61	TACCACTAAGGCCCTGCCCCAGCTTTATCACCTGAGCACTAACAAGTGCTGTGTGGAGTT	120
Sbjct	61	TACCACTAAGGCCCTGCCCCAGCTTTATCACCTGAGCACTAACAAGTGCTGTGTGGAGTT	120
Query	121	CAGTCCATGCTGGTAACTNTTGAGTATTCAGTGGGTCTTTTAAACAATTACCACCGTGGAG	180
Sbjct	121	CAGTCCATGCTGGTAACTNTTGAGTATTCAGTGGGTCTTTTAAACAATTACCACCGTGGAG	180
Query	181	GANANAGCAAGGAAGAGAAATGCTGTGATCTTTTNCTGTTTTTAATTAGNGAAAGAGGGA	240
Sbjct	181	GANANAGCAAGGAAGAGAAATGCTGTGATCTTTTNCTGTTTTTAATTAGNGAAAGAGGGA	240
Query	241	TTANATTAAACAAATGTTACAGAGNTGTGACTNTGATCCCCAGNGGTAAGCAATAATTG	300
Sbjct	241	TTANATTAAACAAATGTTACAGAGNTGTGACTNTGATCCCCAGNGGTAAGCAATAATTG	300
Query	301	TANAGACTGGATTTNANAAGCCCTGAGAGTTTATTTTCAACCTATNTATTATAGNNCAAT	360
Sbjct	301	TANAGACTGGATTTNANAAGCCCTGAGAGTTTATTTTCAACCTATNTATTATAGNNCAAT	360
Query	361	CC 362	
Sbjct	361	CC 362	

Sequence 1028 matched with Sequence 381

Query= Sequence ID 1028
Length=80

SEQ ID NO: 381

ALIGNMENTS

Identities = 80/80 (100%), Gaps = 0/80 (0%)

```
Query 1  ACAAGGCTTGGGGGCTGGACTCCCTCTACTGCCTCTGGCCATACCCCCTCCTGGAGATGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  ACAAGGCTTGGGGGCTGGACTCCCTCTACTGCCTCTGGCCATACCCCCTCCTGGAGATGG 60

Query 61 GGTCAAGGCACCAGGACTGA 80
          ||||||||||||||||
Sbjct 61 GGTCAAGGCACCAGGACTGA 80
```

Sequence 1056 matched with Sequence 382

Query= Sequence ID - 1056 nt: 435
Length=435

SEQ ID NO: 382 nt: 435

ALIGNMENTS

Identities = 435/435 (100%), Gaps = 0/435 (0%)

Query	1	TCGCTTGTAAGCCTGAGACAGCTGCCTGTGTGGGACTGAGATGCAGGATTTCTTCACAC	60
Sbjct	1	TCGCTTGTAAGCCTGAGACAGCTGCCTGTGTGGGACTGAGATGCAGGATTTCTTCACAC	60
Query	61	CTCTCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGT	120
Sbjct	61	CTCTCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGT	120
Query	121	CTGCGTTCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCGTGTCCACCG	180
Sbjct	121	CTGCGTTCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCGTGTCCACCG	180
Query	181	TGACCCCTGTCCCCACACTGACCTGTGTTCCCTCCCGATCATCTTTCCTGTTCCAGAGA	240
Sbjct	181	TGACCCCTGTCCCCACACTGACCTGTGTTCCCTCCCGATCATCTTTCCTGTTCCAGAGA	240
Query	241	AGTGGGCTGGATGTCTCCATCTCTGTCTCAACTTCATGGTGCGCTGAGCTGCAACTTCTT	300
Sbjct	241	AGTGGGCTGGATGTCTCCATCTCTGTCTCAACTTCATGGTGCGCTGAGCTGCAACTTCTT	300
Query	301	ACTTCCCTAATGAAGTTAAGAACCTGAATATAAAATTTGTTTTCTCAAATATTTGCTATGA	360
Sbjct	301	ACTTCCCTAATGAAGTTAAGAACCTGAATATAAAATTTGTTTTCTCAAATATTTGCTATGA	360
Query	361	AGGGTTGATGGATTAATTAAATAAGTCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACC	420
Sbjct	361	AGGGTTGATGGATTAATTAAATAAGTCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACC	420
Query	421	TGAGAACCTTCCAGA	435
Sbjct	421	TGAGAACCTTCCAGA	435

Sequence 1071 matched with Sequence 383

Query= Sequence ID 1071
Length=571

SEQ ID NO: 383

ALIGNMENTS

Identities = 571/571 (100%), Gaps = 0/571 (0%)

Query	1	NGATATAGTNCCGCATGGGAAAAGATGANCAGGTATAACCNAGCNTNATATAGCAAGGACTA	61
Sbjct	1	NGATATAGTNCCGCATGGGAAAAGATGANCAGGTATAACCNAGCNTNATATAGCAAGGACTA	61
Query	62	ACCCCCCTGCCTTCTGCATAATGAATTAAGTAGAAATAACTTNGCAAGGAGAGCCAAAGC	121
Sbjct	62	ACCCCCCTGCCTTCTGCATAATGAATTAAGTAGAAATAACTTNGCAAGGAGAGCCAAAGC	121
Query	122	TAAGACCCCNAAAACCAGACGAGCTACCTAAGAACAGNTAAAAGAGCACACCCGTCTATG	181
Sbjct	122	TAAGACCCCNAAAACCAGACGAGCTACCTAAGAACAGNTAAAAGAGCACACCCGTCTATG	181
Query	182	TAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAG	241
Sbjct	182	TAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAG	241
Query	242	CTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTNGCCACAGAACCCCTCTAAAT	301
Sbjct	242	CTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTNGCCACAGAACCCCTCTAAAT	301
Query	302	CCCCTTGTAATTTAACTGTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAA	361
Sbjct	302	CCCCTTGTAATTTAACTGTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAA	361
Query	362	CCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTA	421
Sbjct	362	CCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTA	421
Query	422	AGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCC	481
Sbjct	422	AGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCC	481

PATENT SEQUENCE ALIGNMENT

```
Query  482  TNACACCCAATTGGACCAATCTATCACCTATAGAAGAACTAATGTTAGTATAAGTAACA  541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   482  TNACACCCAATTGGACCAATCTATCACCTATAGAAGAACTAATGTTAGTATAAGTAACA  541

Query  542  TGAAAACATTCTCCTCCGCATAAGCCTGC  571
          ||||||||||||||||||||
Sbjct   542  TGAAAACATTCTCCTCCGCATAAGCCTGC  571
```

Blast comparison trimmed “N” from both the 3’ end and the 5’ end of both sequences and reported 569 identities. The report has been manually corrected for this. “N” has been appended to both sequences and prepended to both sequences and identity count has been increased to 571.

Sequence 1074 matched with Sequence 384

Query= Sequence ID - 1074 nt: 689
Length=689

SEQ ID NO: 384 nt: 689

ALIGNMENTS

Identities = 689/689 (100%), Gaps = 0/689 (0%)

Query	1	GGGAGGCGGAGGCTGCAGTGAGCTGAGATCGTGCCACTTCATTCCAGCCTGGGCAACAAA	60
Sbjct	1	GGGAGGCGGAGGCTGCAGTGAGCTGAGATCGTGCCACTTCATTCCAGCCTGGGCAACAAA	60
Query	61	GCGAAACTCTGTCTCaaaaaaaaaaaaaaaaaaaaTTTGTGACTGTTGTAATTTAAAGC	120
Sbjct	61	GCGAAACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAATTTGTGACTGTTGTAATTTAAAGC	120
Query	121	TTGTCATTTTTTATTTAGTAATAACACTCATTAGTGTAGTATCTATGATGAACCAGGTTC	180
Sbjct	121	TTGTCATTTTTTATTTAGTAATAACACTCATTAGTGTAGTATCTATGATGAACCAGGTTC	180
Query	181	TGCACAAAGTACCTTATGTTTCATGGCCTCATATCGTCTTCTCCAAAACCTCTGCAAGATAG	240
Sbjct	181	TGCACAAAGTACCTTATGTTTCATGGCCTCATATCGTCTTCTCCAAAACCTCTGCAAGATAG	240
Query	241	GATTCATCACCCTTATAGGGAGAGATCTGAAAGTTTAAAATTGTACCCAAGGTCACACA	300
Sbjct	241	GATTCATCACCCTTATAGGGAGAGATCTGAAAGTTTAAAATTGTACCCAAGGTCACACA	300
Query	301	GCTGGTAAGTGCCAGAGCTGGGATTCCGTAGGGTGTTTCANAGTGCCTCTCCTGCCGTAGG	360
Sbjct	301	GCTGGTAAGTGCCAGAGCTGGGATTCCGTAGGGTGTTTCANAGTGCCTCTCCTGCCGTAGG	360
Query	361	CTTATCACAAAAAGTCAAAGTTTGGTCATAATAAAGCCTGAAGTTTGGCAGGATTTAAAA	420
Sbjct	361	CTTATCACAAAAAGTCAAAGTTTGGTCATAATAAAGCCTGAAGTTTGGCAGGATTTAAAA	420
Query	421	ATAGTCACCANACTTTTGGAGTTGGAGCATCCACCTCACTGCTGTTACCTTCTGTGGCA	480
Sbjct	421	ATAGTCACCANACTTTTGGAGTTGGAGCATCCACCTCACTGCTGTTACCTTCTGTGGCA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGAGAGTCATCATTTCCATTTTCAGCTTGTGGAATATCTTGTCATTAACATTCTCATGCA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGGAGAGTCATCATTTCCATTTTCAGCTTGTGGAATATCTTGTCATTAACATTCTCATGCA  540

Query  541  AAAGCCATTTTATGGTGCCCAATGAANATGGTTAAGCTACTGCCCCAAGCCTNTGGAAGC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AAAGCCATTTTATGGTGCCCAATGAANATGGTTAAGCTACTGCCCCAAGCCTNTGGAAGC  600

Query  601  CTTCTAATTTTGGACTTGCACTATGCAAATTGNATAATATTTTCTCTACCCTAAGCCAA  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  CTTCTAATTTTGGACTTGCACTATGCAAATTGNATAATATTTTCTCTACCCTAAGCCAA  660

Query  661  ATATTTTCTTCACTTTTCATTCTTCTAC  689
          ||||||||||||||||||||
Sbjct   661  ATATTTTCTTCACTTTTCATTCTTCTAC  689
```

Sequence 1081 matched with Sequence 385

Query= Sequence ID 1081
Length=542

SEQ ID NO: 385

ALIGNMENTS

Identities = 542/542 (100%), Gaps = 0/542 (0%)

Query	1	cgccgcccgcgcccgcgtcgctctccaacgccagcgccgcctctcgctcgccgagctccag	60
Sbjct	1	CGCCGCCGCGCCGCCGTCGCTCTCCAACGCCAGCGCCGCCTCTCGCTCGCCGAGCTCCAG	60
Query	61	ccgAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACT	120
Sbjct	61	CCGAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACT	120
Query	121	GCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGC	180
Sbjct	121	GCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGC	180
Query	181	AAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTG	240
Sbjct	181	AAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTG	240
Query	241	GCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTTCGCAAACCTCCC	300
Sbjct	241	GCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTTCGCAAACCTCCC	300
Query	301	TTCCAGCGTCTGGTGCAGAGAAATTGCTCAGGACTTTAAAACAGATCTGCGCTTCCAGAGC	360
Sbjct	301	TTCCAGCGTCTGGTGCAGAGAAATTGCTCAGGACTTTAAAACAGATCTGCGCTTCCAGAGC	360
Query	361	GCANCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGAC	420
Sbjct	361	GCANCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGAC	420
Query	421	ACCAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTA	480
Sbjct	421	ACCAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCACGCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTTCATTC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCACGCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTTCATTC  540

Query  541  TC   542
          ||
Sbjct   541  TC   542
```

Sequence 1083 matched with Sequence 386

Query= Sequence ID - 1083 nt: 198
Length=198

SEQ ID NO: 386 nt: 198

ALIGNMENTS

Identities = 198/198 (100%), Gaps = 0/198 (0%)

Query	1	GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTAAAGGCACAATTAATCACATTGG	60
Sbjct	1	GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTAAAGGCACAATTAATCACATTGG	60
Query	61	TTGTACTCTGNGACAGCCTTCTTTaaaaaaaaataaacaatttaaaacaaaaaaaaa	120
Sbjct	61	TTGTACTCTGNGACAGCCTTCTTTAAAAAAAAAATAACAATTTAAACAAAAAAAAA	120
Query	121	aaa	180
Sbjct	121	AAA	180
Query	181	aaaaaaaaanTTTTAACC	198
Sbjct	181	AAAAAAAAANTTTTAACC	198

Sequence 1084 matched with Sequence 387

Query= Sequence ID - 1084 nt: 198
Length=198

SEQ ID NO: 387 nt: 198

ALIGNMENTS

Identities = 198/198 (100%), Gaps = 0/198 (0%)

Query	1	GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTAAAGGCACAATTAATCACATTGG	60
Sbjct	1	GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTAAAGGCACAATTAATCACATTGG	60
Query	61	TTGTACTCTGNGACAGCCTTCTTTaaaaaaaaataaacaatttaaaacaaaaaaaaa	120
Sbjct	61	TTGTACTCTGNGACAGCCTTCTTTAAAAAAAAAATAACAATTTAAACAAAAAAAAA	120
Query	121	aaa	180
Sbjct	121	AAA	180
Query	181	aaaaaaaaanTTTAAACC	198
Sbjct	181	AAAAAAAAANTTTAAACC	198

Sequence 1099 matched with Sequence 388

Query= Sequence ID - 1099 nt: 561
Length=561

SEQ ID NO: 388 nt: 561

ALIGNMENTS

Identities = 561/561 (100%), Gaps = 0/561 (0%)

Query	1	TGCATGCTTGTGGATTGGAAAACTTTGGGAGACTGATTACTTTTCATTATATATGTGTCA	60
Sbjct	1	TGCATGCTTGTGGATTGGAAAACTTTGGGAGACTGATTACTTTTCATTATATATGTGTCA	60
Query	61	CAGTGAAACAGCTTTTATGTGTCATGTAAGATTACTGCTTGCCTCTCTAAGGAAGGTCGT	120
Sbjct	61	CAGTGAAACAGCTTTTATGTGTCATGTAAGATTACTGCTTGCCTCTCTAAGGAAGGTCGT	120
Query	121	GACTGTTTAAATAGACGGGCAAGGTGGAACCTTTTGAAAGATGAGCTTTTGAATATAAGT	180
Sbjct	121	GACTGTTTAAATAGACGGGCAAGGTGGAACCTTTTGAAAGATGAGCTTTTGAATATAAGT	180
Query	181	TGTCTGCTAGATCATGGTTTGTATTGAACTAACAAGGTTTGCAGATCTGCTGACTTATAT	240
Sbjct	181	TGTCTGCTAGATCATGGTTTGTATTGAACTAACAAGGTTTGCAGATCTGCTGACTTATAT	240
Query	241	AAAGCTTTTTGATTCCTACTAAGCTTTAAGATTTAAAAAATGTTCAATGTTGAAATTTCT	300
Sbjct	241	AAAGCTTTTTGATTCCTACTAAGCTTTAAGATTTAAAAAATGTTCAATGTTGAAATTTCT	300
Query	301	GTGGGGCTCTATTTTTGCTTTGGCTTTCTGGTGAGAGAGTGAGGAAGCATTCTTTCCTTC	360
Sbjct	301	GTGGGGCTCTATTTTTGCTTTGGCTTTCTGGTGAGAGAGTGAGGAAGCATTCTTTCCTTC	360
Query	361	ACTAAGTTTGTCTTTCTTGTCTTCTGGATAGATTGATTTTAAGAGACTAAGGGAATTTAC	420
Sbjct	361	ACTAAGTTTGTCTTTCTTGTCTTCTGGATAGATTGATTTTAAGAGACTAAGGGAATTTAC	420
Query	421	AAACTAAAGATTTTAGTCATCTGGTGGAAGGAGACTTTAAGATTGTTTAGGGCTGGGC	480
Sbjct	421	AAACTAAAGATTTTAGTCATCTGGTGGAAGGAGACTTTAAGATTGTTTAGGGCTGGGC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGGTGACTCACATCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCAGAACACTTGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGGTGACTCACATCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCAGAACACTTGA  540

Query  541  AGGAGTTCAAGACCAGCGTGG  561
          ||||||||||||||||
Sbjct  541  AGGAGTTCAAGACCAGCGTGG  561
```

Sequence 1109 matched with Sequence 389

Length=601

Identities = 601/601 (100%), Gaps = 0/601 (0%)

Query	1	TTTGNCGGTNTTGGannnnnnanaanTTTCTTCCANNCNTNACNTNTTGGTGGNCTAAATT	60
Sbjct	1	TTTGNCGGTNTTGGANNNNNANAANTTTCTTCCANNCNTNACNTNTTGGTGGNCTAAATT	60
Query	61	AANATGGNTTTNGNGGGTTCNTTNCTNNNTNNNNCATGGGANANAATTNATTNTCNTNCN	120
Sbjct	61	AANATGGNTTTNGNGGGTTCNTTNCTNNNTNNNNCATGGGANANAATTNATTNTCNTNCN	120
Query	121	NNTTCCTTNNCCCTNAANCTACCTTCCCCCNATTTTCTCCCCTNTTCNTNAATTANCATC	180
Sbjct	121	NNTTCCTTNNCCCTNAANCTACCTTCCCCCNATTTTCTCCCCTNTTCNTNAATTANCATC	180
Query	181	CTCTCCNCNTANNTCNANACNTTAATGGCAANACTATCTAATANCNANNATAANANCTCC	240
Sbjct	181	CTCTCCNCNTANNTCNANACNTTAATGGCAANACTATCTAATANCNANNATAANANCTCC	240
Query	241	TGTNNNCCACATNTCTTATTNNNCGCNNCANGTTNCANNCCCNAGAGTNAACTCATCCT	300
Sbjct	241	TGTNNNCCACATNTCTTATTNNNCGCNNCANGTTNCANNCCCNAGAGTNAACTCATCCT	300
Query	301	CNNCNNAANTTCATATCGTGNNCTNTNNNCNNTNGCGCGANATATTaannanaccngtan	360
Sbjct	301	CNNCNNAANTTCATATCGTGNNCTNTNNNCNNTNGCGCGANATATTAANNANACCNGTAN	360
Query	361	ntnnnanacannanntnngnaanaanccttctnannTTTTAGCNTCNNGCNNTAACNNNN	420
Sbjct	361	NTNNNANACANNANNTNNGNAANAANCCTTCTNANNTTTTAGCNTCNNGCNNTAACNNNN	420
Query	421	NTCTTNGTGNNNNCNCAGCTTTCNCNNCATNATNCTNCNNCGAANTNTCANNCNTCTCCN	480
Sbjct	421	NTCTTNGTGNNNNCNCAGCTTTCNCNNCATNATNCTNCNNCGAANTNTCANNCNTCTCCN	480
Query	481	CTTNAATGNNTTCCCATGNATTAANTNCCTCGNNNANAGCACTATCGTNNNNGAGNNNAT	540
Sbjct	481	CTTNAATGNNTTCCCATGNATTAANTNCCTCGNNNANAGCACTATCGTNNNNGAGNNNAT	540
Query	541	TATNGNCNNTTTACNTCATGTGGTCCANTNNCGTTNGNCGCNNNNAATNTTCGTNNNNCNN	601

PATENT SEQUENCE ALIGNMENT

```
|||||
Sbjct  541  TATNGNCNNTTTACNTCATGTGGTCCANTNNCGTTNGNCGCNNNNNAATNTTCGTNNNNNCNN 601
```

Blast comparison trimmed “NNNNCNN” from the 3’ end of both sequences and reported 594 identities. The report has been manually corrected for this. “NNNNCNN” has been appended to both sequences and identity count has been increased to 601.

Sequence 1118 matched with Sequence 390

Query= Sequence ID 1118
Length=616

SEQ ID NO: 390

ALIGNMENTS

Identities = 616/616 (100%), Gaps = 0/616 (0%)

Query	1	GGATTTTAGAGGAAGGCGCTNGGTTACATTGGAGAACTGGAGTGGTCTGGAGTTCCACGG	60
Sbjct	1	GGATTTTAGAGGAAGGCGCTNGGTTACATTGGAGAACTGGAGTGGTCTGGAGTTCCACGG	60
Query	61	TGTAGTGGACCAGAGGCCACCTCTCCTGGGCTTCTCAGTGTCTCGCCGGCGGGGTTTCGGC	120
Sbjct	61	TGTAGTGGACCAGAGGCCACCTCTCCTGGGCTTCTCAGTGTCTCGCCGGCGGGGTTTCGGC	120
Query	121	CTGAGCTGGATTGACATAGCCCTTGGCGGATTTAAACAACCTAAACATTAAGCAGTACAG	180
Sbjct	121	CTGAGCTGGATTGACATAGCCCTTGGCGGATTTAAACAACCTAAACATTAAGCAGTACAG	180
Query	181	CTGCCTCAAACCTTTGGGATTTTCAGAATGACTGACACTGCCGAAGCTGTTCCAAAGTTT	240
Sbjct	181	CTGCCTCAAACCTTTGGGATTTTCAGAATGACTGACACTGCCGAAGCTGTTCCAAAGTTT	240
Query	241	GAAGAGATGTTTGCTAGTAGATTACAGAAAATGACAAGGAGTATCAGGAATACCTGAAA	300
Sbjct	241	GAAGAGATGTTTGCTAGTAGATTACAGAAAATGACAAGGAGTATCAGGAATACCTGAAA	300
Query	301	CGCCCTCCTGAGTCTCCTCCAATTGTTGAGGAATGGAATAGCANAGCTGGTGGGAACCAA	360
Sbjct	301	CGCCCTCCTGAGTCTCCTCCAATTGTTGAGGAATGGAATAGCANAGCTGGTGGGAACCAA	360
Query	361	AGAAACAGAGGCAATCGGTTGCAAGACAACAGACAGTTCAGAGGCAGGGACAACAGATGG	420
Sbjct	361	AGAAACAGAGGCAATCGGTTGCAAGACAACAGACAGTTCAGAGGCAGGGACAACAGATGG	420
Query	421	GGGTGGCCAAGTGACAATCGATCCAATCAGTGGCATGGACGATCCTGGGGTAACAACCTAC	480
Sbjct	421	GGGTGGCCAAGTGACAATCGATCCAATCAGTGGCATGGACGATCCTGGGGTAACAACCTAC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCGCAACACAGACAAGAACCTTACTATCCCCAGCAATATGGACATTATGGTTACAACCAG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CCGCAACACAGACAAGAACCTTACTATCCCCAGCAATATGGACATTATGGTTACAACCAG  540

Query  541  CGGCCTCCTTACGGTTACTACTGATAGAAATGTTGGCAGCTTTTAGTAAAAGCATTTACT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CGGCCTCCTTACGGTTACTACTGATAGAAATGTTGGCAGCTTTTAGTAAAAGCATTTACT  600

Query  601  CTGTTACCATGAGAAA  616
          |||||||||||||||
Sbjct   601  CTGTTACCATGAGAAA  616
```

Sequence 1125 matched with Sequence 391

Query= Sequence ID 1125
Length=407

SEQ ID NO: 391

ALIGNMENTS

Identities = 407/407 (100%), Gaps = 0/407 (0%)

```
Query 1      NGA CTGGCTCCCGAAAAGAAGGGTGGCGAGaanaaaaaGGGCCGTTCTGCCATGGACGAAG 61
            |||
Sbjct 1      NGA CTGGCTCCCGAAAAGAAGGGTGGCGAGANA AAAAGGGCCGTTCTGCCATGGACGAAG 61

Query 62     TGGTAACCCGCGAATACACCATCAACATTNACAAGCGCATCCATGGAGTGGGCTTCAAGA 121
            |||
Sbjct 62     TGGTAACCCGCGAATACACCATCAACATTNACAAGCGCATCCATGGAGTGGGCTTCAAGA 121

Query 122    ANCGTGACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAGGAGATGGGAACTC 181
            |||
Sbjct 122    ANCGTGACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAGGAGATGGGAACTC 181

Query 182    CATATGTGCGCATTGACACCAGGCTCAACAAANCTGTCTGGGCCAAAGGAATAAGGAATG 241
            |||
Sbjct 182    CATATGTGCGCATTGACACCAGGCTCAACAAANCTGTCTGGGCCAAAGGAATAAGGAATG 241

Query 242    TGCCATACCGAATCCGTGTGCGGCTGTCCANAAAACGTAATGAGGATGAAGATTACCAA 301
            |||
Sbjct 242    TGCCATACCGAATCCGTGTGCGGCTGTCCANAAAACGTAATGAGGATGAAGATTACCAA 301

Query 302    ATAAGCTNTATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAG 361
            |||
Sbjct 302    ATAAGCTNTATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAG 361

Query 362    TCAATGTGGATGANAACNAATCGCTGATCGTCAGATCaaanaaaNT 407
            |||
Sbjct 362    TCAATGTGGATGANAACNAATCGCTGATCGTCAGATCAAANAAANT 407
```

Blast comparison trimmed "N" from the 5' end of both sequences and trimmed "NT" from the 3' end of both sequences and reported 404 identities. The report has been manually

corrected for this. “N” has been prepended to the 5’ end of both sequences and “NT” has appended to the 3’ end of both sequences and identity count has been increased to 407.

Sequence 1139 matched with Sequence 392

Query= Sequence ID - 1139 nt: 503
Length=503

SEQ ID NO: 392 nt: 503

ALIGNMENTS

Identities = 503/503 (100%), Gaps = 0/503 (0%)

Query	1	CAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTACCCTCATTTACCTGCGCTGTGGA	60
Sbjct	1	CAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTACCCTCATTTACCTGCGCTGTGGA	60
Query	61	CACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGTGACATCATTACAGCGCATGCACCT	120
Sbjct	61	CACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGTGACATCATTACAGCGCATGCACCT	120
Query	121	TCGTCAGTACGAGCTGCTCTAAGAAGGGAACCCCCAAATTTAATTAAAGCCTTAAGCACA	180
Sbjct	121	TCGTCAGTACGAGCTGCTCTAAGAAGGGAACCCCCAAATTTAATTAAAGCCTTAAGCACA	180
Query	181	ATTAATTTAAAGTGAAACGTAATTGTACAAGCAGTTAATCACCCACCATAGGGCATGATT	240
Sbjct	181	ATTAATTTAAAGTGAAACGTAATTGTACAAGCAGTTAATCACCCACCATAGGGCATGATT	240
Query	241	AACAAAGCAACCTTTCCCTTCCCCGAGTGATTTTGCGAAACCCCTTTTCCCTTCAGCT	300
Sbjct	241	AACAAAGCAACCTTTCCCTTCCCCGAGTGATTTTGCGAAACCCCTTTTCCCTTCAGCT	300
Query	301	TGCTTAGATGTTCCAAATTTAGAAAGCTTAAGGCGGCCTACAGaaaaaggaaaaaaggcc	360
Sbjct	301	TGCTTAGATGTTCCAAATTTAGAAAGCTTAAGGCGGCCTACAGAAAAAGGAAAAAAGGCC	360
Query	361	acaaaagttccctctcactttcagtaaaaataaataaaacagcagcagcaacaaataaa	420
Sbjct	361	ACAAAAGTTCCCTCTCACTTTCAGTAAAAATAAATAAAACAGCAGCAGCAAACAAATAAA	420
Query	421	atgaaataaaagaaacaaatgaaataaatattgtgtgtgcagcattaaaaaaatcaaa	480
Sbjct	421	ATGAAATAAAAGAAACAAATGAAATAAATATTGTGTTGTGCAGCATTAAAAAAATCAAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	ataaaaattaaatGTGAGCAAAG	503
Sbjct	481	ATAAAAATTAAATGTGAGCAAAG	503

Sequence 1148 matched with Sequence 393

Query= Sequence ID - 1148 nt: 587
Length=587

SEQ ID NO: 393 nt: 587

ALIGNMENTS

Identities = 587/587 (100%), Gaps = 0/587 (0%)

Query	1	TGAAAAATAAAGTTTTTATGTATATTCTACATATGTATATGTTGGTAGAAAGCAAAAACG	60
Sbjct	1	TGAAAAATAAAGTTTTTATGTATATTCTACATATGTATATGTTGGTAGAAAGCAAAAACG	60
Query	61	CTAGGTAAAAATAAATGTAATACAATTTTAGCTATGAACCAAAAAACCATTGTGGTGTG	120
Sbjct	61	CTAGGTAAAAATAAATGTAATACAATTTTAGCTATGAACCAAAAAACCATTGTGGTGTG	120
Query	121	GATGCAAGAAAGTCTGGATGGGTGCAGAGTTCTCCATGTTTCACTTCTGACATTTGAAAA	180
Sbjct	121	GATGCAAGAAAGTCTGGATGGGTGCAGAGTTCTCCATGTTTCACTTCTGACATTTGAAAA	180
Query	181	TACGCAGTTTGCATTTGATACGTCAAATGTTATTTTAAAGAAAACCAATAAAATCATTA	240
Sbjct	181	TACGCAGTTTGCATTTGATACGTCAAATGTTATTTTAAAGAAAACCAATAAAATCATTA	240
Query	241	AACCGAAAAGGCAGTTTGTCTGTTTTTACCTTAGTTGGAGTTATCTGCAATTGCCGTAT	300
Sbjct	241	AACCGAAAAGGCAGTTTGTCTGTTTTTACCTTAGTTGGAGTTATCTGCAATTGCCGTAT	300
Query	301	TAGTGTTTTAAGGAACTTGTAAGTAAGCTCCTTAGTCCCCTTTAGAGCTACGAAACATGT	360
Sbjct	301	TAGTGTTTTAAGGAACTTGTAAGTAAGCTCCTTAGTCCCCTTTAGAGCTACGAAACATGT	360
Query	361	CAATTTTACTTTTCTCCAGCTTTTGGGAATCTTATCTAAATTACCATGTAGAGTTCTGCA	420
Sbjct	361	CAATTTTACTTTTCTCCAGCTTTTGGGAATCTTATCTAAATTACCATGTAGAGTTCTGCA	420
Query	421	TAGCTTCAAATTCTCTTAGCCAATGTGGTCTGTAAGTGTCTATCGATGAATTTACCGTT	480
Sbjct	421	TAGCTTCAAATTCTCTTAGCCAATGTGGTCTGTAAGTGTCTATCGATGAATTTACCGTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AATTGCCGTAGTATACTGTCCTGTACCGGATGTGAAGAGGAGCAACTCTGCACAGTGCAC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AATTGCCGTAGTATACTGTCCTGTACCGGATGTGAAGAGGAGCAACTCTGCACAGTGCAC  540

Query  541  TGGTTGCTCCCATGGTAGGAANGAATGGCTTATCAATGGTCGGATTT  587
          |||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGTTGCTCCCATGGTAGGAANGAATGGCTTATCAATGGTCGGATTT  587
```

Sequence 1160 matched with Sequence 394

Query= Sequence ID - 1160 nt: 650
Length=650

SEQ ID NO: 394 nt: 650

ALIGNMENTS

Identities = 650/650 (100%), Gaps = 0/650 (0%)

Query	1	GGAGGATGGAGCAGTGAGCGGGTCTGGGCGGCTGCTGGCAGCGCCATGGAGACGGTACAG	60
Sbjct	1	GGAGGATGGAGCAGTGAGCGGGTCTGGGCGGCTGCTGGCAGCGCCATGGAGACGGTACAG	60
Query	61	CTGAGGAACCCGCCGCGCCGGCAGCTGAAAAAGTTGGATGAAGATAGTTTAACCAAACAA	120
Sbjct	61	CTGAGGAACCCGCCGCGCCGGCAGCTGAAAAAGTTGGATGAAGATAGTTTAACCAAACAA	120
Query	121	CCAGAAGAAGTATTTGATGTCTTAGAGAAACTTGGAGAAGGGTGAGTGTAAGAAACTAT	180
Sbjct	121	CCAGAAGAAGTATTTGATGTCTTAGAGAAACTTGGAGAAGGGTGAGTGTAAGAAACTAT	180
Query	181	AGGTAGGTCATTGGGTCCCAGTCTTTTTCTGCCCCAGAAGAAGCAGAAGGATATGAACC	240
Sbjct	181	AGGTAGGTCATTGGGTCCCAGTCTTTTTCTGCCCCAGAAGAAGCAGAAGGATATGAACC	240
Query	241	TTTCAGCATTGTTCTAGGTGGGGTGAAGGTAAATTTACAGCTTGTGATGTCCTTCTTCG	300
Sbjct	241	TTTCAGCATTGTTCTAGGTGGGGTGAAGGTAAATTTACAGCTTGTGATGTCCTTCTTCG	300
Query	301	CTTTACTCCAATCCCTATTATAGACAGATTTAGTGATTCCTGGTCTTTTAAACACGAAGA	360
Sbjct	301	CTTTACTCCAATCCCTATTATAGACAGATTTAGTGATTCCTGGTCTTTTAAACACGAAGA	360
Query	361	ATATCTATTGTTTTCTCTTTTGTAGGATCTGTATGATTTTATCTACTTAACAGATAGCAC	420
Sbjct	361	ATATCTATTGTTTTCTCTTTTGTAGGATCTGTATGATTTTATCTACTTAACAGATAGCAC	420
Query	421	TAATTAGATTAAAATTCTATAAGAAACTTTTTAATTTGCTGTTTCATAATTTCTGATTGGT	480
Sbjct	421	TAATTAGATTAAAATTCTATAAGAAACTTTTTAATTTGCTGTTTCATAATTTCTGATTGGT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATGCAATAACTGTTTCAATGAAAATCAATGTAATTTAGTATTTTAATATTTGCACCTTTG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATGCAATAACTGTTTCAATGAAAATCAATGTAATTTAGTATTTTAATATTTGCACCTTTG  540

Query  541  TGAAATATAGTAAATAAATTAAGCACTATCACCACCTTCACAGCTACTTAGGAGATCCAC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TGAAATATAGTAAATAAATTAAGCACTATCACCACCTTCACAGCTACTTAGGAGATCCAC  600

Query  601  AATCCTGGGTGGGAGCCAGTGGATTCCTGAAACACAGATTTGTTAATG  650
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  AATCCTGGGTGGGAGCCAGTGGATTCCTGAAACACAGATTTGTTAATG  650
```

Sequence 1165 matched with Sequence 395

Query= Sequence ID - 1165 nt: 502
Length=502

SEQ ID NO: 395 nt: 502

ALIGNMENTS

Identities = 502/502 (100%), Gaps = 0/502 (0%)

Query	1	CTCAAGTGAATCCTGGCTTCTTGAAGCGCTTGCCTAGACGAGACACAGTGCATAAAAAAC	60
Sbjct	1	CTCAAGTGAATCCTGGCTTCTTGAAGCGCTTGCCTAGACGAGACACAGTGCATAAAAAAC	60
Query	61	AACTTTTGGGGACAGGTATGTTTTCTTGCAGCTGCGGTTGTAAGGTCTTGGCAAGACAA	120
Sbjct	61	AACTTTTGGGGACAGGTATGTTTTCTTGCAGCTGCGGTTGTAAGGTCTTGGCAAGACAA	120
Query	121	GCAGTGTGGCCAGAATTTTGAACCTTCTGATGAATGTGTAATGCAAAGGACCTTGTACAtt	180
Sbjct	121	GCAGTGTGGCCAGAATTTTGAACCTTCTGATGAATGTGTAATGCAAAGGACCTTGTACATT	180
Query	181	tttttGTTTCAAGGTCCTCAAAATGAGCACATGAAGAGGTTGCTGTGAAACTTTAAGTGG	240
Sbjct	181	TTTTTGTTTCAAGGTCCTCAAAATGAGCACATGAAGAGGTTGCTGTGAAACTTTAAGTGG	240
Query	241	CCCTACTGCGCAGAAGCATTTCAGATGTCACTTGATGATCTGTAAGGGAACCTTGCTGATTT	300
Sbjct	241	CCCTACTGCGCAGAAGCATTTCAGATGTCACTTGATGATCTGTAAGGGAACCTTGCTGATTT	300
Query	301	GGGAATGTGCTTAGGGAACACACATTCCTTTTGACAGGGTCTGTCACTGGGTGGGTGATG	360
Sbjct	301	GGGAATGTGCTTAGGGAACACACATTCCTTTTGACAGGGTCTGTCACTGGGTGGGTGATG	360
Query	361	AATTATACAGATGACATGTGCTtttttttcttttttCAACCTCAATGGTATTCCTACAGG	420
Sbjct	361	AATTATACAGATGACATGTGCTTTTTTTCTTTTTTCAACCTCAATGGTATTCCTACAGG	420
Query	421	AAATGGATAACCATTTTAACTGTATTTTTTGCAGCCCGTACCTTCTTGGAATACAATTG	480
Sbjct	421	AAATGGATAACCATTTTAACTGTATTTTTTGCAGCCCGTACCTTCTTGGAATACAATTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCTAACTTTTTATTTTGGTCT	502
Sbjct	481	TCTAACTTTTTATTTTGGTCT	502

Sequence 1172 matched with Sequence 396

Query= Sequence ID - 1172 nt: 648
Length=648

SEQ ID NO: 396 nt: 648

ALIGNMENTS

Identities = 648/648 (100%), Gaps = 0/648 (0%)

Query	1	CCACAATAATAAGAGAAAAACAGGAGCAAAAGGATATACAAAACCACCAGAAAACAAATA	60
Sbjct	1	CCACAATAATAAGAGAAAAACAGGAGCAAAAGGATATACAAAACCACCAGAAAACAAATA	60
Query	61	ACAAAGTGACAGGAGTAAGTCCTTAAGTGGCAATAATAACCATGAATCTAAATGGATTCC	120
Sbjct	61	ACAAAGTGACAGGAGTAAGTCCTTAAGTGGCAATAATAACCATGAATCTAAATGGATTCC	120
Query	121	ATTTCCCACTTAAAAGATAAAGACATGCTGAATGGATAAAAAGCTGTCACCCAGTTATAT	180
Sbjct	121	ATTTCCCACTTAAAAGATAAAGACATGCTGAATGGATAAAAAGCTGTCACCCAGTTATAT	180
Query	181	GCTGCCTACAACAACTCACTTCACCTGTAAACATACATATGGATGGAAAGAGAAGGCAT	240
Sbjct	181	GCTGCCTACAACAACTCACTTCACCTGTAAACATACATATGGATGGAAAGAGAAGGCAT	240
Query	241	GGGAAAAGATACTCTACTCAAATGAAAACAAAAACCAAACAAAGGTGGCTATTCTTATAT	300
Sbjct	241	GGGAAAAGATACTCTACTCAAATGAAAACAAAAACCAAACAAAGGTGGCTATTCTTATAT	300
Query	301	GAGATAATACAGACATTTAAATCAAAAACTGGAAACAAACACAAAGTCATTGTATAATGAT	360
Sbjct	301	GAGATAATACAGACATTTAAATCAAAAACTGGAAACAAACACAAAGTCATTGTATAATGAT	360
Query	361	GAATTCAATTATATCATGATGAATTCAATTATATCCTCCTTCCTGATCAATTCAGAAAGG	420
Sbjct	361	GAATTCAATTATATCATGATGAATTCAATTATATCCTCCTTCCTGATCAATTCAGAAAGG	420
Query	421	AGGATATAATCTTTTTAAATATATATACACCCAACACCAGAGCATATAAATATGTAAAGG	480
Sbjct	421	AGGATATAATCTTTTTAAATATATATACACCCAACACCAGAGCATATAAATATGTAAAGG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAGATAAAGGGAGTCCTGTGATCAAGAATAAATATAACAATTATAAAATATTTTATCTAAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AAGATAAAGGGAGTCCTGTGATCAAGAATAAATATAACAATTATAAAATATTTTATCTAAA  540

Query  541  GTGATAGATAGACTGTAATACAATAATAGGGTGGTGACATTAACACCCCCTCTCACATTG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GTGATAGATAGACTGTAATACAATAATAGGGTGGTGACATTAACACCCCCTCTCACATTG  600

Query  601  GACTGATCATCTAGAAGGGAGAAAAAGCTTTATGATTGGAAAAGCCAT  648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GACTGATCATCTAGAAGGGAGAAAAAGCTTTATGATTGGAAAAGCCAT  648
```

Sequence 1178 matched with Sequence 397

Query= Sequence ID 1178
Length=705

SEQ ID NO: 397

ALIGNMENTS

Identities = 705/705 (100%), Gaps = 0/705 (0%)

Query	1	ATTGTGTTGGCCACCCGGAATTCGCGGCCGCGTCGACCTACGCACACGAGAACATGCCT	60
Sbjct	1	ATTGTGTTGGCCACCCGGAATTCGCGGCCGCGTCGACCTACGCACACGAGAACATGCCT	60
Query	61	CTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAGAAGAGGAAACACAAGAAGAAA	120
Sbjct	61	CTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAGAAGAGGAAACACAAGAAGAAA	120
Query	121	CGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCAGGTGAGGAGACG	180
Sbjct	121	CGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCAGGTGAGGAGACG	180
Query	181	GCTTGCTGTAGTGGGGAAAGCACTGGACCTCAACAGTTGGAAAATGTTGTAGTGTAGCT	240
Sbjct	181	GCTTGCTGTAGTGGGGAAAGCACTGGACCTCAACAGTTGGAAAATGTTGTAGTGTAGCT	240
Query	241	GTCTCGTATCCTTGAAGCTGTGCAGCAGCTTCAGTTTCTTCGCCTGTGGAAAATATTTTC	300
Sbjct	241	GTCTCGTATCCTTGAAGCTGTGCAGCAGCTTCAGTTTCTTCGCCTGTGGAAAATATTTTC	300
Query	301	CCTGATACTCTTAAAATTTGAATGTATGAGACTGGCAAAGTTTTGCATCTTAGGAGGAGT	360
Sbjct	301	CCTGATACTCTTAAAATTTGAATGTATGAGACTGGCAAAGTTTTGCATCTTAGGAGGAGT	360
Query	361	GATTCATTTACCGTGATCTCTCATCACATTTACATACAACCCCTACGtttttttGTGT	420
Sbjct	361	GATTCATTTACCGTGATCTCTCATCACATTTACATACAACCCCTACGTTTTTTTGTGT	420
Query	421	TGGGAAACAATGTAATGGATGATGAGTTGGGCATAAGTGCAGGAAAGACGGGTGTAATAG	480
Sbjct	421	TGGGAAACAATGTAATGGATGATGAGTTGGGCATAAGTGCAGGAAAGACGGGTGTAATAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGGaaaaaaaTGTTATCTGCTTTTCTTTCAGGATGCTATAAAATCACCACGGTCTTTAGC  540
          |||
Sbjct   481  AGGAAAAAAATGTTATCTGCTTTTCTTTCAGGATGCTATAAAATCACCACGGTCTTTAGC  540

Query  541  CATGCACAAACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGA  600
          |||
Sbjct   541  CATGCACAAACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGA  600

Query  601  GGAAAAGCAAGGCTTACAGAAGGATGTTCTTCAGGAGGAAGCAGCACTAAAAGCACTCT  660
          |||
Sbjct   601  GGAAAAGCAAGGCTTACAGAAGGATGTTCTTCAGGAGGAAGCAGCACTAAAAGCACTCT  660

Query  661  GAGTCAANATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT  705
          |||
Sbjct   661  GAGTCAANATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT  705
```

Sequence 1180 matched with Sequence 398

Query= Sequence ID - 1180 nt: 622
Length=622

SEQ ID NO: 398 nt: 622

ALIGNMENTS

Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query	1	CTTTTCCTCCCGCTGTCCCCACGGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGT	60
Sbjct	1	CTTTTCCTCCCGCTGTCCCCACGGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGT	60
Query	61	GAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTC	120
Sbjct	61	GAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTC	120
Query	121	GGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACT	180
Sbjct	121	GGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACT	180
Query	181	AACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCAGATGAGGCAGCTGTGACTGTGT	240
Sbjct	181	AACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCAGATGAGGCAGCTGTGACTGTGT	240
Query	241	CAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGG	300
Sbjct	241	CAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGG	300
Query	301	AAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACT	360
Sbjct	301	AAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACT	360
Query	361	ATTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGTCTG	420
Sbjct	361	ATTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGTCTG	420
Query	421	GGTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGAT	480
Sbjct	421	GGTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGA  540

Query  541  AGAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACANCCA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AGAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACANCCA  600

Query  601  CAATCATGAGGATGATGTGTTG  622
          ||||||||||||||||
Sbjct   601  CAATCATGAGGATGATGTGTTG  622
```

Sequence 1181 matched with Sequence 399

Query= Sequence ID - 1181 nt: 155
Length=155

SEQ ID NO: 399 nt: 155

ALIGNMENTS

Identities = 155/155 (100%), Gaps = 0/155 (0%)

Query	1	CGCCACTTATCCAGTGAACCACTATCACGaaaaaaCTCTACCTCTCTATACTAATCTCC	60
Sbjct	1	CGCCACTTATCCAGTGAACCACTATCACGAAAAAACTCTACCTCTCTATACTAATCTCC	60
Query	61	CTACAAATCTCCTTAATTATAACATTACAGCCACAGAACTAATCATATTaaaaaaaaa	120
Sbjct	61	CTACAAATCTCCTTAATTATAACATTACAGCCACAGAACTAATCATATTAaaaaaaaaa	120
Query	121	aaaaaaaaaaaaaaaaaaaaaaaaaaaaa	155
Sbjct	121	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	155

Sequence 1182 matched with Sequence 400

Query= Sequence ID 1182
Length=700

SEQ ID NO: 400

ALIGNMENTS

Identities = 700/700 (100%), Gaps = 0/700 (0%)

Query	1	CATTGTGTTGGCNCCCGGAATTCGCGGCCGCGTCGACTTTTTGTGTTGTTGGAGCAGA	60
Sbjct	1	CATTGTGTTGGCNCCCGGAATTCGCGGCCGCGTCGACTTTTTGTGTTGTTGGAGCAGA	60
Query	61	AATACTAAAGAAGATTCCGGGCCGAGTATCCACAGAAGTGGACGCAAGGCTCTCCTTTGA	120
Sbjct	61	AATACTAAAGAAGATTCCGGGCCGAGTATCCACAGAAGTGGACGCAAGGCTCTCCTTTGA	120
Query	121	TAAAGATGCGATGGTGGCCAGAGCCAGGCGGCTCATCGAGCTCTACAAGGAAGCTGGGAT	180
Sbjct	121	TAAAGATGCGATGGTGGCCAGAGCCAGGCGGCTCATCGAGCTCTACAAGGAAGCTGGGAT	180
Query	181	CAGCAAGGACCGAATTCTTATAAAGCTGTCATCAACCTGGGAAGGAATTCAGGCTGGAAA	240
Sbjct	181	CAGCAAGGACCGAATTCTTATAAAGCTGTCATCAACCTGGGAAGGAATTCAGGCTGGAAA	240
Query	241	GGAGCTCGAGGAGCAGCACGGCATCCACTGCAACATGACGTTACTCTTCTCCTTCGCCCA	300
Sbjct	241	GGAGCTCGAGGAGCAGCACGGCATCCACTGCAACATGACGTTACTCTTCTCCTTCGCCCA	300
Query	301	GGCTGTGGCCTGTGCCGAGGCGGGTGTGACCCTCATCTCCCATTGTTGGGCGCATCCT	360
Sbjct	301	GGCTGTGGCCTGTGCCGAGGCGGGTGTGACCCTCATCTCCCATTGTTGGGCGCATCCT	360
Query	361	TGATTGGCATGTGGCAAACACCGACAAGAAATCCTATGAGCCCCTGGAAGACCCTGGGGT	420
Sbjct	361	TGATTGGCATGTGGCAAACACCGACAAGAAATCCTATGAGCCCCTGGAAGACCCTGGGGT	420
Query	421	AAAGAGTGTCACTAAAATCTACAACACTACTACAAGAAGTTTAGCTACAAAACCATTGTCAT	480
Sbjct	421	AAAGAGTGTCACTAAAATCTACAACACTACTACAAGAAGTTTAGCTACAAAACCATTGTCAT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGGCGCCTCCTTCGCAACACGGGCGAGATCAAAGCACTGGCCGGCTGTGACTTCCTCAC	540
Sbjct	481	GGGCGCCTCCTTCGCAACACGGGCGAGATCAAAGCACTGGCCGGCTGTGACTTCCTCAC	540
Query	541	CATCTCACCCAAGCTCCTGGGAGAGCTGCTGCAGGACAACGCCAAGCTGGTGCCTGTGCT	600
Sbjct	541	CATCTCACCCAAGCTCCTGGGAGAGCTGCTGCAGGACAACGCCAAGCTGGTGCCTGTGCT	600
Query	601	CTCAGCCAAGGCGGCCCAAGCCAGTGACCTGGAAAAATCCACCTGGATGAGAAGTCTTT	660
Sbjct	601	CTCAGCCAAGGCGGCCCAAGCCAGTGACCTGGAAAAATCCACCTGGATGAGAAGTCTTT	660
Query	661	CCGTTGGTTGCACAACGAGGACCAGATGGCTGTGGAGAAG	700
Sbjct	661	CCGTTGGTTGCACAACGAGGACCAGATGGCTGTGGAGAAG	700

Sequence 1183 matched with Sequence 401

Query= Sequence ID - 1183 nt: 479
Length=479

SEQ ID NO: 401 nt: 479

ALIGNMENTS

Identities = 479/479 (100%), Gaps = 0/479 (0%)

Query	1	CGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTCAGACCCCTTGTGAAGCCCAAG	60
Sbjct	1	CGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTCAGACCCCTTGTGAAGCCCAAG	60
Query	61	ATCGTCAAAAAGAGAACCAAGAAGTTCATCCGGCACCAGTCAGACCGATATGTCAAAATT	120
Sbjct	61	ATCGTCAAAAAGAGAACCAAGAAGTTCATCCGGCACCAGTCAGACCGATATGTCAAAATT	120
Query	121	AAGCGTAACTGGCGGAAACCCAGAGGCATTGACAACAGGGTTCGTAGAAGATTCAAGGGC	180
Sbjct	121	AAGCGTAACTGGCGGAAACCCAGAGGCATTGACAACAGGGTTCGTAGAAGATTCAAGGGC	180
Query	181	CAGATCTTGATGCCCAACATTGGTTATGGAAGCAACaaaaaaaaCAAAGCACATGCTGCCC	240
Sbjct	181	CAGATCTTGATGCCCAACATTGGTTATGGAAGCAACAAAAAACAAGCACATGCTGCCC	240
Query	241	AGTGGCTTCCGGAAGTTCCTGGTCCACAACGTCAAGGAGCTGGAAGTGCTGCTGATGTGC	300
Sbjct	241	AGTGGCTTCCGGAAGTTCCTGGTCCACAACGTCAAGGAGCTGGAAGTGCTGCTGATGTGC	300
Query	301	AACAAATCTTACTGTGCCGAGATCGCTCACAATGTTTCCTCCAAGAACCGCAAAGCCATC	360
Sbjct	301	AACAAATCTTACTGTGCCGAGATCGCTCACAATGTTTCCTCCAAGAACCGCAAAGCCATC	360
Query	361	GTGGAAAGAGCTGCCCAACTGGCCATCAGAGTCACCAACCCCAATGCCAGGCTGCGCAGT	420
Sbjct	361	GTGGAAAGAGCTGCCCAACTGGCCATCAGAGTCACCAACCCCAATGCCAGGCTGCGCAGT	420
Query	421	GAAGAAAATGAGTAGGCAGCTCATGTGCACGTTTTCTGTTTAAATAAATGTAAAACTG	479
Sbjct	421	GAAGAAAATGAGTAGGCAGCTCATGTGCACGTTTTCTGTTTAAATAAATGTAAAACTG	479

Sequence 1185 matched with Sequence 402

Query= Sequence ID - 1185 nt: 628
Length=628

SEQ ID NO: 402 nt: 628

ALIGNMENTS

Identities = 628/628 (100%), Gaps = 0/628 (0%)

Query	1	CTTTGATTACCTTTGAGTATTAGGTTGAAAGCTTCTCTGTGCTTGATTGAACATTGTGAT	60
Sbjct	1	CTTTGATTACCTTTGAGTATTAGGTTGAAAGCTTCTCTGTGCTTGATTGAACATTGTGAT	60
Query	61	GATGTTGATTGGGTCATGTCAGATTTAGACAGTGTTGTGTTTAAGATAAAATGTTTAATGG	120
Sbjct	61	GATGTTGATTGGGTCATGTCAGATTTAGACAGTGTTGTGTTTAAGATAAAATGTTTAATGG	120
Query	121	CTCTTAGCAGTGTTTCATGCCTCCCCTTTTCCCCTGATACTTTAAAAACAGAATATACAGA	180
Sbjct	121	CTCTTAGCAGTGTTTCATGCCTCCCCTTTTCCCCTGATACTTTAAAAACAGAATATACAGA	180
Query	181	AAAGGGGAGTTGGGTGAAGAATCACCATATTCTCATTACCAGAGTAGTGCTACCAGCTG	240
Sbjct	181	AAAGGGGAGTTGGGTGAAGAATCACCATATTCTCATTACCAGAGTAGTGCTACCAGCTG	240
Query	241	TTTTCACATTTTTCTGTTTCCTTCTGTCCTTGGAATCCttttttAGATCCTTGTAATAC	300
Sbjct	241	TTTTCACATTTTTCTGTTTCCTTCTGTCCTTGGAATCCTTTTTTTTAGATCCTTGTAATAC	300
Query	301	TAGTAAAGATATTCCACTCTGTGTTGTAAGCATTTTTCCATTTTGCTCCATGGTCTTCAT	360
Sbjct	301	TAGTAAAGATATTCCACTCTGTGTTGTAAGCATTTTTCCATTTTGCTCCATGGTCTTCAT	360
Query	361	AATGCCCTGTGGTCCTTTATTAAGGGGATGCACCATGTAGAGGTGAAAGGCTTTCCTTGA	420
Sbjct	361	AATGCCCTGTGGTCCTTTATTAAGGGGATGCACCATGTAGAGGTGAAAGGCTTTCCTTGA	420
Query	421	CTTGGCCACCATTTCTGTATTTTCCTTAGAGGAGGAGGTTTCCAACATTTCTTTTTTAGA	480
Sbjct	421	CTTGGCCACCATTTCTGTATTTTCCTTAGAGGAGGAGGTTTCCAACATTTCTTTTTTAGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GACAGAGTCTCGTTCTGACACGCAGGCAGGAGTGCAGTGGCATGATAACAGCTCACTGCA	540
Sbjct	481	GACAGAGTCTCGTTCTGACACGCAGGCAGGAGTGCAGTGGCATGATAACAGCTCACTGCA	540
Query	541	GCCTCGAACTCCTGGGCTCAAGTTATCCTCCACCTCAGCTTCCTGAGTAGCTAGGACTG	600
Sbjct	541	GCCTCGAACTCCTGGGCTCAAGTTATCCTCCACCTCAGCTTCCTGAGTAGCTAGGACTG	600
Query	601	CAGGTGCCTGCCACCACACCCAGCTAAT	628
Sbjct	601	CAGGTGCCTGCCACCACACCCAGCTAAT	628

Sequence 1186 matched with Sequence 403

Query= Sequence ID - 1186 nt: 494
Length=494

SEQ ID NO: 403 nt: 494

ALIGNMENTS

Identities = 494/494 (100%), Gaps = 0/494 (0%)

Query	1	CAGCCCTCCGTCACCTCTTACCGCACCCCTCGGACTgcccccaaggccccgcgcgcgcct	60
Sbjct	1	CAGCCCTCCGTCACCTCTTACCGCACCCCTCGGACTGCCCAAGGCCCGCCGCCGCT	60
Query	61	ccagcgccgcgcagccaccgcccgcgcgcgcctctccttagtcgcccATGACGACC	120
Sbjct	61	CCAGCGCCGCGCAGCCACCGCCGCCGCCGCGCCTCTCCTTAGTCGCCGCCATGACGACC	120
Query	121	GCGTCCACCTCGCAGGTGCGCCAGAACTACCACCAGGACTCAGAGGCCGCCATCAACCGC	180
Sbjct	121	GCGTCCACCTCGCAGGTGCGCCAGAACTACCACCAGGACTCAGAGGCCGCCATCAACCGC	180
Query	181	CAGATCAACCTGGAGCTCTACGCCTCCTACGTTTACCTGTCCATGTCTTACTACTTTGAC	240
Sbjct	181	CAGATCAACCTGGAGCTCTACGCCTCCTACGTTTACCTGTCCATGTCTTACTACTTTGAC	240
Query	241	CGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAG	300
Sbjct	241	CGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAG	300
Query	301	AGGGGAACATGCTGAGAACTGATGAAGCTGCAGAACCAACGAGGGTGGCCGAATCTTCC	360
Sbjct	301	AGGGGAACATGCTGAGAACTGATGAAGCTGCAGAACCAACGAGGGTGGCCGAATCTTCC	360
Query	361	TTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGT	420
Sbjct	361	TTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGT	420
Query	421	GTGCATTACATTTGGaaaaaaTGGAATCAGTCACTACTGGAAGTGCACAACTGGCCA	480
Sbjct	421	GTGCATTACATTTGGAAAAAAATGGAATCAGTCACTACTGGAAGTGCACAACTGGCCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGACAAAAATGAC	494
Sbjct	481	CTGACAAAAATGAC	494

Sequence 1188 matched with Sequence 404

Query= Sequence ID - 1188 nt: 599
Length=599

SEQ ID NO: 404 nt: 599

ALIGNMENTS

Identities = 599/599 (100%), Gaps = 0/599 (0%)

Query	1	GGGAGACAAGCCCAGCCTTTCGGCGAGNATACGTCTAACCTGTGCAACAGCCACTACAT	60
Sbjct	1	GGGAGACAAGCCCAGCCTTTCGGCGAGNATACGTCTAACCTGTGCAACAGCCACTACAT	60
Query	61	TACTTCAAAGTGAATCCTTCCTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAG	120
Sbjct	61	TACTTCAAAGTGAATCCTTCCTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAG	120
Query	121	TCTTCCTCCCTGTGTATTCTCATGATTATTATTTAGTGGGGCGGGGTGGGAAAG	180
Sbjct	121	TCTTCCTCCCTGTGTATTCTCATGATTATTATTTAGTGGGGCGGGGTGGGAAAG	180
Query	181	ATTACTTTTTCTTTATGTGTTTGACGGGAAACAAAGTAAATCTACAGTACACCA	240
Sbjct	181	ATTACTTTTTCTTTATGTGTTTGACGGGAAACAAAGTAAATCTACAGTACACCA	240
Query	241	CAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAGGGGCAGGCCANA	300
Sbjct	241	CAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAGGGGCAGGCCANA	300
Query	301	GCTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAA	360
Sbjct	301	GCTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAA	360
Query	361	CCTCTTCCCCGCGCGTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAG	420
Sbjct	361	CCTCTTCCCCGCGCGTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAG	420
Query	421	GCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCAGCTCAGGGC	480
Sbjct	421	GCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCAGCTCAGGGC	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCTTTCCTCCACACCATTTCAGGTCTTTCTTTCCGAGGCCCTGTCTCAGGGTGAGGTGCT	540
Sbjct	481	TCTTTCCTCCACACCATTTCAGGTCTTTCTTTCCGAGGCCCTGTCTCAGGGTGAGGTGCT	540
Query	541	TGAGTCTCCAACGGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAG	599
Sbjct	541	TGAGTCTCCAACGGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAG	599

Sequence 1189 matched with Sequence 405

Query= Sequence ID 1189
Length=610

SEQ ID NO: 405

ALIGNMENTS

Identities = 610/610 (100%), Gaps = 0/610 (0%)

Query	1	GGGAGACAAGCCCAGCCTTTCGGCGAGATACGTCTAACCCCTGTGCAACAGCCACTACATT	60
Sbjct	1	GGGAGACAAGCCCAGCCTTTCGGCGAGATACGTCTAACCCCTGTGCAACAGCCACTACATT	60
Query	61	ACTTCAAAGTGAATCCTTCTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAGT	120
Sbjct	61	ACTTCAAAGTGAATCCTTCTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAGT	120
Query	121	CTTCTCCCTGTGTATTCATTCTCATGATTATTATTTTAGTGGGGGCGGGTGGGAAAGA	180
Sbjct	121	CTTCTCCCTGTGTATTCATTCTCATGATTATTATTTTAGTGGGGGCGGGTGGGAAAGA	180
Query	181	TTACTTTTTCTTTATGTGTTTGACGGGAAACAAAAGTAAATCTACAGTACACCAC	240
Sbjct	181	TTACTTTTTCTTTATGTGTTTGACGGGAAACAAAAGTAAATCTACAGTACACCAC	240
Query	241	AAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGAAAGGGGCAGGCCAGAG	300
Sbjct	241	AAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGAAAGGGGCAGGCCAGAG	300
Query	301	CTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAAC	360
Sbjct	301	CTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAAC	360
Query	361	CTCTTCCCCGCCCGTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAGG	420
Sbjct	361	CTCTTCCCCGCCCGTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAGG	420
Query	421	CACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCAGCTCAGGGCT	480
Sbjct	421	CACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCAGCTCAGGGCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTTTCCTCCACACCATTTCAGGTCTTTCTTTCCGAGGCCCTGTCTCAGGGTGAGGTGCTT	540
Sbjct	481	CTTTCCTCCACACCATTTCAGGTCTTTCTTTCCGAGGCCCTGTCTCAGGGTGAGGTGCTT	540
Query	541	GAGTCTCCAACGGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAGCC	600
Sbjct	541	GAGTCTCCAACGGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAGCC	600
Query	601	TCGAGGAGGT	610
Sbjct	601	TCGAGGAGGT	610

Sequence 1190 matched with Sequence 406

Query= Sequence ID 1190
Length=644

SEQ ID NO: 406

ALIGNMENTS

Identities = 644/644 (100%), Gaps = 0/644 (0%)

Query	1	GTTTAAATTTGACAACTAAAGCTNATNACTGCTATAAGAGTAATAACTGCTCATTTTCC	60
Sbjct	1	GTTTAAATTTGACAACTAAAGCTNATNACTGCTATAAGAGTAATAACTGCTCATTTTCC	60
Query	61	ATAACTCATTCTTAAAGTTTGTAGTAATGTAAAAGTTAttttttGCAGTAAGTTATAATG	120
Sbjct	61	ATAACTCATTCTTAAAGTTTGTAGTAATGTAAAAGTTATTTTTTGCAGTAAGTTATAATG	120
Query	121	ATAGAAGCTTACATGTTTTTTCATGCCTCATCTGTTCCCTTAAACTATAATTATCAG	180
Sbjct	121	ATAGAAGCTTACATGTTTTTTCATGCCTCATCTGTTCCCTTAAACTATAATTATCAG	180
Query	181	TAAAGTCCTGTGGTATTTTTCAATTTGTAAGAACTAGGCTATATATACATTGGGAAAAA	240
Sbjct	181	TAAAGTCCTGTGGTATTTTTCAATTTGTAAGAACTAGGCTATATATACATTGGGAAAAA	240
Query	241	CAGCCTTCATTTGTCAATGCACTAGTGTCCAAAGGTTTCTGGTAATTGTGTGCTATTGC	300
Sbjct	241	CAGCCTTCATTTGTCAATGCACTAGTGTCCAAAGGTTTCTGGTAATTGTGTGCTATTGC	300
Query	301	TTTTTGTTGACTTGCAaaaaaaaaaaaaaaaaaTTACTATGACTTGNGGTAGCCCTGCA	360
Sbjct	301	TTTTTGTTGACTTGCAAAAAAAAAAAAAAAAAAATTACTATGACTTGNGGTAGCCCTGCA	360
Query	361	ACCTTCGGAAGTGCTTAGCCCAGTCTGACCATACATTTATATTTANAATGCTTAGGTAAA	420
Sbjct	361	ACCTTCGGAAGTGCTTAGCCCAGTCTGACCATACATTTATATTTANAATGCTTAGGTAAA	420
Query	421	TAAATAATATGCCTAAACCCAATGCTATAAGATACTATATAATATCTCATAATTTTAAAA	480
Sbjct	421	TAAATAATATGCCTAAACCCAATGCTATAAGATACTATATAATATCTCATAATTTTAAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATCACTGTTTTGTATAATAATAAAACAAGGCAGGCAAGCTGTTCTACAATGACTGTTGGT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATCACTGTTTTGTATAATAATAAAACAAGGCAGGCAAGCTGTTCTACAATGACTGTTGGT  540

Query  541  AAGGGTGCTGAGGAAGAAAAACAAACAATCTTGATTCAGGGATAGTGAATAGACAAAAAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AAGGGTGCTGAGGAAGAAAAACAAACAATCTTGATTCAGGGATAGTGAATAGACAAAAAA  600

Query  601  TGTCTAATCAATGAAGCTGTGTGATGATTCTGATTGACAGAGA  644
          |||||||||||||||||||||||||||||||||||||||
Sbjct   601  TGTCTAATCAATGAAGCTGTGTGATGATTCTGATTGACAGAGA  644
```


Sequence 1191 matched with Sequence 407

Query= Sequence ID 1191
Length=653

SEQ ID NO: 407

ALIGNMENTS

Identities = 653/653 (100%), Gaps = 0/653 (0%)

Query	1	GTGCAAAGTGTTATATCCACTTTCAACAAAGAGAGAAGCTGAAAAGCTAACCCAATGTTA	60
Sbjct	1	GTGCAAAGTGTTATATCCACTTTCAACAAAGAGAGAAGCTGAAAAGCTAACCCAATGTTA	60
Query	61	ATTTTGGATCACACACATTTCAGTGTAGACTTTAAGATTTTACTTCTGTTGGAGTAGCTAT	120
Sbjct	61	ATTTTGGATCACACACATTTCAGTGTAGACTTTAAGATTTTACTTCTGTTGGAGTAGCTAT	120
Query	121	ATTATTTCTAGTTAAAAAAGCTCTCTATATACATATTTATTTGTTTTTCTACTTGTTTAAAT	180
Sbjct	121	ATTATTTCTAGTTAAAAAAGCTCTCTATATACATATTTATTTGTTTTTCTACTTGTTTAAAT	180
Query	181	ATTTTTCTCTTCCAATTAGGAACTCAATATGGAATAAAAAATATTTAAATGTATTTTACT	240
Sbjct	181	ATTTTTCTCTTCCAATTAGGAACTCAATATGGAATAAAAAATATTTAAATGTATTTTACT	240
Query	241	CAAACGTGTGTGTATATATGTTTGTGTGCATGATAAGgagagtgagagcaagagtaagag	300
Sbjct	241	CAAACGTGTGTGTATATATGTTTGTGTGCATGATAAGGAGAGTGAGAGCAAGAGTAAGAG	300
Query	301	agagagagCACGCATAGATGGAAGCACACATTTAATGTCTATGAAATGAGAAAACATTAA	360
Sbjct	301	AGAGAGAGCACGCATAGATGGAAGCACACATTTAATGTCTATGAAATGAGAAAACATTAA	360
Query	361	GGCTAAGATATTTTTCCTTCTGAACTAGCAGATTGTATCAATGGCTGGTCACTTAAATTA	420
Sbjct	361	GGCTAAGATATTTTTCCTTCTGAACTAGCAGATTGTATCAATGGCTGGTCACTTAAATTA	420
Query	421	ATCAGTTTGTAAAGATATTTAAAAGGTATGTCTACCTTCTTGCAATTAATTTGATTATGT	480
Sbjct	421	ATCAGTTTGTAAAGATATTTAAAAGGTATGTCTACCTTCTTGCAATTAATTTGATTATGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCTAATGGCATGGCAAGAGAAATGAAAGAAGATAACTAAAAGTTAAAAGTCGTTGCATGT	540
Sbjct	481	TCTAATGGCATGGCAAGAGAAATGAAAGAAGATAACTAAAAGTTAAAAGTCGTTGCATGT	540
Query	541	TTTTGTTGCAGCATACCCTTCTTTCAGGCTACCGAATAACCTTGATTGACATTGGATTAG	600
Sbjct	541	TTTTGTTGCAGCATACCCTTCTTTCAGGCTACCGAATAACCTTGATTGACATTGGATTAG	600
Query	601	TAGTAGAATACCTCATTGGTAGAGCATATCGCAGCANCTACACTAGAAAACAT	653
Sbjct	601	TAGTAGAATACCTCATTGGTAGAGCATATCGCAGCANCTACACTAGAAAACAT	653

Sequence 1192 matched with Sequence 408

Query= Sequence ID 1192
Length=452

SEQ ID NO: 408

ALIGNMENTS

Identities = 452/452 (100%), Gaps = 0/452 (0%)

Query	1	GTCTGGA ACTCCAGACCTCAGGTGATACCCCTGCCTCAGCCTCCCAATGTGCTGGGATTA	60
Sbjct	1	GTCTGGA ACTCCAGACCTCAGGTGATACCCCTGCCTCAGCCTCCCAATGTGCTGGGATTA	60
Query	61	CAGCTGTGAAGCCACCGCGCCCGGCTGCTGTGATAGTTGAGATGTAAACCAAAAATAAAA	120
Sbjct	61	CAGCTGTGAAGCCACCGCGCCCGGCTGCTGTGATAGTTGAGATGTAAACCAAAAATAAAA	120
Query	121	TTCTAAGCCACCCAATCCGACTGAATGGACCCTTCCTGTTGAGCAAGGACATTCCAAAGT	180
Sbjct	121	TTCTAAGCCACCCAATCCGACTGAATGGACCCTTCCTGTTGAGCAAGGACATTCCAAAGT	180
Query	181	AAACTGAAAAGACCAGCTTAGGCCATGATGGGAAGGGGAGGTGTCAACATGCCTCATTCT	240
Sbjct	181	AAACTGAAAAGACCAGCTTAGGCCATGATGGGAAGGGGAGGTGTCAACATGCCTCATTCT	240
Query	241	ACCTTCCTCCCTCTGGAATCCAGACACA ACTGACCAGCATTAACATTAAAAACAGAGATCT	300
Sbjct	241	ACCTTCCTCCCTCTGGAATCCAGACACA ACTGACCAGCATTAACATTAAAAACAGAGATCT	300
Query	301	TAAGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGAT	360
Sbjct	301	TAAGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGAT	360
Query	361	CACCTGAGGTCGGAAGTTCAAGACCAGCCTGGCCGGTATGGTGAAGCCATGTCTCTACTG	420
Sbjct	361	CACCTGAGGTCGGAAGTTCAAGACCAGCCTGGCCGGTATGGTGAAGCCATGTCTCTACTG	420
Query	421	AAAATGCAAAATTGGCCGGACATTGTGGTGCA	452
Sbjct	421	AAAATGCAAAATTGGCCGGACATTGTGGTGCA	452

Sequence 1193 matched with Sequence 409

Query= Sequence ID 1193
Length=900

SEQ ID NO: 409

ALIGNMENTS

Identities = 900/900 (100%), Gaps = 0/900 (0%)

```
Query 1      TNCNttttttttCCCNCGGGAAAGCGCGCCATTGTGTTGGTCCCCGGAATTCGCGGCCGCGTC 64
|||||
Sbjct 1      TNCNTTTTTTTTCCCNCGGGAAAGCGCGCCATTGTGTTGGTCCCCGGAATTCGCGGCCGCGTC 64

Query 65     GACGAGAAATGGCTTGAACCCAGTAGGCAGAGGTTGTAGTGAGCCCAGAATNGGNCACCT 124
|||||
Sbjct 65     GACGAGAAATGGCTTGAACCCAGTAGGCAGAGGTTGTAGTGAGCCCAGAATNGGNCACCT 124

Query 125    GCACNTTANCCNTGGGTGACAAAANTGAAACTTTGTCTnaaaaaaaaaaaaaaaaaaat 184
|||||
Sbjct 125    GCACNTTANCCNTGGGTGACAAAANTGAAACTTTGTCTNAAAAAAAAAAAAAAAAAAAT 184

Query 185    tttaantnaaatnaaaaaancctttncnttntttttnaaannggggggggNNTTTTNGGG 244
|||||
Sbjct 185    TTTAANTNAAATNAAAAANCCTTTNCNTTNTTTTTNAAANNGGGGGGGGNNTTTTNGGG 244

Query 245    NTTNGNNNTGGTAAAAANTNNNtttttttttttaggggccnanncccnttttanaaa 304
|||||
Sbjct 245    NTTNGNNNTGGTAAAAANTNNNTTTTTTTTTTTTAGGGGCCNANNCCCNTTTANAAA 304

Query 305    anccngnttttnaaaaaantttttNCCCNCNNTTNggggggggggNTTTTNANCNNTNT 364
|||||
Sbjct 305    ANCCNGNTTTTNAAAAAANTTTTTNCCCNCNNTTNGGGGGGGGGNTTTTNANCNNTNT 364

Query 365    TNgggggggNCCCCCTNTTANNACCNCAaantttttantttttgnnnaannnccccct 424
|||||
Sbjct 365    TNGGGGGGNCCCCCTNTTANNACCNCAAANTTTTTANTTTTTGNNAANNNCCCCCT 424

Query 425    tttttnntttttttGNggggggggggNNGCCCCCNCCCTTNggggggggggNTTNNGn 484
|||||
Sbjct 425    TTTTNTTTTTTTTTTGNGGGGGGGGGNNGCCCCCNCCCTTNGGGGGGGGGNNTTNNGN 484
```

PATENT SEQUENCE ALIGNMENT

Query	485	aaaannacttttnaaaannaGGGNNGGGGNANATNNccccccNGGNtttttttttta	544
Sbjct	485	AAAANNACTTTTNAANAAGGGNNGGGGNANATNNCCCCCNGGNTTTTTTTTTTA	544
Query	545	aaaantnaannggggggggnnctnantnggggcncccanngggggttanaannaTTTT	604
Sbjct	545	AAAANTNAANNGGGGGGGNNCTNANTNGGGGCNCCANNGGGGNTTANAANNATTTT	604
Query	605	CTNCCCAAACCCCGNTTTTATNNccccccccccNCNNNNGAANGGGNGGNCCNttt	664
Sbjct	605	CTNCCCAAACCCCGNTTTTATNNCCCCCCCCCCCCNCNNNNGAANGGGNGGNCCNTTT	664
Query	665	tttttatttttNNGGNGGNaaaaaantttnaaaaannannaTNTTTTTTccccccccc	724
Sbjct	665	TTTTTATTTTNNGGNGGNAAAAAANTTTNAANAANNATNTTTTTTCCCCCCCCC	724
Query	725	ccNCTTTTNGGNAAANCCNNGGGGGNTCCTTTTTTnaaannnncccccaaaaaaanttt	784
Sbjct	725	CCNCTTTTNGGNAAANCCNNGGGGGNTCCTTTTTTNAANNNNCCCCAAAAAAAANTTT	784
Query	785	tttnttntntttttctctnggggnccnnantnttananttttncnccnaaaaaaangg	844
Sbjct	785	TTTTNTNTNTTTTTCTCTNGGGGNCCNNANTTNTANANTTTTNCNCCNAAAAAAAANGG	844
Query	845	gnccccttttttncnggnnggncccaaannttttttttnaaaaaaaaaaaaa	900
Sbjct	845	GNCCCCTTTTTTNCNGGNNGGNCCCAAAANNTTTTTTTTNAAAAAAAAAAAAAA	900

Blast comparison trimmed “TNCN” from the 5’ end of both sequences and reported 896 identities. The report has been manually corrected for this. “TNCN” has been prepended to both sequences and identity count has been increased to 900.

Sequence 1195 matched with Sequence 410

Query= Sequence ID 1195
Length=271

SEQ ID NO: 410

ALIGNMENTS

Identities = 271/271 (100%), Gaps = 0/271 (0%)

Query	1	GTTCGTGACNTTCGGAGCTACCTGACAGAGCAGAGTCAACCAGGNTCTGCCCAAAGAGAG	60
Sbjct	1	GTTCGTGACNTTCGGAGCTACCTGACAGAGCAGAGTCAACCAGGNTCTGCCCAAAGAGAG	60
Query	61	TGTTAGGCCTGAGCTTGAGAGCCCTGGAGAGACGTGTGCACAAAATGTGACCTGAGGCCC	120
Sbjct	61	TGTTAGGCCTGAGCTTGAGAGCCCTGGAGAGACGTGTGCACAAAATGTGACCTGAGGCCC	120
Query	121	TAGTCTAGCAAGAGGACATAGCACCCCTCATCTGGGAATAGGGAAGGCACCTTGCAGAAAA	180
Sbjct	121	TAGTCTAGCAAGAGGACATAGCACCCCTCATCTGGGAATAGGGAAGGCACCTTGCAGAAAA	180
Query	181	TATGAGCAATTTGATATTAACCTAACATCTTCAATGTGCCATAGACCTTCCCACAAAGACT	240
Sbjct	181	TATGAGCAATTTGATATTAACCTAACATCTTCAATGTGCCATAGACCTTCCCACAAAGACT	240
Query	241	GTCCAATAATAAGAGATGCTTATCTATTTTA	271
Sbjct	241	GTCCAATAATAAGAGATGCTTATCTATTTTA	271

Sequence 1196 matched with Sequence 411

Query= Sequence ID - 1196 nt: 412
Length=412

SEQ ID NO: 411 nt: 412

ALIGNMENTS

Identities = 412/412 (100%), Gaps = 0/412 (0%)

```
Query 1   GTCGACGCGGCCGCGTCTGGAGNCGATCAACTCTAGGCTCCAACTCGTTATGAAAAG 60
          |||
Sbjct 1   GTCGACGCGGCCGCGTCTGGAGNCGATCAACTCTAGGCTCCAACTCGTTATGAAAAG 60

Query 61  TGGGAAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAA 120
          |||
Sbjct 61  TGGGAAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAA 120

Query 121 ATTGGTCATTCTCGCTAACAACTGCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGC 180
          |||
Sbjct 121 ATTGGTCATTCTCGCTAACAACTGCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGC 180

Query 181 TATGTTGGCTAAAACCTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGC 240
          |||
Sbjct 181 TATGTTGGCTAAAACCTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGC 240

Query 241 ATGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACAT 300
          |||
Sbjct 241 ATGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACAT 300

Query 301 CATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTAAACCTTTTCACCTACAAAATTTCA 360
          |||
Sbjct 301 CATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTAAACCTTTTCACCTACAAAATTTCA 360

Query 361 CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTGTTTT 412
          |||
Sbjct 361 CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTGTTTT 412
```


Sequence 1197 matched with Sequence 412

Query= Sequence ID 1197
Length=460

SEQ ID NO: 412

ALIGNMENTS

Identities = 460/460 (100%), Gaps = 0/460 (0%)

Query	1	CCGCCAACATGGGCCGCGTTCGCACCAAAACCGTGAAGAAGGCGGCCCGGGTCATCATAG	60
Sbjct	1	CCGCCAACATGGGCCGCGTTCGCACCAAAACCGTGAAGAAGGCGGCCCGGGTCATCATAG	60
Query	61	AAAAGTACTACACGCGCCTGGGCAACGACTTCCACACGAACAAGCGCGTGTGCGAGGAGA	120
Sbjct	61	AAAAGTACTACACGCGCCTGGGCAACGACTTCCACACGAACAAGCGCGTGTGCGAGGAGA	120
Query	121	TCGCCATTATCCCCAGCAAAAAGCTCCGCAACAAGATAGCAGGTTATGTCACGCATCTGA	180
Sbjct	121	TCGCCATTATCCCCAGCAAAAAGCTCCGCAACAAGATAGCAGGTTATGTCACGCATCTGA	180
Query	181	TGAAGCGAATTCAGAGAGGCCAGTAAGAGGTATCTCCATCAAGCTGCAGGAGGAGGAGA	240
Sbjct	181	TGAAGCGAATTCAGAGAGGCCAGTAAGAGGTATCTCCATCAAGCTGCAGGAGGAGGAGA	240
Query	241	GAGAAAGGAGAGACAATTATGTTCTGAGGTCTCAGCCTTGGATCAGGAGATTATTGAAG	300
Sbjct	241	GAGAAAGGAGAGACAATTATGTTCTGAGGTCTCAGCCTTGGATCAGGAGATTATTGAAG	300
Query	301	TAGATCCTGACACTAAGGAAATGCTGAAGCTTTTGGACTTCGGCAGTCTGTCCAACCTTC	360
Sbjct	301	TAGATCCTGACACTAAGGAAATGCTGAAGCTTTTGGACTTCGGCAGTCTGTCCAACCTTC	360
Query	361	AGGTCACTCAGCCTACAGTTGGGATGAATTTCAAACGCCTCGGGGACCTGTTTGAATTT	420
Sbjct	361	AGGTCACTCAGCCTACAGTTGGGATGAATTTCAAACGCCTCGGGGACCTGTTTGAATTT	420
Query	421	TTTCTGTAGTGCTGTATTATTTCAATAAATCTGGGACAA	460
Sbjct	421	TTTCTGTAGTGCTGTATTATTTCAATAAATCTGGGACAA	460

Sequence 1198 matched with Sequence 413

Query= Sequence ID 1198
Length=245

SEQ ID NO: 413

ALIGNMENTS

Identities = 245/245 (100%), Gaps = 0/245 (0%)

Query	1	CAGAGGTGGGAGGATTGCTTCAGTTCAAGAGTTTGAGACCAGCCTGGGTAACATGGCGAA	60
Sbjct	1	CAGAGGTGGGAGGATTGCTTCAGTTCAAGAGTTTGAGACCAGCCTGGGTAACATGGCGAA	60
Query	61	ACCCTGTCTTTACAAAAATGCAAACCTTTGCCGCATGTGTTGGGGTGCGCCTGTAGTCC	120
Sbjct	61	ACCCTGTCTTTACAAAAATGCAAACCTTTGCCGCATGTGTTGGGGTGCGCCTGTAGTCC	120
Query	121	CAGCTTCTCGGGAGGCTGAGGTGGGGGGACCACCTGAGCCATGGAGGTTGAGGCTGCAGT	180
Sbjct	121	CAGCTTCTCGGGAGGCTGAGGTGGGGGGACCACCTGAGCCATGGAGGTTGAGGCTGCAGT	180
Query	181	GAGCCGTGATACCACCACTGTACTCTAGCCTGGGCCATAGAGTGAGACACCCTGCCTCAG	240
Sbjct	181	GAGCCGTGATACCACCACTGTACTCTAGCCTGGGCCATAGAGTGAGACACCCTGCCTCAG	240
Query	241	AAATA	245
Sbjct	241	AAATA	245

Sequence 1199 matched with Sequence 414

Query= Sequence ID - 1199 nt: 439
Length=439

SEQ ID NO: 414 nt: 439

ALIGNMENTS

Identities = 439/439 (100%), Gaps = 0/439 (0%)

Query	1	CCCATCCCCTCGACCGCTCGCGTCGCATTTGGCCGCCTCCCTACCGCTCCAAGCCCAGCC	60
Sbjct	1	CCCATCCCCTCGACCGCTCGCGTCGCATTTGGCCGCCTCCCTACCGCTCCAAGCCCAGCC	60
Query	61	CTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATCTTCCACAA	120
Sbjct	61	CTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATCTTCCACAA	120
Query	121	GTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGAAGGAGCTGAT	180
Sbjct	121	GTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGAAGGAGCTGAT	180
Query	181	CCAGAAGGAGCTCACCATTGGCTCGAAGCTGCAGGATGCTGAAATTGCAAGGCTGATGGA	240
Sbjct	181	CCAGAAGGAGCTCACCATTGGCTCGAAGCTGCAGGATGCTGAAATTGCAAGGCTGATGGA	240
Query	241	AGACTTGGACCGGAACAAGGACCAGGAGGTGAACTTCCAGGAGTATGTCACCTTCCTGGG	300
Sbjct	241	AGACTTGGACCGGAACAAGGACCAGGAGGTGAACTTCCAGGAGTATGTCACCTTCCTGGG	300
Query	301	GGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGCTGAAAATAAATAGGGAAGATGGA	360
Sbjct	301	GGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGCTGAAAATAAATAGGGAAGATGGA	360
Query	361	GACACCCTCTGGGGGTCCTCTCTGAGTCAAATCCAGTGGTGGGTAATTGTACAATAAAtt	420
Sbjct	361	GACACCCTCTGGGGGTCCTCTCTGAGTCAAATCCAGTGGTGGGTAATTGTACAATAAATT	420
Query	421	tttttttGGTCAAATTTAA	439
Sbjct	421	TTTTTTTGGTCAAATTTAA	439

Sequence 1200 matched with Sequence 415

Query= Sequence ID - 1200 nt: 526
Length=526

SEQ ID NO: 415 nt: 526

ALIGNMENTS

Identities = 526/526 (100%), Gaps = 0/526 (0%)

Query	1	CTGGAGACGACGTGCAGAAATGGCACCTCGAAAGGGAAGGAAAAGAAGGAAGAACAGGT	60
Sbjct	1	CTGGAGACGACGTGCAGAAATGGCACCTCGAAAGGGAAGGAAAAGAAGGAAGAACAGGT	60
Query	61	CATCAGCCTCGGACCTCAGGTGGCTGAAGGAGAGAATGTATTTGGTGTCTGCCATATCTT	120
Sbjct	61	CATCAGCCTCGGACCTCAGGTGGCTGAAGGAGAGAATGTATTTGGTGTCTGCCATATCTT	120
Query	121	TGCATCCTTCAATGACACTTTTGTCCATGTCACTGATCTTTCTGGCAAGGAAACCATCTG	180
Sbjct	121	TGCATCCTTCAATGACACTTTTGTCCATGTCACTGATCTTTCTGGCAAGGAAACCATCTG	180
Query	181	CCGTGTGACTGGTGGGATGAAGGTAAAGGCAGACCGAGATGAATCCTCACCATATGCTGC	240
Sbjct	181	CCGTGTGACTGGTGGGATGAAGGTAAAGGCAGACCGAGATGAATCCTCACCATATGCTGC	240
Query	241	TATGTTGGCTGCCCAGGATGTGGCCCAGAGGTGCAAGGAGCTGGGTATCACCGCCCTACA	300
Sbjct	241	TATGTTGGCTGCCCAGGATGTGGCCCAGAGGTGCAAGGAGCTGGGTATCACCGCCCTACA	300
Query	301	CATCAAACCTCCGGGCCACAGGAGGAAATAGGACCAAGACCCCTGGACCTGGGGCCCAGTC	360
Sbjct	301	CATCAAACCTCCGGGCCACAGGAGGAAATAGGACCAAGACCCCTGGACCTGGGGCCCAGTC	360
Query	361	GGCCCTCANAGCCCTTGCCCGCTCGGGTATGAAGATCGGGCGGATTGAGGATGTCACCCC	420
Sbjct	361	GGCCCTCANAGCCCTTGCCCGCTCGGGTATGAAGATCGGGCGGATTGAGGATGTCACCCC	420
Query	421	CATCCCCTCTGACAGCACTCGCAGGAAGGGGGGTCGCCGTGGTCGCCGTCTGTGAACAAG	480
Sbjct	421	CATCCCCTCTGACAGCACTCGCAGGAAGGGGGGTCGCCGTGGTCGCCGTCTGTGAACAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	ATTCCTCAAAATATTTTCTGTTAATAAATTGCCTTCATGTAAACTG	526
Sbjct	481	ATTCCTCAAAATATTTTCTGTTAATAAATTGCCTTCATGTAAACTG	526

Sequence 1201 matched with Sequence 416

Query= Sequence ID - 1201 nt: 613
Length=613

SEQ ID NO: 416 nt: 613

ALIGNMENTS

Identities = 613/613 (100%), Gaps = 0/613 (0%)

Query	1	CTTAAGTATGCCCTGACAGGAGNATGAAGTAAAGAAGATTTGCATGCAGCGGTTTCATTAA	60
Sbjct	1	CTTAAGTATGCCCTGACAGGAGNATGAAGTAAAGAAGATTTGCATGCAGCGGTTTCATTAA	60
Query	61	AATCGATGGCAAGGTCCGAACTGATATAACCTACCCTGCTGGATTCATGGATGTCATCAG	120
Sbjct	61	AATCGATGGCAAGGTCCGAACTGATATAACCTACCCTGCTGGATTCATGGATGTCATCAG	120
Query	121	CATTGACAAGACGGGAGAGAATTTCCGTCTGATCTATGACACCAAGGGTCGCTTTGCTGT	180
Sbjct	121	CATTGACAAGACGGGAGAGAATTTCCGTCTGATCTATGACACCAAGGGTCGCTTTGCTGT	180
Query	181	ACATCGTATTACACCTGAGGAGGCCAAGTACAAGTTGTGCAAAGTGAGAAAGATCTTTGT	240
Sbjct	181	ACATCGTATTACACCTGAGGAGGCCAAGTACAAGTTGTGCAAAGTGAGAAAGATCTTTGT	240
Query	241	GGGCACAAAAGGAATCCCTCATCTGGTGACTCATGATGCCCCGACCATCCGCTACCCCGA	300
Sbjct	241	GGGCACAAAAGGAATCCCTCATCTGGTGACTCATGATGCCCCGACCATCCGCTACCCCGA	300
Query	301	TCCCCTCATCAAGGTGAATGATACCATTTCAGATTGATTTAGAGACTGGCAAGATTACTGA	360
Sbjct	301	TCCCCTCATCAAGGTGAATGATACCATTTCAGATTGATTTAGAGACTGGCAAGATTACTGA	360
Query	361	TTTCATCAAGTTCGACACTGGTAACCTGTGTATGGTGACTGGAGGTGCTAACCTAGGAAG	420
Sbjct	361	TTTCATCAAGTTCGACACTGGTAACCTGTGTATGGTGACTGGAGGTGCTAACCTAGGAAG	420
Query	421	AATTGGTGTGATCACCAACAGAGAGAGGCACCCTGGATCTTTTGACGTGGTTCACGTGAA	480
Sbjct	421	AATTGGTGTGATCACCAACAGAGAGAGGCACCCTGGATCTTTTGACGTGGTTCACGTGAA	480

PATENT SEQUENCE ALIGNMENT

Query 481 AGATGCCAATGGCAACAGCTTTGCCACTCGACTTTCCAACATTTTGTATTGGCAAGGG 540
|||||
Sbjct 481 AGATGCCAATGGCAACAGCTTTGCCACTCGACTTTCCAACATTTTGTATTGGCAAGGG 540

Query 541 CAACAAACCATGGATTTCTCTTCCCCGAGGAAAGGGTATCCGCCTCACCATTGCTGAAGA 600
|||||
Sbjct 541 CAACAAACCATGGATTTCTCTTCCCCGAGGAAAGGGTATCCGCCTCACCATTGCTGAAGA 600

Query 601 GAGAGACAAAAGA 613
|||||
Sbjct 601 GAGAGACAAAAGA 613

Sequence 1202 matched with Sequence 417

Query= Sequence ID 1202
Length=663

SEQ ID NO: 417

ALIGNMENTS

Identities = 663/663 (100%), Gaps = 0/663 (0%)

Query	1	GGAATTCGCGGCCGCGTCGACCTCTGCTCGAATTGACAGAAAAGGATTCTGTGAAGAGTG	60
Sbjct	1	GGAATTCGCGGCCGCGTCGACCTCTGCTCGAATTGACAGAAAAGGATTCTGTGAAGAGTG	60
Query	61	ATGAGATTTCCATCCATGCTGACTTTGAGAATACATGTTCCCGAATTGTGGTCCCCAAAG	120
Sbjct	61	ATGAGATTTCCATCCATGCTGACTTTGAGAATACATGTTCCCGAATTGTGGTCCCCAAAG	120
Query	121	CTGCCATTGTGGCCCGCCACACTTACCTTGCCAATGGCCAGACCAAGGTGCTGACTCAGA	180
Sbjct	121	CTGCCATTGTGGCCCGCCACACTTACCTTGCCAATGGCCAGACCAAGGTGCTGACTCAGA	180
Query	181	AGTTGTCATCAGTCAGAGGCAATCATATTATCTCAGGGACATGCGCATCATGGCGTGGCA	240
Sbjct	181	AGTTGTCATCAGTCAGAGGCAATCATATTATCTCAGGGACATGCGCATCATGGCGTGGCA	240
Query	241	AGAGCCTTCGGGTTTCAGAAGATCAGGCCTTCTATCCTGGGCTGCAACATCCTTCGAGTTG	300
Sbjct	241	AGAGCCTTCGGGTTTCAGAAGATCAGGCCTTCTATCCTGGGCTGCAACATCCTTCGAGTTG	300
Query	301	AATATTCCTTACTGATCTATGTTAGCGTTCCTGGATCCAAGAAGGTCATCCTTGACCTGC	360
Sbjct	301	AATATTCCTTACTGATCTATGTTAGCGTTCCTGGATCCAAGAAGGTCATCCTTGACCTGC	360
Query	361	CCCTGGTAATTGGCAGCAGATCAGGTCTAAGCAGCAGAACATCCAGCATGGCCAGCCGAA	420
Sbjct	361	CCCTGGTAATTGGCAGCAGATCAGGTCTAAGCAGCAGAACATCCAGCATGGCCAGCCGAA	420
Query	421	CCAGCTCTGAGATGAGTTGGGTAGATCTGAACATCCCTGATACCCAGAAAGCTCCTCCCT	480
Sbjct	421	CCAGCTCTGAGATGAGTTGGGTAGATCTGAACATCCCTGATACCCAGAAAGCTCCTCCCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GCTATATGGATGTCATTCCTGAAGATCACCGATTGGAGAGCCCAACCACTCCTCTGCTAG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCTATATGGATGTCATTCCTGAAGATCACCGATTGGAGAGCCCAACCACTCCTCTGCTAG  540

Query  541  ATGACATGGATGGCTCTCAAGACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATGACATGGATGGCTCTCAAGACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCA  600

Query  601  TGCCACCACCGACTTATACTGAGGTGGATCCCTGCATCCTCAACAACAATGTGCAGTGAG  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TGCCACCACCGACTTATACTGAGGTGGATCCCTGCATCCTCAACAACAATGTGCAGTGAG  660

Query  661  CAT  663
          |||
Sbjct   661  CAT  663
```

Sequence 1203 matched with Sequence 418

Query= Sequence ID - 1203 nt: 692
Length=692

SEQ ID NO: 418 nt: 692

ALIGNMENTS

Identities = 692/692 (100%), Gaps = 0/692 (0%)

Query	1	TGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACCTAAAGGGAAACTTTC	60
Sbjct	1	TGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACCTAAAGGGAAACTTTC	60
Query	61	ACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTT	120
Sbjct	61	ACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTT	120
Query	121	GCAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTAT	180
Sbjct	121	GCAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTAT	180
Query	181	AAAAGGAAAAGTGATGGCATCTATATCATAAATCTCAAGAGGACCTGGGAGAAGCTTCTG	240
Sbjct	181	AAAAGGAAAAGTGATGGCATCTATATCATAAATCTCAAGAGGACCTGGGAGAAGCTTCTG	240
Query	241	CTGGCAGCTCGTGCAATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCTCC	300
Sbjct	241	CTGGCAGCTCGTGCAATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCTCC	300
Query	301	AGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATT	360
Sbjct	301	AGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATT	360
Query	361	GCTGGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCA	420
Sbjct	361	GCTGGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCA	420
Query	421	CGGCTTCTTGTGGTTACTGACCCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTAT	480
Sbjct	421	CGGCTTCTTGTGGTTACTGACCCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTAACCTACCTACCATTGCGCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTTAACCTACCTACCATTGCGCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATT  540

Query  541  GCCATCCCATGCAACAACAAGGGAGCTCACTCAGTGGGTTTAATGTGGTGGATGCTGGCT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GCCATCCCATGCAACAACAAGGGAGCTCACTCAGTGGGTTTAATGTGGTGGATGCTGGCT  600

Query  601  CGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTAACACCCATGGGAGGTCATGCCT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  CGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTAACACCCATGGGAGGTCATGCCT  660

Query  661  GATCTGTACTTCTACAGAGATCCTGAAGAGAT  692
          |||||||||||||||||||||||||
Sbjct   661  GATCTGTACTTCTACAGAGATCCTGAAGAGAT  692
```

Sequence 1204 matched with Sequence 419

Query= Sequence ID 1204
Length=365

SEQ ID NO: 419

ALIGNMENTS

Identities = 365/365 (100%), Gaps = 0/365 (0%)

```
Query 1      ttttttttttttCCTGCGGGAAAGCGCGCCATTGTGTTGGTACCCGGGAAATTCGCGGC 60
            |||
Sbjct 1      TTTTTCCTGCGGGAAAGCGCGCCATTGTGTTGGTACCCGGGAAATTCGCGGC 60

Query 61     CGCGTCGACACAGGCCCCAGCATCAAGATCTGGGATTTAGAGAGGAAAGATCATTGTAGA 120
            |||
Sbjct 61     CGCGTCGACACAGGCCCCAGCATCAAGATCTGGGATTTAGAGAGGAAAGATCATTGTAGA 120

Query 121    TGAAGTGAAGCAAGAAGTTATCAGTACCAGCAGCAAGGCAGAACCCAGTGCACCTC 180
            |||
Sbjct 121    TGAAGTGAAGCAAGAAGTTATCAGTACCAGCAGCAAGGCAGAACCCAGTGCACCTC 180

Query 181    CCTGGCCTGGTCTGCTGATGACACAGGTTGGGC 213
            |||
Sbjct 181    CCTGGCCTGGTCTGCTGATGACACAGGTTGGGC 213

Query 214    NGGNNCNCNGGGGNGGNNNNGNNNGCNGNNGGNNCNGNNNCNNNNNGCNNNNGNNNN 272
            |||
Sbjct 214    NGGNNCNCNGGGGNGGNNNNGNNNGCNGNNGGNNCNGNNNCNNNNNGCNNNNGNNNN 272

Query 273    TNNNCNNNGNNCNNNNNNNNNNNNNNNNNGNTCNNNGNNGCNGGGGCCNGNCGNCGCGG 331
            |||
Sbjct 273    TNNNCNNNGNNCNNNNNNNNNNNNNNNNNGNTCNNNGNNGCNGGGGCCNGNCGNCGCGG 331

Query 332    NCGCGNNTNNNNGGGTNCNNNCNCNNNGGCGCGC 365
            |||
Sbjct 332    NCGCGNNTNNNNGGGTNCNNNCNCNNNGGCGCGC 365
```

Blast comparison trimmed

“NGGNNCNCNGGGGNG GNNNNGNNNNNGCNGNNGGNNCNGNNNN CNNNNNGC-
NNNNGNNNNNTNNNCNNNG NNCNNNNNNNNNNNNNN NNNNGNTCNNNGNNGC NGGGGC-

CNGGNCGNCGCGGNCG CGNNTNNNNGGGTNCNNNCN CNNNGGCGCGC” from the 3’ end of both sequences and reported 213 identities. The report has been manually corrected for this.

“NGGNNCNCNGGGGNGGNNN NGNNNNGCNGNNGGNNCNGNNN CNNNNNGC-
NNNNGNNNTNNNCNNNG NNCNNNNNNNNNNN NNNNNNGNTCNGNNGC NGGGGC-
CNGGNCGNCGCGGNCG CGNNTNNNNGGGTNC NNCNCNNNGGCGCGC” has been
appended to both sequences and identity count has been increased to 365.

Sequence 1205 matched with Sequence 420

Query= Sequence ID 1205
Length=299

SEQ ID NO: 420

ALIGNMENTS

Identities = 299/299 (100%), Gaps = 0/299 (0%)

```
Query 1  CAGACTCTGACCCAGCCTCAGTCCTAACTCCTGGGGCTGGGCTGAGGGGAACAAGCATTT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  CAGACTCTGACCCAGCCTCAGTCCTAACTCCTGGGGCTGGGCTGAGGGGAACAAGCATTT 60

Query 61 GCTGAAACTTGaaaaacaaagcaaataaaaaacaggaaaaaattgtacctggtactttt 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GCTGAAACTTGAAAAACAAAGCAAATCAAAAACAGGAAAAAATTGTACCTGGTACTTTT 120

Query 121 ttttagaaaaaaagattaaaaaagaaagaataaattcttgtttggaaacttgaaaaaaa 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TTTTAGAAAAAAGATTAAAAAAGAAAGAATAAATTCTTGTTTGAAACTTGAAAAA 180

Query 181 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaattttaactc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTAACTC 240

Query 241 tTNNNNNTNNCNNCNANTAANNCANNTCNANNNNANNNNAATTACTTNNANGTNNNTCACN 299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TTNNNNNTNNCNNCNANTAANNCANNTCNANNNNANNNNAATTACTTNNANGTNNNTCACN 299
```

Blast comparison trimmed

“TNNNNNTNNCNNCNANTAANNCANNTCNANNNNANNNNAATTACTTNNANGTNNNTCACN”
from the 3' end of both sequences and reported 241 identities. The report has been manually corrected for this.

“TNNNNNTNNCNNCNANTAANNCANNTCNANNNNANNNNAATTACTTNNANGTNNNTCACN”
has been appended to both sequences and identity count has been increased to 299.

Sequence 1207 matched with Sequence 421

Query= Sequence ID - 1207 nt: 642
Length=642

SEQ ID NO: 421 nt: 642

ALIGNMENTS

Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query	1	ACGAGAAGCCAGATACTAAAGAGAAGAANCCCGAAGCCAAGAAGGTTGATGCTGGTGGCA	60
Sbjct	1	ACGAGAAGCCAGATACTAAAGAGAAGAANCCCGAAGCCAAGAAGGTTGATGCTGGTGGCA	60
Query	61	AGGTGAAAAAGGGTAACCTCAAAGCTAAAAAGCCCAAGAAGGGGAAGCCCCATTGCAGCC	120
Sbjct	61	AGGTGAAAAAGGGTAACCTCAAAGCTAAAAAGCCCAAGAAGGGGAAGCCCCATTGCAGCC	120
Query	121	GCAACCCTGTCCTTGTCTCAGAGGAATTGGCAGGTATTCCCGATCTGCCATGTATTCCANAA	180
Sbjct	121	GCAACCCTGTCCTTGTCTCAGAGGAATTGGCAGGTATTCCCGATCTGCCATGTATTCCANAA	180
Query	181	AGGCCATGTACAAGAGGAAGTACTCAGCCGCTAAATCCAAGGTTGAAAAAGAAAAAGAAGG	240
Sbjct	181	AGGCCATGTACAAGAGGAAGTACTCAGCCGCTAAATCCAAGGTTGAAAAAGAAAAAGAAGG	240
Query	241	AGAAGGTTCTCGCAACTGTTACAAAACCAAGTTGGTGGTGACAAGAACGGCGGTACCCGGG	300
Sbjct	241	AGAAGGTTCTCGCAACTGTTACAAAACCAAGTTGGTGGTGACAAGAACGGCGGTACCCGGG	300
Query	301	TGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAAAGCTGT	360
Sbjct	301	TGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAAAGCTGT	360
Query	361	TGAGCCACGGCAAAAAACCCCTTCAGTCAGCACGTGAGAAAAGTGGAGCCAGCATTACCC	420
Sbjct	361	TGAGCCACGGCAAAAAACCCCTTCAGTCAGCACGTGAGAAAAGTGGAGCCAGCATTACCC	420
Query	421	CCGGGACCATTCTGATCATCCTCACTGGACGCCACAGGGGCAAGAGGGTGGTTTTCTGA	480
Sbjct	421	CCGGGACCATTCTGATCATCCTCACTGGACGCCACAGGGGCAAGAGGGTGGTTTTCTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGCAGCTGGCTAGTGGCTTATTACTTGTGACTGGACCTCTGGTCCTCAATCGAGTTCCTC  540
          |||
Sbjct   481  AGCAGCTGGCTAGTGGCTTATTACTTGTGACTGGACCTCTGGTCCTCAATCGAGTTCCTC  540

Query  541  TACGAAGAACACACCAGAAATTTGTCATTGCCACTTCAACCAAAATCGATATCAGCAATG  600
          |||
Sbjct   541  TACGAAGAACACACCAGAAATTTGTCATTGCCACTTCAACCAAAATCGATATCAGCAATG  600

Query  601  TAAAAATCCCAAACATCTTACTGATGCTTACTTCAAAAAGA  642
          |||
Sbjct   601  TAAAAATCCCAAACATCTTACTGATGCTTACTTCAAAAAGA  642
```

Sequence 1208 matched with Sequence 422

Query= Sequence ID 1208
Length=503

SEQ ID NO: 422

ALIGNMENTS

Identities = 503/503 (100%), Gaps = 0/503 (0%)

Query	1	CCCTATACCTTCTGCATAATGAATTANCTAGAAATAACTTTGCAAGGGAGAGCCAAAGCT	60
Sbjct	1	CCCTATACCTTCTGCATAATGAATTANCTAGAAATAACTTTGCAAGGGAGAGCCAAAGCT	60
Query	61	AAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGT	120
Sbjct	61	AAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGT	120
Query	121	AGCAAAATAGTGGGAAGATTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAGC	180
Sbjct	121	AGCAAAATAGTGGGAAGATTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAGC	180
Query	181	TGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCCCTCTAAATC	240
Sbjct	181	TGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCCCTCTAAATC	240
Query	241	CCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAAC	300
Sbjct	241	CCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAAC	300
Query	301	CTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTAA	360
Sbjct	301	CTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTAA	360
Query	361	GAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCCT	420
Sbjct	361	GAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCCT	420
Query	421	CACACCCAATTGGACCAATCTATCACCCATAGAAGAATAATGTTAGTATAAGTAACAT	480
Sbjct	421	CACACCCAATTGGACCAATCTATCACCCATAGAAGAATAATGTTAGTATAAGTAACAT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GAAAACATTCTCCTCCGCATAAG	503
Sbjct	481	GAAAACATTCTCCTCCGCATAAG	503

Sequence 1209 matched with Sequence 423

Query= Sequence ID - 1209 nt: 620
Length=620

SEQ ID NO: 423 nt: 620

ALIGNMENTS

Identities = 620/620 (100%), Gaps = 0/620 (0%)

Query	1	CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG	60
Sbjct	1	CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG	60
Query	61	TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCGACGTCCACCGTGATCCACATCC	120
Sbjct	61	TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCGACGTCCACCGTGATCCACATCC	120
Query	121	GCAGCGAGACCTCCGTGCCCCGACCATGTGCTGCTGGTCCCTGTTCAACACCCTCTTCATGA	180
Sbjct	121	GCAGCGAGACCTCCGTGCCCCGACCATGTGCTGCTGGTCCCTGTTCAACACCCTCTTCATGA	180
Query	181	ACACCTGCTGCCTGGGCTTCATAGCATTGCGCTACTCCGTGAAGTCTAGGGACAGGAAGA	240
Sbjct	181	ACACCTGCTGCCTGGGCTTCATAGCATTGCGCTACTCCGTGAAGTCTAGGGACAGGAAGA	240
Query	241	TGGTTGGCGACGTGACCGGGGCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT	300
Sbjct	241	TGGTTGGCGACGTGACCGGGGCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT	300
Query	301	GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG	360
Sbjct	301	GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG	360
Query	361	TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCGTGACCTG	420
Sbjct	361	TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCGTGACCTG	420
Query	421	TATCCCACGTACTCTATCTTCCATTCCCTCGCCCTGCCCCAGAGGCCAGGAGCTCTGCCC	480
Sbjct	421	TATCCCACGTACTCTATCTTCCATTCCCTCGCCCTGCCCCAGAGGCCAGGAGCTCTGCCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTGACCTGTATTCCACTTACTCCACCTTCCATTCTCGCCCTGTCCCCACAGCCGAGTCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTGACCTGTATTCCACTTACTCCACCTTCCATTCTCGCCCTGTCCCCACAGCCGAGTCC  540

Query  541  TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT  600

Query  601  TTCTGGTGCTGCTGTGACTT  620
          ||||||||||||||||
Sbjct   601  TTCTGGTGCTGCTGTGACTT  620
```

Sequence 1210 matched with Sequence 424

Query= Sequence ID 1210
Length=702

SEQ ID NO: 424

ALIGNMENTS

Identities = 702/702 (100%), Gaps = 0/702 (0%)

Query	1	TTCGTAATTAGAATACTGTTTGGACTTGCTCAACAAGCACCTTATCTTAACAAAAAGTAA	60
Sbjct	1	TTCGTAATTAGAATACTGTTTGGACTTGCTCAACAAGCACCTTATCTTAACAAAAAGTAA	60
Query	61	CTTATAGAAAAGGGAGACATTCATTTAACTTCAAGCCCATATTATTCTTAAAAGCTGACT	120
Sbjct	61	CTTATAGAAAAGGGAGACATTCATTTAACTTCAAGCCCATATTATTCTTAAAAGCTGACT	120
Query	121	CTTGAAATAGTATTTATTGAGTCATAGTGGAGTCATGGGACTTTTTAAGGGCCGGAAGGG	180
Sbjct	121	CTTGAAATAGTATTTATTGAGTCATAGTGGAGTCATGGGACTTTTTAAGGGCCGGAAGGG	180
Query	181	ACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAGGAAACTGAGGCCTAGA	240
Sbjct	181	ACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAGGAAACTGAGGCCTAGA	240
Query	241	TAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAGTAGTCTATCCGTAAGAGACA	300
Sbjct	241	TAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAGTAGTCTATCCGTAAGAGACA	300
Query	301	ACATGGAGAAAGAAATACAACGTTTTTATAGTGAATTATCATCTTACAAAGAATATTCTT	360
Sbjct	301	ACATGGAGAAAGAAATACAACGTTTTTATAGTGAATTATCATCTTACAAAGAATATTCTT	360
Query	361	CCCATATCGCACTTTTAAAAAGTGGGTACCTTAGTCAAATAGGAGAAAAAACCACTTGAG	420
Sbjct	361	CCCATATCGCACTTTTAAAAAGTGGGTACCTTAGTCAAATAGGAGAAAAAACCACTTGAG	420
Query	421	TAGTTTCATCCTCAGGTTTTAGGTGAGGAAACTGATACTCAGATTAAATAACTTTAAGCA	480
Sbjct	421	TAGTTTCATCCTCAGGTTTTAGGTGAGGAAACTGATACTCAGATTAAATAACTTTAAGCA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CACAGAGCCTGAATGATAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CACAGAGCCTGAATGATAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTT  540

Query  541  AGGTGTTTTCACTTGCAATTCCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGGTGTTTTCACTTGCAATTCCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGT  600

Query  601  ACTACGTTAGGTGTTTTCACTTGCAATTCCTTGTTTGACGTTGACAATAAATCGTGAAGC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ACTACGTTAGGTGTTTTCACTTGCAATTCCTTGTTTGACGTTGACAATAAATCGTGAAGC  660

Query  661  TGCCTTATCTAAGGAAGTCCTAAAGTAAATCATTGGAACACA  702
          |||||||||||||||||||||||||||||||||||
Sbjct  661  TGCCTTATCTAAGGAAGTCCTAAAGTAAATCATTGGAACACA  702
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

Sequence 1211 matched with Sequence 425

Query= Sequence ID 1211
Length=632

SEQ ID NO: 425

ALIGNMENTS

Identities = 632/632 (100%), Gaps = 0/632 (0%)

Query	1	CCATTGTGTTGGNACCCGGAATTCGCGGCCGCGTCGACGGAGTTTACCTTATTACACT	60
Sbjct	1	CCATTGTGTTGGNACCCGGAATTCGCGGCCGCGTCGACGGAGTTTACCTTATTACACT	60
Query	61	TTAATCTCTGGATTTACCCCATCTCATTTCTCTTTTAGGAAAAGTGTGTATGTGGTGG	120
Sbjct	61	TTAATCTCTGGATTTACCCCATCTCATTTCTCTTTTAGGAAAAGTGTGTATGTGGTGG	120
Query	121	CTTTGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAACTAGAAATGAATG	180
Sbjct	121	CTTTGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAACTAGAAATGAATG	180
Query	181	GAAGATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAA	240
Sbjct	181	GAAGATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAA	240
Query	241	CACCATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAAGTCTA	300
Sbjct	241	CACCATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAAGTCTA	300
Query	301	TAACCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTAAACAAATTTA	360
Sbjct	301	TAACCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTAAACAAATTTA	360
Query	361	AGACCCTCTCAAACCTAACAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTG	420
Sbjct	361	AGACCCTCTCAAACCTAACAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTG	420
Query	421	AATAAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTG	480
Sbjct	421	AATAAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CATACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CATACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATG  540

Query  541  AAGGTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAAC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AAGGTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAAC  600

Query  601  CAAGAATTGATTGGGCACATCATTTCAGAAG  632
          |||||||||||||||||||||||||||
Sbjct   601  CAAGAATTGATTGGGCACATCATTTCAGAAG  632
```

Sequence 1212 matched with Sequence 426

Query= Sequence ID - 1212 nt: 374
Length=374

SEQ ID NO: 426 nt: 374

ALIGNMENTS

Identities = 374/374 (100%), Gaps = 0/374 (0%)

```
Query 1  AGAGCAGCAGCCATGGCCCTACGCTACCCTATGGCCGTGGGCCTCAACAAGGGCCACAAA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  AGAGCAGCAGCCATGGCCCTACGCTACCCTATGGCCGTGGGCCTCAACAAGGGCCACAAA 60

Query 61 GTGACCAAGAACGTGAGCAAGCCCAGGCACAGCCGACGCCGCGGGCGTCTGACCAAACAC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GTGACCAAGAACGTGAGCAAGCCCAGGCACAGCCGACGCCGCGGGCGTCTGACCAAACAC 120

Query 121 ACCAAGTTCGTGCGGGACATGATTCTGGGAGGTGTGTGGCTTTGCCCCGTACGAGCGGCGC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 ACCAAGTTCGTGCGGGACATGATTCTGGGAGGTGTGTGGCTTTGCCCCGTACGAGCGGCGC 180

Query 181 GCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCTCAAATTTATCAAGAAAAGG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 GCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCTCAAATTTATCAAGAAAAGG 240

Query 241 GTGGGGACGCACATCCGCGCCAAGAGGAAGCGGGAGGAGCTGAGCAACGTACTGGCCGCC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 GTGGGGACGCACATCCGCGCCAAGAGGAAGCGGGAGGAGCTGAGCAACGTACTGGCCGCC 300

Query 301 ATGAGGAAAGCTGCTGCCAAGAAAGACTGAGCCCCTCCCCTGCCCTCTCCCTGAAATAAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATGAGGAAAGCTGCTGCCAAGAAAGACTGAGCCCCTCCCCTGCCCTCTCCCTGAAATAAA 360

Query 361 GAACAGCTTGACAG 374
          ||||||||||||
Sbjct 361 GAACAGCTTGACAG 374
```

Sequence 1213 matched with Sequence 427

Query= Sequence ID - 1213 nt: 567
Length=567

SEQ ID NO: 427 nt: 567

ALIGNMENTS

Identities = 567/567 (100%), Gaps = 0/567 (0%)

Query	1	GAATTATTGACTTTGAATTGCATTTTCAGTACCATGAAGTCAAAGTCAGTGGTGTATTTGC	60
Sbjct	1	GAATTATTGACTTTGAATTGCATTTTCAGTACCATGAAGTCAAAGTCAGTGGTGTATTTGC	60
Query	61	TCATTTGTTTCATTCTTTCTTTTCCACCAACATTACTGCCTGCAGAGCCAGAGGTGAGTGC	120
Sbjct	61	TCATTTGTTTCATTCTTTCTTTTCCACCAACATTACTGCCTGCAGAGCCAGAGGTGAGTGC	120
Query	121	AGAAATCCTGTCAATTCGTCACTTGTGGACAACCTGCAGCTTGCCACAGCCTACAGTTCC	180
Sbjct	121	AGAAATCCTGTCAATTCGTCACTTGTGGACAACCTGCAGCTTGCCACAGCCTACAGTTCC	180
Query	181	ACCACTGTGACCTCTGAAAACCTCCTGAACAAAAGGAAGGAGACTTGAAAATCCTGAATG	240
Sbjct	181	ACCACTGTGACCTCTGAAAACCTCCTGAACAAAAGGAAGGAGACTTGAAAATCCTGAATG	240
Query	241	GGCTTGGAGACATTAAGGGAGAACTGCCTCCCTGGACCAAGGCAGAATTCAATAGAACCA	300
Sbjct	241	GGCTTGGAGACATTAAGGGAGAACTGCCTCCCTGGACCAAGGCAGAATTCAATAGAACCA	300
Query	301	GCAAGAAATTTTCCTATGAATGGGAAAGCAGGTGGCAGGGGGCAGGGGTGAAAAGCTTT	360
Sbjct	301	GCAAGAAATTTTCCTATGAATGGGAAAGCAGGTGGCAGGGGGCAGGGGTGAAAAGCTTT	360
Query	361	GTACAGGAATTGTGAAAAGCTTTTGCATTATCTCTAGTCTGAAAGTCACATTTCTCAGT	420
Sbjct	361	GTACAGGAATTGTGAAAAGCTTTTGCATTATCTCTAGTCTGAAAGTCACATTTCTCAGT	420
Query	421	TCCTTTCCACTCTCTTCTGTCAACTTGCTGTGAGTAAATGACATCTGTCACCTGTGACAC	480
Sbjct	421	TCCTTTCCACTCTCTTCTGTCAACTTGCTGTGAGTAAATGACATCTGTCACCTGTGACAC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGCCAGGGACTATCACCATATGGCCCCCACACATTATCTAGTACCAGCCTGCCTGGGCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGGCCAGGGACTATCACCATATGGCCCCCACACATTATCTAGTACCAGCCTGCCTGGGCC  540

Query  541  ATGCCTTTTCCAGTCACTGTACCAGCC  567
          ||||||||||||||||||||
Sbjct   541  ATGCCTTTTCCAGTCACTGTACCAGCC  567
```

Sequence 1214 matched with Sequence 428

Query= Sequence ID - 1214 nt: 620
Length=620

SEQ ID NO: 428 nt: 620

ALIGNMENTS

Identities = 620/620 (100%), Gaps = 0/620 (0%)

Query	1	CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG	60
Sbjct	1	CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG	60
Query	61	TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCGACGTCCACCGTGATCCACATCC	120
Sbjct	61	TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCGACGTCCACCGTGATCCACATCC	120
Query	121	GCAGCGAGACCTCCGTGCCCCGACCATGTGCTGCTGGTCCCTGTTCAACACCCTCTTCATGA	180
Sbjct	121	GCAGCGAGACCTCCGTGCCCCGACCATGTGCTGCTGGTCCCTGTTCAACACCCTCTTCATGA	180
Query	181	ACACCTGCTGCCTGGGCTTCATAGCATTGCGCTACTCCGTGAAGTCTAGGGACAGGAAGA	240
Sbjct	181	ACACCTGCTGCCTGGGCTTCATAGCATTGCGCTACTCCGTGAAGTCTAGGGACAGGAAGA	240
Query	241	TGGTTGGCGACGTGACCGGGGCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT	300
Sbjct	241	TGGTTGGCGACGTGACCGGGGCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT	300
Query	301	GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG	360
Sbjct	301	GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG	360
Query	361	TCCAGGCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCGTGACCTG	420
Sbjct	361	TCCAGGCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCGTGACCTG	420
Query	421	TATCCCACGTACTCTATCTTCCATTCCCTCGCCCTGCCCCAGAGGCCAGGAGCTCTGCCC	480
Sbjct	421	TATCCCACGTACTCTATCTTCCATTCCCTCGCCCTGCCCCAGAGGCCAGGAGCTCTGCCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTGACCTGTATTCCACTTACTCCACCTTCCATTCTCGCCCTGTCCCCACAGCCGAGTCC  540
          |||
Sbjct  481  TTGACCTGTATTCCACTTACTCCACCTTCCATTCTCGCCCTGTCCCCACAGCCGAGTCC  540

Query  541  TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT  600
          |||
Sbjct  541  TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT  600

Query  601  TTCTGGTGCTGCTGTGACTT  620
          |||
Sbjct  601  TTCTGGTGCTGCTGTGACTT  620
```

Sequence 1215 matched with Sequence 429

Query= Sequence ID 1215
Length=669

SEQ ID NO: 429

ALIGNMENTS

Identities = 669/669 (100%), Gaps = 0/669 (0%)

Query	1	CACAAGATAGAATGGTaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaTTTTAAGTGA	60
Sbjct	1	CACAAGATAGAATGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTTAAGTGA	60
Query	61	CAGTGCCATAGTTTGGACAGTACCTTTCAATGATTAATTTTAATAGCCTGTGAGTCCAAG	120
Sbjct	61	CAGTGCCATAGTTTGGACAGTACCTTTCAATGATTAATTTTAATAGCCTGTGAGTCCAAG	120
Query	121	TAAATGATCACTTTATTTGCTAGGGAGGGAAGTCCTAGGGTGGTTTCAGTTTCTCCCAGA	180
Sbjct	121	TAAATGATCACTTTATTTGCTAGGGAGGGAAGTCCTAGGGTGGTTTCAGTTTCTCCCAGA	180
Query	181	CATACCTAAATTTTTACATCAATCCTTTTAAAGAAAATCTGTATTTCAAAGAATCTTTCT	240
Sbjct	181	CATACCTAAATTTTTACATCAATCCTTTTAAAGAAAATCTGTATTTCAAAGAATCTTTCT	240
Query	241	CTGCAGTAAATCTCGCAGGGGAATTTGCACTATTACACTTGAAAGTTGTTATTGTTAACC	300
Sbjct	241	CTGCAGTAAATCTCGCAGGGGAATTTGCACTATTACACTTGAAAGTTGTTATTGTTAACC	300
Query	301	TTTTCGGCAGCTTTTAATAGGAAAGTTAAACGTTTTAAACATGGTAGTACTGGAAATTTT	360
Sbjct	301	TTTTCGGCAGCTTTTAATAGGAAAGTTAAACGTTTTAAACATGGTAGTACTGGAAATTTT	360
Query	361	ACAAGACTTTTACCTAGCACTTAAATATGTATAAATGTACATAAAGACAAACTAGTAAGC	420
Sbjct	361	ACAAGACTTTTACCTAGCACTTAAATATGTATAAATGTACATAAAGACAAACTAGTAAGC	420
Query	421	ATGACCTGGGGAAATGGTCAGACCTTGTATTGTGTTTTTGGCCTTGAAAGTAGCAAGTGA	480
Sbjct	421	ATGACCTGGGGAAATGGTCAGACCTTGTATTGTGTTTTTGGCCTTGAAAGTAGCAAGTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CCAGAATCTGCCATGGCAACAGGCTTTAAAAAAGACCCTTAAAAAGACACTGTCTCAACT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CCAGAATCTGCCATGGCAACAGGCTTTAAAAAAGACCCTTAAAAAGACACTGTCTCAACT  540

Query  541  GTGGTGTTAGCACCAGCCAGCTCTCTGTACATTTGCTAGCTTGTAGTTTCTAAGACTGA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GTGGTGTTAGCACCAGCCAGCTCTCTGTACATTTGCTAGCTTGTAGTTTCTAAGACTGA  600

Query  601  GTAAACTTCTTATTTTTAGAAAAGTGGAGGTCTGGTTTGTAAC TTCCTTGACTTAATTG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GTAAACTTCTTATTTTTAGAAAAGTGGAGGTCTGGTTTGTAAC TTCCTTGACTTAATTG  660

Query  661  GGTAAAAGT  669
          ||||||||
Sbjct   661  GGTAAAAGT  669
```

Sequence 1216 matched with Sequence 430

Query= Sequence ID - 1216 nt: 484
Length=484

SEQ ID NO: 430 nt: 484

ALIGNMENTS

Identities = 484/484 (100%), Gaps = 0/484 (0%)

Query	1	CAACCTTAGCCAAACCATTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGGCG	60
Sbjct	1	CAACCTTAGCCAAACCATTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGGCG	60
Query	61	CAATAGATATAGTACCGCAAGGAAAGATGAAAAATTATAACCAAGCATAATATAGCAAG	120
Sbjct	61	CAATAGATATAGTACCGCAAGGAAAGATGAAAAATTATAACCAAGCATAATATAGCAAG	120
Query	121	GACTAACCCCTATACCTTCTGCATAATGAATTAAGTAACTAGAAATAACTTTGCAAGGAGAGCC	180
Sbjct	121	GACTAACCCCTATACCTTCTGCATAATGAATTAAGTAACTAGAAATAACTTTGCAAGGAGAGCC	180
Query	181	AAAGCTAAGACCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGT	240
Sbjct	181	AAAGCTAAGACCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGT	240
Query	241	CTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGT	300
Sbjct	241	CTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGT	300
Query	301	GATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCCCTC	360
Sbjct	301	GATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAACCCCTC	360
Query	361	TAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGA	420
Sbjct	361	TAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGA	420
Query	421	AAAAACCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACC	480
Sbjct	421	AAAAACCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACC	480

PATENT SEQUENCE ALIGNMENT

Query	481	AATT	484
Sbjct	481	AATT	484

Sequence 1217 matched with Sequence 431

Query= Sequence ID 1217
Length=576

SEQ ID NO: 431

ALIGNMENTS

Identities = 576/576 (100%), Gaps = 0/576 (0%)

Query	1	GACAGGCGGGGGCCCAGCGCCGGGTGAAGGCCGGGTGGCTCTGTGAATCAAAGGAGAGT	60
Sbjct	1	GACAGGCGGGGGCCCAGCGCCGGGTGAAGGCCGGGTGGCTCTGTGAATCAAAGGAGAGT	60
Query	61	CCCAGAAAACCTGTGACTGTTGAAGAAAATTCATCTGTGAATTTTTATATTCAAGGAGTC	120
Sbjct	61	CCCAGAAAACCTGTGACTGTTGAAGAAAATTCATCTGTGAATTTTTATATTCAAGGAGTC	120
Query	121	AGTATTTATATTCATCTTTTAAACTGGGAAGATTTATATTTTACTTTAAAACTTCTTGAT	180
Sbjct	121	AGTATTTATATTCATCTTTTAAACTGGGAAGATTTATATTTTACTTTAAAACTTCTTGAT	180
Query	181	AATAATTTACAATGAATGGACACAGTGATGAAGAAAGTGTTAGAAACAGTAGTGGAAGAT	240
Sbjct	181	AATAATTTACAATGAATGGACACAGTGATGAAGAAAGTGTTAGAAACAGTAGTGGAAGAT	240
Query	241	CAAGGTAAGTAAGCACTTTGTTATCAATTGTTTACTATGAAGAGAGTTGAAAACTTGACT	300
Sbjct	241	CAAGGTAAGTAAGCACTTTGTTATCAATTGTTTACTATGAAGAGAGTTGAAAACTTGACT	300
Query	301	TTTTCTTTATTGTTATTGTTGTTATTTAGTTTTCTCATAGGTAGCAGAGTTTTTCAGGT	360
Sbjct	301	TTTTCTTTATTGTTATTGTTGTTATTTAGTTTTCTCATAGGTAGCAGAGTTTTTCAGGT	360
Query	361	TTTCCTCTTAGCTATCCAAATACTaaaaaaTTCTGATATACGAACCTTTTTTCATAATA	420
Sbjct	361	TTTCCTCTTAGCTATCCAAATACTAAAAAATTCTGATATACGAACCTTTTTTCATAATA	420
Query	421	CAGGTTTTAATTATATTTTTCATTCAGATACACAGTAGATCTTAAATATAGAAAGTTTTT	480
Sbjct	421	CAGGTTTTAATTATATTTTTCATTCAGATACACAGTAGATCTTAAATATAGAAAGTTTTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTTACTTAAATCTATTTGGAAGTTTATATTTGAGCTAATAATTAAGCTGGAGCATGTAT  540
          |||
Sbjct  481  GTTACTTAAATCTATTTGGAAGTTTATATTTGAGCTAATAATTAAGCTGGAGCATGTAT  540

Query  541  AATAGATTTAAATTGTTTGGACTGTTAGTGAAATTT  576
          |||
Sbjct  541  AATAGATTTAAATTGTTTGGACTGTTAGTGAAATTT  576
```

Sequence 1218 matched with Sequence 432

Query= Sequence ID 1218
Length=669

SEQ ID NO: 432

ALIGNMENTS

Identities = 669/669 (100%), Gaps = 0/669 (0%)

Query	1	CTCACTTGGTGGGTGAGCCTCCAATGACTACACCCAAGGAGGATTTAACACAGGGATTTT	60
Sbjct	1	CTCACTTGGTGGGTGAGCCTCCAATGACTACACCCAAGGAGGATTTAACACAGGGATTTT	60
Query	61	ATGACTTGCAACAAGTCAGGAGGACATGGGGTTGGGGTAGTTCAGCAGTGCCTGTCTGAA	120
Sbjct	61	ATGACTTGCAACAAGTCAGGAGGACATGGGGTTGGGGTAGTTCAGCAGTGCCTGTCTGAA	120
Query	121	CAAAGGTGAAAATTGGGCTTTTATTGGGCTGATCAAGGGGGAGTAAAGGCAGCCAGGAGC	180
Sbjct	121	CAAAGGTGAAAATTGGGCTTTTATTGGGCTGATCAAGGGGGAGTAAAGGCAGCCAGGAGC	180
Query	181	AGTCGCCTGTCATGCTTCTACCTATATTGCATGTATAGAAAAGGGAAAAATAAACTCCTTC	240
Sbjct	181	AGTCGCCTGTCATGCTTCTACCTATATTGCATGTATAGAAAAGGGAAAAATAAACTCCTTC	240
Query	241	CTGGGCAGGGTTTTAGTATGCTAAGGAGGGGAGTTATTCAACTTCAATCCAACCTCAAGCA	300
Sbjct	241	CTGGGCAGGGTTTTAGTATGCTAAGGAGGGGAGTTATTCAACTTCAATCCAACCTCAAGCA	300
Query	301	TCAGCATTGCTGCGTCCATCCCAGTTTTGTTTTGCTGGGGCTGAACTTCTTCCTATAACT	360
Sbjct	301	TCAGCATTGCTGCGTCCATCCCAGTTTTGTTTTGCTGGGGCTGAACTTCTTCCTATAACT	360
Query	361	TTTTGAAACAACAAGAACTCAAGGTGTGACAGTTACAAGTGGGCCCTTTTTCACAGTGTG	420
Sbjct	361	TTTTGAAACAACAAGAACTCAAGGTGTGACAGTTACAAGTGGGCCCTTTTTCACAGTGTG	420
Query	421	TACCTAAACACGTGAGGACCCTGGATTACAGAATGACAGACTCGAAGTGACTCAAGTTCC	480
Sbjct	421	TACCTAAACACGTGAGGACCCTGGATTACAGAATGACAGACTCGAAGTGACTCAAGTTCC	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGTTGTTTCATCTTTAGATGGTAAAGATGGCTGTACGTACTATCCTTGCTTATTTCCAATC	540
Sbjct	481	GGTTGTTTCATCTTTAGATGGTAAAGATGGCTGTACGTACTATCCTTGCTTATTTCCAATC	540
Query	541	TATTGTTTAAACTCTTGTATATGTAATACCGCAGAGGCTAGAGATACAACCTTTGACCAA	600
Sbjct	541	TATTGTTTAAACTCTTGTATATGTAATACCGCAGAGGCTAGAGATACAACCTTTGACCAA	600
Query	601	ATGAGTGAATTCAAGTAATCCATTACTAATGTGATCTGGAAACAAACATGGTGTGAATG	660
Sbjct	601	ATGAGTGAATTCAAGTAATCCATTACTAATGTGATCTGGAAACAAACATGGTGTGAATG	660
Query	661	TGCATATGT	669
Sbjct	661	TGCATATGT	669

Sequence 1219 matched with Sequence 433

Query= Sequence ID - 1219 nt: 559
Length=559

SEQ ID NO: 433 nt: 559

ALIGNMENTS

Identities = 559/559 (100%), Gaps = 0/559 (0%)

Query	1	CTTGGCAGCTCCGTTATGTGCCCAGCTCTTTGCAAGGGCATACTGGGAAATGAGTGGAGA	60
Sbjct	1	CTTGGCAGCTCCGTTATGTGCCCAGCTCTTTGCAAGGGCATACTGGGAAATGAGTGGAGA	60
Query	61	TAAAGGACCCAATCATAAGCATTTTACAGTATGGATACCCATTTTAAAAAGGTAAACTG	120
Sbjct	61	TAAAGGACCCAATCATAAGCATTTTACAGTATGGATACCCATTTTAAAAAGGTAAACTG	120
Query	121	AGGCACAATGCAAttttttttttttttAAGGAGTTTATTTGAGCAAACAGTGATTCATG	180
Sbjct	121	AGGCACAATGCAATTTTTTTTTTTTAAAGGAGTTTATTTGAGCAAACAGTGATTCATG	180
Query	181	AATCAGGCAGCACCAAACCAGAAGGAGGCTTTGCTGAANAAGGATGAGGGACAAGCATTT	240
Sbjct	181	AATCAGGCAGCACCAAACCAGAAGGAGGCTTTGCTGAANAAGGATGAGGGACAAGCATTT	240
Query	241	ATAAAGTGAATGTAGATGTAATACAAAGAAAATATTTGAACCGGGTGCGGTGGCTTACAC	300
Sbjct	241	ATAAAGTGAATGTAGATGTAATACAAAGAAAATATTTGAACCGGGTGCGGTGGCTTACAC	300
Query	301	TTGTAATCCCAACACTTTGGGAGGCCAAGGCGGGCAGATCACAAGATCAAGAGATCGAGA	360
Sbjct	301	TTGTAATCCCAACACTTTGGGAGGCCAAGGCGGGCAGATCACAAGATCAAGAGATCGAGA	360
Query	361	CCATCCTGGTCAACATGGTGAAACCCCATCTNTACTAAAAAATACAAAAATTANCTGGGC	420
Sbjct	361	CCATCCTGGTCAACATGGTGAAACCCCATCTNTACTAAAAAATACAAAAATTANCTGGGC	420
Query	421	GTGGTGGTGCGTGCCTGTAGTCCCAGCTACTTGGGCGGCTGAGGCAGGANAATTGCTTGA	480
Sbjct	421	GTGGTGGTGCGTGCCTGTAGTCCCAGCTACTTGGGCGGCTGAGGCAGGANAATTGCTTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ACCCGGGAGGTGGAGGTTGCAGTAAGCCGAGATTGCACCATTGCACTACTCCAGCCTGGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ACCCGGGAGGTGGAGGTTGCAGTAAGCCGAGATTGCACCATTGCACTACTCCAGCCTGGT  540

Query  541  GACAGAGAGAGACTCCATC  559
          ||||||||||||||
Sbjct   541  GACAGAGAGAGACTCCATC  559
```

Length=1354

Query	1	GANNNGTGCGATANNATGNNTGTCTtttttttttAAAGTNTTTCNNATNGNAGNGAANCCCCCNAN	65
Sbjct	1	GANNNGTGCGATANNATGNNTGTCTTTTTTTTTAAAGTNTTTCNNATNGNAGNGAANCCCCCNAN	65
Query	66	NTNNCATAANGAGAGATNACTACNGTACANATAGNGNCANACNGATAGTAGTANCAANAT	125
Sbjct	66	NTNNCATAANGAGAGATNACTACNGTACANATAGNGNCANACNGATAGTAGTANCAANAT	125
Query	126	TGTNTTAGCTANATNANTCAATAGATATCNAGATanaaanaanCNNGGATATACAGCGA	185
Sbjct	126	TGTNTTAGCTANATNANTCAATAGATATCNAGATANAANAANANCNNGGATATACAGCGA	185
Query	186	TGTNTNANNGGnnnnnnnnanGGAACGAACATCNACNTTAANNATAAGCTNGNGGAGAGAG	245
Sbjct	186	TGTNTNANNGGNNNNNNANGGAACGAACATCNACNTTAANNATAAGCTNGNGGAGAGAG	245
Query	246	ACANGTANGTTATANANNAGAATNGNAGTAGGNGTGATCATAATAGnnnnnnannTANTAT	305
Sbjct	246	ACANGTANGTTATANANNAGAATNGNAGTAGGNGTGATCATAATAGNNNNNNANNTANTAT	305
Query	306	ATANGATNTTANTGNNCTNTNNTNNGTTTATCNNNAATNTCTATNCTNGAGAGNAGCNNN	365
Sbjct	306	ATANGATNTTANTGNNCTNTNNTNNGTTTATCNNNAATNTCTATNCTNGAGAGNAGCNNN	365
Query	366	ATNNNNAGGCGANGANATTGGGNNTNCTCNTNATAGANANCTGGTGTCnnanaantacn	425
Sbjct	366	ATNNNNAGGCGANGANATTGGGNNTNCTCNTNATAGANANCTGGTGTCNNANAANTACN	425
Query	426	tcatctattnanctctcacnanatggnannatanagnagnnnntnnanaggantangca	485
Sbjct	426	TCATCTATTNANCTCTCACNANATGGNANNATANAGNAGNGNNNTNNANAGGANTANGCA	485
Query	486	tagngnntnctnaaacaaaannnataaganntctcgnaananGGGCCTNTNNTNTAGC	545
Sbjct	486	TAGNGNNTNCTNAAACAAAANNNATAAGANNTCTCGNNAANANGGGCCTNTNNTNTAGC	545
Query	546	GAGGNNTTANTTTNTATANTTTTCNCTCTtnnaatanntangatanatganctngnngt	605

PATENT SEQUENCE ALIGNMENT

Sbjct	546	 GAGGNNTTANTTTNTATANTTNTTCNCTCTTNNAATANNTANGATANATGANCTNGNNGT	605
Query	606	gatanatannnnntacngtnaanntntantcntataatagatanaaatataggatntTNC	665
Sbjct	606	 GATANATANNNNTACNGTNAANNTNTANTCNTATAATAGATANAAATATAGGATNTTNC	665
Query	666	TCTGGCNGGTNGAANANTTNNTNCNNTTTNAATAATGNTGTTAGNGACNGNGNTNTnana	725
Sbjct	666	 TCTGGCNGGTNGAANANTTNNTNCNNTTTNAATAATGNTGTTAGNGACNGNGNTNTNANA	725
Query	726	nnnnnTTAGAAAGGTACTCTATATACTNNTATGNTNCGGCNNATAATANAAACAGATGTTT	785
Sbjct	726	 NNNNNTTAGAAAGGTACTCTATATACTNNTATGNTNCGGCNNATAATANAAACAGATGTTT	785
Query	786	GTATNAATATnaaanaaGGTCNNTTTCGNCAAGAGAANNNTGNCTGGTNATAGAATTAGC	845
Sbjct	786	 GTATNAATATNAAANAAGGTTCNNTTTCGNCAAGAGAANNNTGNCTGGTNATAGAATTAGC	845
Query	846	ATAANTTANNTANTATGATNNANTNNTNCTACNANTNTTAGCNNTTNGCAGNAGTCATTN	905
Sbjct	846	 ATAANTTANNTANTATGATNNANTNNTNCTACNANTNTTAGCNNTTNGCAGNAGTCATTN	905
Query	906	NGNATNTATNNNGNNTANTAGTNANTTGGGNCTNNTNCagantatatnttngnaanatga	965
Sbjct	906	 NGNATNTATNNNGNNTANTAGTNANTTGGGNCTNNTNCAGANTATATTNTGNGAANATGA	965
Query	966	anntacgnantcctnngnantatnatnntgantangananaancnananntntntannant	1025
Sbjct	966	 ANNTACGNANTCCTNNGNANTATNATNNTGANTANGANAANCNANANNTNTTNTANNANT	1025
Query	1026	gnctatanattgccnngatanattntnnnaatgaanCGATAGCCCGCNCTAAGGanntnn	1085
Sbjct	1026	 GNCTATANATTGCCNNGATANATTNTNNNAATGAANCGATAGCCCGCNCTAAGGANNTNN	1085
Query	1086	gtnanntaaanntctcagataanntacntnttnnttattaancnannatcacantatanC	1145
Sbjct	1086	 GTNANNTAAANNTCTCAGATAANNTACNTNTTNTTATTAANCNANNATCACANTATANC	1145
Query	1146	NGNGACANNNGCGANANTATATGTATGNNANTATNACNGNTCCNNNCCGNGAANNTANTC	1205
Sbjct	1146	 NGNGACANNNGCGANANTATATGTATGNNANTATNACNGNTCCNNNCCGNGAANNTANTC	1205

PATENT SEQUENCE ALIGNMENT

```
Query  1206  NTANNAGGCATTTCNGNNGAGCTNTTCTNCTAGACNATTTnnantgaaannatgcngnnaa  1265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1206  NTANNAGGCATTTCNGNNGAGCTNTTCTNCTAGACNATTTNNANTGAAANNATGCNGNNAA  1265

Query  1266  aaaCGACNNNCTTNAANTTNTGTCTACANTCCGCNNTNTTTNTACAGATNGCAGNTAAGN  1325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1266  AAACGACNNNCTTNAANTTNTGTCTACANTCCGCNNTNTTTNTACAGATNGCAGNTAAGN  1325

Query  1326  NNANTNANNGCTCTCANCTNGCTNNNACT  1354
          ||||||||||||||||||||||||
Sbjct   1326  NNANTNANNGCTCTCANCTNGCTNNNACT  1354
```

Blast comparison trimmed “GANNN” from the 5’ end of both sequences and trimmed “NNNACT” from the 3’ end of both sequences and reported 1343 identities. The report has been manually corrected for this. “GANNN” has been prepended to the 5’ end of both sequences and “NNNACT” has appended to the 3’ end of both sequences and identity count has been increased to 1354.

Sequence 1221 matched with Sequence 435

Query= Sequence ID - 1221 nt: 741
Length=741

SEQ ID NO: 435 nt: 741

ALIGNMENTS

Identities = 741/741 (100%), Gaps = 0/741 (0%)

Query	1	AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGAGCCA	60
Sbjct	1	AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGAGCCA	60
Query	61	CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCCTGG	120
Sbjct	61	CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCCTGG	120
Query	121	TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC	180
Sbjct	121	TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC	180
Query	181	CATTATTTTCTTTAATGTAGAAATGATTAATACATATTCTACAAGGGGCAGTAAGGTAGT	240
Sbjct	181	CATTATTTTCTTTAATGTAGAAATGATTAATACATATTCTACAAGGGGCAGTAAGGTAGT	240
Query	241	AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACCTTG	300
Sbjct	241	AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACCTTG	300
Query	301	TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT	360
Sbjct	301	TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT	360
Query	361	ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGGAAAGACTGTAAATCAC	420
Sbjct	361	ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGGAAAGACTGTAAATCAC	420
Query	421	TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA	480
Sbjct	421	TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA  540

Query  541  AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT  600

Query  601  GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC  660

Query  661  CTAATTTGAGATCACCTAAACACTGGAAAAAGaaaaaaaTGAAAGGGCAGTATGTCCATA  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  CTAATTTGAGATCACCTAAACACTGGAAAAAGAAAAAAAATGAAAGGGCAGTATGTCCATA  720

Query  721  AACCAACAAATAATTTGGCTG  741
          |||||||||||||||
Sbjct   721  AACCAACAAATAATTTGGCTG  741
```

Sequence 1224 matched with Sequence 436

Query= Sequence ID - 1224 nt: 485
Length=485

SEQ ID NO: 436 nt: 485

ALIGNMENTS

Identities = 485/485 (100%), Gaps = 0/485 (0%)

Query	1	CGAAATTTCTTGTGACACAGAGGAAGGGCAAAGGTCTGAGCCCAGAGTTGACGGAGGGA	60
Sbjct	1	CGAAATTTCTTGTGACACAGAGGAAGGGCAAAGGTCTGAGCCCAGAGTTGACGGAGGGA	60
Query	61	GTATTTTCAGGGTTCACCTCAGGGGCTCCCAAAGCGACAAGATCGTTAGGGAGAGAGGCCC	120
Sbjct	61	GTATTTTCAGGGTTCACCTCAGGGGCTCCCAAAGCGACAAGATCGTTAGGGAGAGAGGCCC	120
Query	121	AGGGTGGGGACTGGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGGTTCAAGGAACTT	180
Sbjct	121	AGGGTGGGGACTGGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGGTTCAAGGAACTT	180
Query	181	CTGTGCAAGCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGCCCCCGCGCTAGCTGT	240
Sbjct	181	CTGTGCAAGCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGCCCCCGCGCTAGCTGT	240
Query	241	GAGCTGAGCAAAGCCCTGGGCTCACAGCACCCCAAAGCCTGTGGCTTCAGTCCTGCGTC	300
Sbjct	241	GAGCTGAGCAAAGCCCTGGGCTCACAGCACCCCAAAGCCTGTGGCTTCAGTCCTGCGTC	300
Query	301	TGACCACACAATCAAAAGGATCGTTTTGTTTTGTTTTTAAAGAAAGGTGAGATTGGCTT	360
Sbjct	301	TGACCACACAATCAAAAGGATCGTTTTGTTTTGTTTTTAAAGAAAGGTGAGATTGGCTT	360
Query	361	GGTTCTTCATGAGCACATTTGATATAGCTCTTTTTCTGTTTTTCCTTGCTCATTTTCGTTT	420
Sbjct	361	GGTTCTTCATGAGCACATTTGATATAGCTCTTTTTCTGTTTTTCCTTGCTCATTTTCGTTT	420
Query	421	TGGGGAAGAAATCTGTACTGTATTGGGATTGTAAAGAACATCTCTGCACTCAGACAGTTT	480
Sbjct	421	TGGGGAAGAAATCTGTACTGTATTGGGATTGTAAAGAACATCTCTGCACTCAGACAGTTT	480

PATENT SEQUENCE ALIGNMENT

Query	481	ACAGA	485
Sbjct	481	ACAGA	485

Sequence 1226 matched with Sequence 437

Query= Sequence ID 1226
Length=637

SEQ ID NO: 437

ALIGNMENTS

Identities = 637/637 (100%), Gaps = 0/637 (0%)

Query	1	GGTTTTTATACTTGCCATGAAACTGTTCTTTGGGATATTATTTTGTTCAGGTTCCCCACT	60
Sbjct	1	GGTTTTTATACTTGCCATGAAACTGTTCTTTGGGATATTATTTTGTTCAGGTTCCCCACT	60
Query	61	TGGACAGCAGAGGGGGTGACTCTGCCCATCCCTGCCACTGGTAGCCAGGCGGGCAATGTC	120
Sbjct	61	TGGACAGCAGAGGGGGTGACTCTGCCCATCCCTGCCACTGGTAGCCAGGCGGGCAATGTC	120
Query	121	TGCTAGCAGTCTGCTTCTGTCTGAACTCAGCCAGCAGAGGCAAACCTCCCGTTCCCCGAG	180
Sbjct	121	TGCTAGCAGTCTGCTTCTGTCTGAACTCAGCCAGCAGAGGCAAACCTCCCGTTCCCCGAG	180
Query	181	AAACACTCTGAAGGCAGGGTGGGTGACTCCACCCACCACCGCCTCTCCTAGCCATGCAGG	240
Sbjct	181	AAACACTCTGAAGGCAGGGTGGGTGACTCCACCCACCACCGCCTCTCCTAGCCATGCAGG	240
Query	241	CCATGTCTGCTAGAGCTTCCAGCGCAGTGGTCCTAATTCTGTCTGAATCCGGCTGAGGGG	300
Sbjct	241	CCATGTCTGCTAGAGCTTCCAGCGCAGTGGTCCTAATTCTGTCTGAATCCGGCTGAGGGG	300
Query	301	TGCAGCCTCCTGTTACTGCCCAGGGAAACACCCAGATGGCAGGGTGGGTGACTCCAACCA	360
Sbjct	301	TGCAGCCTCCTGTTACTGCCCAGGGAAACACCCAGATGGCAGGGTGGGTGACTCCAACCA	360
Query	361	CCTCTGCCTGTGGTAGCCAGATGGGCCACACCTGCTAGAGCTTCCAGCCCAGCAGTCCCG	420
Sbjct	361	CCTCTGCCTGTGGTAGCCAGATGGGCCACACCTGCTAGAGCTTCCAGCCCAGCAGTCCCG	420
Query	421	CTACTCTGTGGGTGGGTGCCATCCCCTGTTCTCTGGGAAGCACCCAGACAGCTGATTAC	480
Sbjct	421	CTACTCTGTGGGTGGGTGCCATCCCCTGTTCTCTGGGAAGCACCCAGACAGCTGATTAC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTGACCCACCCACTTCTGCAGATCCTAGCTGAGCAGGACTTGCTGGTTTGGACAATGCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTGACCCACCCACTTCTGCAGATCCTAGCTGAGCAGGACTTGCTGGTTTGGACAATGCC  540

Query  541  CAAGCAGGGAAGAGCCCTCATTCTTTATCACTGACAGAGGTGAGATGTCCGANTTTGTA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CAAGCAGGGAAGAGCCCTCATTCTTTATCACTGACAGAGGTGAGATGTCCGANTTTGTA  600

Query  601  NGCTGGTGGAGGAGTGAGGTGGAGGAGGTATGCCTCT  637
          ||||||||||||||||||||||||||||
Sbjct   601  NGCTGGTGGAGGAGTGAGGTGGAGGAGGTATGCCTCT  637
```

Sequence 1228 matched with Sequence 438

Query= Sequence ID 1228
Length=420

SEQ ID NO: 438

ALIGNMENTS

Identities = 420/420 (100%), Gaps = 0/420 (0%)

Query	1	GTTATTTCAGGTATCCATCAAAATTTTATAAGAGGGCCGAAACATCGGCTCACACCTGTA	60
Sbjct	1	GTTATTTCAGGTATCCATCAAAATTTTATAAGAGGGCCGAAACATCGGCTCACACCTGTA	60
Query	61	ATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGTTCACTTGAGGTCAGGAGTTCGAGACCA	120
Sbjct	61	ATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGTTCACTTGAGGTCAGGAGTTCGAGACCA	120
Query	121	GCCTGGCCAACATGGCAAAACCCCGTCACTATTAATAACAAAACATTAGCTGGGTGTA	180
Sbjct	121	GCCTGGCCAACATGGCAAAACCCCGTCACTATTAATAACAAAACATTAGCTGGGTGTA	180
Query	181	GTGGCAGGTGCCTGTAATCCCAGCTATTCGGGAGGCCTAGGAAGGAAAAATGGCTTGAACC	240
Sbjct	181	GTGGCAGGTGCCTGTAATCCCAGCTATTCGGGAGGCCTAGGAAGGAAAAATGGCTTGAACC	240
Query	241	TGGGGGTGGAGGTTGGAGTGAGGCAAGATCACACCACTGCACTCCAGCCTGGGCGACAGA	300
Sbjct	241	TGGGGGTGGAGGTTGGAGTGAGGCAAGATCACACCACTGCACTCCAGCCTGGGCGACAGA	300
Query	301	GCGAGACTCCATCTCAAAAGAAAGaaaaaaaaaacaacaaaaaaaaCCTTTATCAGATTATC	360
Sbjct	301	GCGAGACTCCATCTCAAAAGAAAGAAAAAAAAAACAACAAAAAACCTTTATCAGATTATC	360
Query	361	AGAGGTTATCACTACAGAGGGAGGTAAAATTGGAGGGAAAAGGTACAAATTTATTTTAC	420
Sbjct	361	AGAGGTTATCACTACAGAGGGAGGTAAAATTGGAGGGAAAAGGTACAAATTTATTTTAC	420

Sequence 1230 matched with Sequence 439

Query= Sequence ID - 1230 nt: 741
Length=741

SEQ ID NO: 439 nt: 741

ALIGNMENTS

Identities = 741/741 (100%), Gaps = 0/741 (0%)

Query	1	AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGAGCCA	60
Sbjct	1	AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGAGCCA	60
Query	61	CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCCTGG	120
Sbjct	61	CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCCTGG	120
Query	121	TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC	180
Sbjct	121	TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC	180
Query	181	CATTATTTTCTTTAATGTAGAAATGATTAATACATATTCTACAAGGGGCAGTAAGGTAGT	240
Sbjct	181	CATTATTTTCTTTAATGTAGAAATGATTAATACATATTCTACAAGGGGCAGTAAGGTAGT	240
Query	241	AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACCTTG	300
Sbjct	241	AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACCTTG	300
Query	301	TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT	360
Sbjct	301	TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT	360
Query	361	ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGAAAGACTGTTAAATCAC	420
Sbjct	361	ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGAAAGACTGTTAAATCAC	420
Query	421	TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA	480
Sbjct	421	TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA	540
Sbjct	481	CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA	540
Query	541	AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT	600
Sbjct	541	AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT	600
Query	601	GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC	660
Sbjct	601	GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC	660
Query	661	CTAATTTGAGATCACCTAAACACTGGAAAAAGaaaaaaaTGAAAGGGCAGTATGTCCATA	720
Sbjct	661	CTAATTTGAGATCACCTAAACACTGGAAAAAGAAAAAAATGAAAGGGCAGTATGTCCATA	720
Query	721	AACCAACAAATAATTTGGCTG	741
Sbjct	721	AACCAACAAATAATTTGGCTG	741

Sequence 1231 matched with Sequence 440

Query= Sequence ID - 1231 nt: 203
Length=203

SEQ ID NO: 440 nt: 203

ALIGNMENTS

Identities = 203/203 (100%), Gaps = 0/203 (0%)

```
Query 1   TTGAGGAAGGGTCTACTGTCTTTTAAATGGCACAATTTTAAGAGGTTTGAGAGGTACAG  60
          |||
Sbjct 1   TTGAGGAAGGGTCTACTGTCTTTTAAATGGCACAATTTTAAGAGGTTTGAGAGGTACAG  60

Query 61  TCCCTTAACCTGCCACGGGAGAGGGGCCCCAACTTTCTTCCCCCACACTTCTGGTTT  120
          |||
Sbjct 61  TCCCTTAACCTGCCACGGGAGAGGGGCCCCAACTTTCTTCCCCCACACTTCTGGTTT  120

Query 121 TCTGTGTGGAGGGGAGCAGGGATATCTAAGCTGTGGTGTGAAAGGGTAGGAGAGATGCT  180
          |||
Sbjct 121 TCTGTGTGGAGGGGAGCAGGGATATCTAAGCTGTGGTGTGAAAGGGTAGGAGAGATGCT  180

Query 181 GGAGGTGGGGGTGCTGTGTTCTA  203
          |||
Sbjct 181 GGAGGTGGGGGTGCTGTGTTCTA  203
```

Sequence 1239 matched with Sequence 441

Query= Sequence ID 1239
Length=874

SEQ ID NO: 441

ALIGNMENTS

Identities = 874/874 (100%), Gaps = 0/874 (0%)

Query	1	TTTCCTCGGGAAGCGGCCATTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACAttt	60
Sbjct	1	TTTCCTCGGGAAGCGGCCATTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACATTT	60
Query	61	ttttttttttttttttttttttAGAATGATTAACAATTTATTGAGTTTTATTATCTACAAAAA	120
Sbjct	61	TTTTTTTTTTTTTTTTTTTAGAATGATTAACAATTTATTGAGTTTTATTATCTACAAAAA	120
Query	121	TATAGCAATACAGNGAACTTCACCAAATCCTAAATATTCAGTACCTGAACTGGCTACAAC	180
Sbjct	121	TATAGCAATACAGNGAACTTCACCAAATCCTAAATATTCAGTACCTGAACTGGCTACAAC	180
Query	181	ACCGNGTGCACACCCAGTTCCTGCAGAATCTCTTGCAGATATGGGAGAGTCAGCCAGTGA	240
Sbjct	181	ACCGNGTGCACACCCAGTTCCTGCAGAATCTCTTGCAGATATGGGAGAGTCAGCCAGTGA	240
Query	241	AAAGATCCATTTCTTGGGAATCCTTGTCAACAAGACCAGTTCAGAAATCCAGGATATATA	300
Sbjct	241	AAAGATCCATTTCTTGGGAATCCTTGTCAACAAGACCAGTTCAGAAATCCAGGATATATA	300
Query	301	GAAGCCTACTGTAATTTaaaaacagtaacaaaaaccccaacaaaacccaaatcaacaaaG	360
Sbjct	301	GAAGCCTACTGTAATTTAAAAACAGTAACAAAAACCCCAACAAAACCCAAATCAACAAAG	360
Query	361	ACCAAGATAAAGGNGTGATAAACATTAATTGTAATGGTTTTCTTTACATGCAATACATG	420
Sbjct	361	ACCAAGATAAAGGNGTGATAAACATTAATTGTAATGGTTTTCTTTACATGCAATACATG	420
Query	421	CATTTTAAAATCACTAAGAAACACGAAATTTTGTAGAGCAAAGTTTGNGTTTCACGTAAG	480
Sbjct	421	CATTTTAAAATCACTAAGAAACACGAAATTTTGTAGAGCAAAGTTTGNGTTTCACGTAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TGCAAATGAatatatatattttattttttataactatttaaattatatatatattttttCCATACA	540
Sbjct	481	TGCAAATGAATATATATTTTATTTTATATACTATTAAATTATATATATTTTTCATACA	540
Query	541	AAAGCACACAGTGTTAATCTATAAAATGACATCCAAGTGGATGATGATTGTTTTTGCATG	600
Sbjct	541	AAAGCACACAGTGTTAATCTATAAAATGACATCCAAGTGGATGATGATTGTTTTTGCATG	600
Query	601	TCCCCCTGCTTAGAttttttttaaataatatagtcaaaaattaacatccttcttttaaaaat	660
Sbjct	601	TCCCCCTGCTTAGATTTTTTTTAAATATATAGTCAAAAATTAACATCCTTCTTTAAAT	660
Query	661	acagaagggaangggcaaaaaaaaaaTCTAGACTCGAGCAAGCTTATGCATGCATG	720
Sbjct	661	ACAGAAGGGAAAAANGGGCAAAAAAAAAAATCTAGACTCGAGCAAGCTTATGCATGCATG	720
Query	721	CGGCCGCAATTCGANCTCGNCGACTTGGCCAATTCGCCCTATAGNGAGTCGNATTACAA	780
Sbjct	721	CGGCCGCAATTCGANCTCGNCGACTTGGCCAATTCGCCCTATAGNGAGTCGNATTACAA	780
Query	781	TTCACTGGGCCGNCGNTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCNNCTNA	840
Sbjct	781	TTCACTGGGCCGNCGNTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCNNCTNA	840
Query	841	TCGNCTTGNAACAATNCCNNTTNGCCAGNGGGG	874
Sbjct	841	TCGNCTTGNAACAATNCCNNTTNGCCAGNGGGG	874

Sequence 1255 matched with Sequence 442

Query= Sequence ID 1255
Length=928

SEQ ID NO: 442

ALIGNMENTS

Identities = 928/928 (100%), Gaps = 0/928 (0%)

Query	1	TCACTTCGTATNGAANCTGTTTGGACTTGCTCAACAAGACCTTATCTTAACAAAAAGTAA	60
Sbjct	1	TCACTTCGTATNGAANCTGTTTGGACTTGCTCAACAAGACCTTATCTTAACAAAAAGTAA	60
Query	61	CTTATAGAAAAGGGAGACATTCATTTAACTTCAAGCCCATATTATTCTTAAAAGCTGACT	120
Sbjct	61	CTTATAGAAAAGGGAGACATTCATTTAACTTCAAGCCCATATTATTCTTAAAAGCTGACT	120
Query	121	CTTGAAATAGTATTTATTGAGTCATAGTGGAGTCATGGGACTTTTTAAGGGCCGGAAGGG	180
Sbjct	121	CTTGAAATAGTATTTATTGAGTCATAGTGGAGTCATGGGACTTTTTAAGGGCCGGAAGGG	180
Query	181	ACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAGGAAACTGAGGCCTAGA	240
Sbjct	181	ACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAGGAAACTGAGGCCTAGA	240
Query	241	TAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAGTAGTCTATCCGTAAGAGACA	300
Sbjct	241	TAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAGTAGTCTATCCGTAAGAGACA	300
Query	301	ACATGGAGAAAGAAATACAACGTTTTTATAGTGAATTATCATCTTACAAAGAATATTCTT	360
Sbjct	301	ACATGGAGAAAGAAATACAACGTTTTTATAGTGAATTATCATCTTACAAAGAATATTCTT	360
Query	361	CCCATATCGCACTTTTAAAAAGTGGGTACCTTAGTCAAATAGGAGAAAAAACCACTTGAG	420
Sbjct	361	CCCATATCGCACTTTTAAAAAGTGGGTACCTTAGTCAAATAGGAGAAAAAACCACTTGAG	420
Query	421	TAGTTTCATCCTCAGGTTTTAGGTGAGGAAACTGATACTCAGATTAAATAACTTTAAGCA	480
Sbjct	421	TAGTTTCATCCTCAGGTTTTAGGTGAGGAAACTGATACTCAGATTAAATAACTTTAAGCA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CACAGAGCCTGAATGATAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTT	540
Sbjct	481	CACAGAGCCTGAATGATAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTT	540
Query	541	AGGTGTTTTCACTTGCAATTCCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGT	600
Sbjct	541	AGGTGTTTTCACTTGCAATTCCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGT	600
Query	601	ACTACGTTAGGTGTTTTCACTTGCAATTCCTTGTTTGACGTTGACAATAAATCGTGAAGC	660
Sbjct	601	ACTACGTTAGGTGTTTTCACTTGCAATTCCTTGTTTGACGTTGACAATAAATCGTGAAGC	660
Query	661	TGCCTTATCTAAGNAGTCCTAAAGTAAATCATTGGAACACATGTANCCAGTTTGTGT	720
Sbjct	661	TGCCTTATCTAAGNAGTCCTAAAGTAAATCATTGGAACACATGTANCCAGTTTGTGT	720
Query	721	TTATTTGCCAGGTNTCAAATATAACTGAAAACCCATGCTAACTGACTNATTTTAAAGNT	780
Sbjct	721	TTATTTGCCAGGTNTCAAATATAACTGAAAACCCATGCTAACTGACTNATTTTAAAGNT	780
Query	781	GTNTGGGGCATGAAANGATTGCTCTGCCTGGGCGGGNGGTTNANCCTGNGTCCCCN	840
Sbjct	781	GTNTGGGGCATGAAANGATTGCTCTGCCTGGGCGGGNGGTTNANCCTGNGTCCCCN	840
Query	841	NGGAGNCCACCCANGANGCGATATTTNAGGGNNGATTNAAACCCCTGGCACGNGNNAAC	900
Sbjct	841	NGGAGNCCACCCANGANGCGATATTTNAGGGNNGATTNAAACCCCTGGCACGNGNNAAC	900
Query	901	CCCNTTTTAAANANAAAAANANCGGNNG	928
Sbjct	901	CCCNTTTTAAANANAAAAANANCGGNNG	928

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

Sequence 1256 matched with Sequence 443

Query= Sequence ID 1256
Length=954

SEQ ID NO: 443

ALIGNMENTS

Identities = 954/954 (100%), Gaps = 0/954 (0%)

Query	1	TTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACGGAGTTTACCTTATTACACTTTA	60
Sbjct	1	TTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACGGAGTTTACCTTATTACACTTTA	60
Query	61	ATCTCTGGATTTACCCCATCTCATTCTCTTTTAGGAAAAGTGGTGTATGTGGTGGCTT	120
Sbjct	61	ATCTCTGGATTTACCCCATCTCATTCTCTTTTAGGAAAAGTGGTGTATGTGGTGGCTT	120
Query	121	TGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAAGTAAATGAATGGAA	180
Sbjct	121	TGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAAGTAAATGAATGGAA	180
Query	181	GATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAACAC	240
Sbjct	181	GATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAACAC	240
Query	241	CATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTATAA	300
Sbjct	241	CATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTATAA	300
Query	301	CCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTCCAGTTTAAACAAATTTAAGA	360
Sbjct	301	CCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTCCAGTTTAAACAAATTTAAGA	360
Query	361	CCCTCTCAAACAAAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTGAAT	420
Sbjct	361	CCCTCTCAAACAAAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTGAAT	420
Query	421	AAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTGCAT	480
Sbjct	421	AAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTGCAT	480

PATENT SEQUENCE ALIGNMENT

```

Query  481  ACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAG  540

Query  541  GTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAACCAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAACCAA  600

Query  601  GAATTGATTGGGCACATCATTTCAAGAAGTCCCCTCTCCTCCACATTGTGTTTGCCAATT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GAATTGATTGGGCACATCATTTCAAGAAGTCCCCTCTCCTCCACATTGTGTTTGCCAATT  660

Query  661  TGCACATTAAATGACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGGNTTAA  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  TGCACATTAAATGACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGGNTTAA  720

Query  721  ANATGTAAACAGTTGGGTTTTTTAAGGGNCCTTTTTTCATAACTGGAACACTCTNTACAAG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721  ANATGTAAACAGTTGGGTTTTTTAAGGGNCCTTTTTTCATAACTGGAACACTCTNTACAAG  780

Query  781  GNTNCTTNTTAAATAAAATAACTTGACTTTTTTGTGTTTNTAAANGNANCTTCNTGCTTCCA  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   781  GNTNCTTNTTAAATAAAATAACTTGACTTTTTTGTGTTTNTAAANGNANCTTCNTGCTTCCA  840

Query  841  TaaaaaaaaaaaaTTTAANTNGNCANCTNTGCTGCTGCGNCCANTTNGCTNGNCCNTGGCA  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   841  TAAAAAAAAAAAAATTTAANTNGNCANCTNTGCTGCTGCGNCCANTTNGCTNGNCCNTGGCA  900

Query  901  TTCCCTAGGGANGNTNAATANTGGCNNNTTAACNNGGCNGNAACNNNNNCCANT  954
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   901  TTCCCTAGGGANGNTNAATANTGGCNNNTTAACNNGGCNGNAACNNNNNCCANT  954

```

Blast comparison trimmed “NNNTTAACNNGGCNGNAACNNNNNCCANT” from the 3’ end of both sequences and reported 925 identities. The report has been manually corrected for this. “NNNTTAACNNGGCNGNAACNNNNNCCANT” has been appended to both sequences and identity count has been increased to 954.

Sequence 1331 matched with Sequence 444

Query= Sequence ID 1331
Length=787

SEQ ID NO: 444

ALIGNMENTS

Identities = 787/787 (100%), Gaps = 0/787 (0%)

Query	1	GGGCGATGCATGCTTTATTAAGGCTCTTGTTTCACCTGGCAGTGTACTGTATCAACGTAT	60
Sbjct	1	GGGCGATGCATGCTTTATTAAGGCTCTTGTTTCACCTGGCAGTGTACTGTATCAACGTAT	60
Query	61	AATACAGaaaaaaaTCTCTTTAAGGTCCTCCTTCACAAAGACATAGAGTGAAACTCCCT	120
Sbjct	61	AATACAGAAAAAAATCTCTTTAAGGTCCTCCTTCACAAAGACATAGAGTGAAACTCCCT	120
Query	121	TTACATGTCAGTATTTGTTCAACACTTTAGGCAACTTGACTGTCAGTGTAAAATGGAAA	180
Sbjct	121	TTACATGTCAGTATTTGTTCAACACTTTAGGCAACTTGACTGTCAGTGTAAAATGGAAA	180
Query	181	ACAGGAAAATGGAAAAATCTGACCAATTCTGCCACCTTGAGACTTTCATATAGACCTTGC	240
Sbjct	181	ACAGGAAAATGGAAAAATCTGACCAATTCTGCCACCTTGAGACTTTCATATAGACCTTGC	240
Query	241	ACAACAATTGTATAGATCACACACCGGCTGTATTTAATATGTAACATTTTCACACATATT	300
Sbjct	241	ACAACAATTGTATAGATCACACACCGGCTGTATTTAATATGTAACATTTTCACACATATT	300
Query	301	AAAGATACAGAAGTATTAaaaaaACCCCAATGTTAATGTATTTGCTTAAAAGGCACAAGT	360
Sbjct	301	AAAGATACAGAAGTATTAaaaaaACCCCAATGTTAATGTATTTGCTTAAAAGGCACAAGT	360
Query	361	TTCACATATCTGTCTAGCTATCTGTTGGTAATACAGAAAGTATACTACTTTTTTAAAAAA	420
Sbjct	361	TTCACATATCTGTCTAGCTATCTGTTGGTAATACAGAAAGTATACTACTTTTTTAAAAAA	420
Query	421	GTGGGCAGAATTCTtgtgtatgtatatatttgtgtgtacagtatgtgtatgtgtgtatatat	480
Sbjct	421	GTGGGCAGAATTCTTGTGTATGTATTTGTGTGTACAGTATGTGTATGTGTGTATATAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  atatattatatatatagataaatatataaatatTTTTTTAAGGAGAACTAGAATGTTTA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATATATTATATATATAGATAATATATAAAATATTTTTTTAAGGAGAACTAGAATGTTTA  540

Query  541  GCTAGAAAATTCCACAGCCTGTGAAGAAATATTTCAAATGGCCATAAAGGAGGTAAAAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GCTAGAAAATTCCACAGCCTGTGAAGAAATATTTCAAATGGCCATAAAGGAGGTAAAAA  600

Query  601  TGAAAACCATAACCTAACTTTTATAGAGGCTTTATCTTTAATTTAACGATGTGCGGAGGA  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TGAAAACCATAACCTAACTTTTATAGAGGCTTTATCTTTAATTTAACGATGTGCGGAGGA  660

Query  661  CTTTCTTGCTTGAATCTGTTCCGGGCTGTCTGCTCTGTCCATCAAATGGGCAGGTCTGGG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  CTTTCTTGCTTGAATCTGTTCCGGGCTGTCTGCTCTGTCCATCAAATGGGCAGGTCTGGG  720

Query  721  AATGAGGCACCTTCGGCCGTTTCAAGTGGCCTGAACAGAATGCTGGAACCCAGGCTGGA  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721  AATGAGGCACCTTCGGCCGTTTCAAGTGGCCTGAACAGAATGCTGGAACCCAGGCTGGA  780

Query  781  CTCGGAC   787
          |||||
Sbjct   781  CTCGGAC   787
```

Sequence 1332 matched with Sequence 445

Query= Sequence ID 1332
Length=689

SEQ ID NO: 445

ALIGNMENTS

Identities = 689/689 (100%), Gaps = 0/689 (0%)

Query	1	CAAACCTGCATGTTCTGCACATGTATCCAGGAACCTAAAAAAAAAAAAAGATAGTTTGTG	60
Sbjct	1	CAAACCTGCATGTTCTGCACATGTATCCAGGAACCTAAAAAAAAAAAAAGATAGTTTGTG	60
Query	61	TGTCTTAATTGAATAATAGTAGATTTATAGATTAAAGATCTATGGGTTTTTAATATGGAT	120
Sbjct	61	TGTCTTAATTGAATAATAGTAGATTTATAGATTAAAGATCTATGGGTTTTTAATATGGAT	120
Query	121	TAGAAATCTGTGGGTTTTTGATATGGATTAGAAATCTGTGGGTTTTTAATATGGATTGGA	180
Sbjct	121	TAGAAATCTGTGGGTTTTTGATATGGATTAGAAATCTGTGGGTTTTTAATATGGATTGGA	180
Query	181	AATCTGTGGGTTTTTAATATGGATTAAAAACATCTGTGGGTTTTTAATATGGATTAAAC	240
Sbjct	181	AATCTGTGGGTTTTTAATATGGATTAAAAACATCTGTGGGTTTTTAATATGGATTAAAC	240
Query	241	ATCTGTGGGTTTTTAATATGGATTAAACATCTGGGTTTTTAATATGGATTAAACATCTGT	300
Sbjct	241	ATCTGTGGGTTTTTAATATGGATTAAACATCTGGGTTTTTAATATGGATTAAACATCTGT	300
Query	301	GGGTTTTTAATATGGGTTAAAAATCAAAAGAAAATGAACTATTTGCTCCAGTGCAGGAAA	360
Sbjct	301	GGGTTTTTAATATGGGTTAAAAATCAAAAGAAAATGAACTATTTGCTCCAGTGCAGGAAA	360
Query	361	ATACAGGCAATACTGGATACAATTAGATGGTCAGGAGCGATAACCCGGTTGCCATTGTTT	420
Sbjct	361	ATACAGGCAATACTGGATACAATTAGATGGTCAGGAGCGATAACCCGGTTGCCATTGTTT	420
Query	421	GAAGAAGAGAATAAGGTGCTAGCATTCCATCCGTAGATAATTTGACAGCTAGGAAATAG	480
Sbjct	421	GAAGAAGAGAATAAGGTGCTAGCATTCCATCCGTAGATAATTTGACAGCTAGGAAATAG	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAATGAACTATTATATGCAGTTATCGTAGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAATGAACTATTATATGCAGTTATCGTAGA  540

Query  541  AGAGTACTCAAAAAAATCTGTAAAAAATAAAGAAAGGCCGGGCGCGGTGGCTCACGCCTG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AGAGTACTCAAAAAAATCTGTAAAAAATAAAGAAAGGCCGGGCGCGGTGGCTCACGCCTG  600

Query  601  TAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCATGAGGTCAGGAGATCGAGACCA  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCATGAGGTCAGGAGATCGAGACCA  660

Query  661  TCCTGGCTACCANGGTGAAACCCCGTCT  689
          ||||||||||||||||||||
Sbjct   661  TCCTGGCTACCANGGTGAAACCCCGTCT  689
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

Sequence 1335 matched with Sequence 446

Query= Sequence ID 1335
Length=688

SEQ ID NO: 446

ALIGNMENTS

Identities = 688/688 (100%), Gaps = 0/688 (0%)

Query	1	CAAGACTCCATCTCaaaaaaaaaaaaaTCTACAGTGCTGAGTATATAAAATTATTAAC	60
Sbjct	1	CAAGACTCCATCTCAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTATTAAC	60
Query	61	ACATTTTACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Sbjct	61	ACATTTTACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAACAGGTAAT	120
Query	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Sbjct	121	TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT	180
Query	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Sbjct	181	GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT	240
Query	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Sbjct	241	TTGTTCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT	300
Query	301	GCCAAATATGGGTAAATAAGGGAAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT	360
Sbjct	301	GCCAAATATGGGTAAATAAGGGAAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT	360
Query	361	GAATATTTGAATTTTGTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Sbjct	361	GAATATTTGAATTTTGTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA	420
Query	421	GAGGAAAGATGGATTTTCACTCTGTATTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480
Sbjct	421	GAGGAAAGATGGATTTTCACTCTGTATTTTAAACATCATTTATTTTAAATCTGGTGCTGA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAAATAAGaaaaaaaTTAAACTGCATTCTGCTGTTCTTCTTTAGAAGCATTCTGCGTAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AAAATAAGAAAAAAATTAAACTGCATTCTGCTGTTCTTCTTTAGAAGCATTCTGCGTAA  540

Query  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600

Query  601  GTGtttttttgtttttttCCTAGAAATGTTTGTCTTCCCCCACCTGTTGATCCAGGTTA  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GTGTTTTTTTGTTTTTTTCCTAGAAATGTTTGTCTTCCCCCACCTGTTGATCCAGGTTA  660

Query  661  AGGAATACTTTTTTACACTTTATTCAAA  688
          ||||||||||||||||||||
Sbjct   661  AGGAATACTTTTTTACACTTTATTCAAA  688
```

Sequence 1336 matched with Sequence 447

Query= Sequence ID 1336
Length=724

SEQ ID NO: 447

ALIGNMENTS

Identities = 724/724 (100%), Gaps = 0/724 (0%)

Query	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCGCTGCATCCTTTCTGTG	60
Sbjct	1	CTTTTCCTCCCGCTGTCCCCACGGAGGGGACTGCTCTCCCCGCTGCATCCTTTCTGTG	60
Query	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Sbjct	61	AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCTG	120
Query	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Sbjct	121	GGAAGTGTTTTTGAGAAGTCTCGGTCCGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA	180
Query	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Sbjct	181	ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC	240
Query	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Sbjct	241	AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA	300
Query	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTA	360
Sbjct	301	AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTA	360
Query	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGCTGG	420
Sbjct	361	TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCTACAACAGTGCTGG	420
Query	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480
Sbjct	421	GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA	540
Sbjct	481	CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA	540
Query	541	GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACAACCAC	600
Sbjct	541	GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACCTCTGACAACCAC	600
Query	601	AATCATGAGGATGATGTGTTGGGGTTTCCCAGCAATCAGGACTTGTATTGGTCAGAGGAC	660
Sbjct	601	AATCATGAGGATGATGTGTTGGGGTTTCCCAGCAATCAGGACTTGTATTGGTCAGAGGAC	660
Query	661	GATCAAGAGCTCATAATCCCATGCCTTGCGCTGGTGAGAGCATCCAAAGCCTGCCTGAAG	720
Sbjct	661	GATCAAGAGCTCATAATCCCATGCCTTGCGCTGGTGAGAGCATCCAAAGCCTGCCTGAAG	720
Query	721	AAAA 724	
Sbjct	721	AAAA 724	

Sequence 1337 matched with Sequence 448

Query= Sequence ID 1337
Length=622

SEQ ID NO: 448

ALIGNMENTS

Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query	1	CAAGAACTCTGGGACATTTGCAAAGGGTATGGCATATGTGTAATGGGAATACCAGAGGAG	60
Sbjct	1	CAAGAACTCTGGGACATTTGCAAAGGGTATGGCATATGTGTAATGGGAATACCAGAGGAG	60
Query	61	AGGAAAGACAGGAAGTCaaaaaaaGAATTTTTTCCAAATTAATGATAGGTTCCAAACCACA	120
Sbjct	61	AGGAAAGACAGGAAGTCAAAAAAGAATTTTTTCCAAATTAATGATAGGTTCCAAACCACA	120
Query	121	GATGCAGGAAGCTTAAACACCAACAGGATAAAATAAAACAAAATCTACGCTTAAGCATATC	180
Sbjct	121	GATGCAGGAAGCTTAAACACCAACAGGATAAAATAAAACAAAATCTACGCTTAAGCATATC	180
Query	181	ATACTTAACCTGCAGAAAAATTACAGACAAAGAAAAAACACCAGAGGGGAAGCTGGCAGAA	240
Sbjct	181	ATACTTAACCTGCAGAAAAATTACAGACAAAGAAAAAACACCAGAGGGGAAGCTGGCAGAA	240
Query	241	ACATACCACCTATAGCGGAAGAAGAATAAGAATTACATCAGACTTCCCTTCAGAAATCTT	300
Sbjct	241	ACATACCACCTATAGCGGAAGAAGAATAAGAATTACATCAGACTTCCCTTCAGAAATCTT	300
Query	301	GCAAACAAAAAGATGTAGCACAATATTTAAAGTATTAAAGGAGGCCGGGCCGGTGGCTC	360
Sbjct	301	GCAAACAAAAAGATGTAGCACAATATTTAAAGTATTAAAGGAGGCCGGGCCGGTGGCTC	360
Query	361	GGGCCTGTAATCCTAACACTTTGGGAGGCTGAGGCAGGAGGACCATGAGGTCAGGAGATC	420
Sbjct	361	GGGCCTGTAATCCTAACACTTTGGGAGGCTGAGGCAGGAGGACCATGAGGTCAGGAGATC	420
Query	421	GAGACCATCCTGGTGATGGTGATACCCCATCTCTACTAAAAATACAAAAAATTAACCGGG	480
Sbjct	421	GAGACCATCCTGGTGATGGTGATACCCCATCTCTACTAAAAATACAAAAAATTAACCGGG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CATGGTGACACGCACCTGTAATCCCAGCTACTTGGGAGGCTGAAGCAGGAGAATCGTTTG	540
Sbjct	481	CATGGTGACACGCACCTGTAATCCCAGCTACTTGGGAGGCTGAAGCAGGAGAATCGTTTG	540
Query	541	AGCCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATCACATCACTGCACGCCTGGGCAACAG	600
Sbjct	541	AGCCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATCACATCACTGCACGCCTGGGCAACAG	600
Query	601	AGCGAGACTCCATCTCAAAAAA	622
Sbjct	601	AGCGAGACTCCATCTCAAAAAA	622

Sequence 1338 matched with Sequence 449

Query= Sequence ID 1338
Length=834

SEQ ID NO: 449

ALIGNMENTS

Identities = 834/834 (100%), Gaps = 0/834 (0%)

Query	1	CGACCCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCC	60
Sbjct	1	CGACCCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCC	60
Query	61	TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTA	120
Sbjct	61	TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTA	120
Query	121	AATGTTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGG	180
Sbjct	121	AATGTTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGG	180
Query	181	GAATATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTA	240
Sbjct	181	GAATATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTA	240
Query	241	GAATCAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTTCAT	300
Sbjct	241	GAATCAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTTCAT	300
Query	301	ATGCAAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTTAAAAAACTGACCC	360
Sbjct	301	ATGCAAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTTAAAAAACTGACCC	360
Query	361	TATTCTCAGGATGAAAATAATACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTA	420
Sbjct	361	TATTCTCAGGATGAAAATAATACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTA	420
Query	421	AGGAGGTACAATTAATAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCT	480
Sbjct	421	AGGAGGTACAATTAATAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCCTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGA	540
Sbjct	481	TCCTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGA	540
Query	541	TTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTG	600
Sbjct	541	TTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTG	600
Query	601	CATGCTTATCTTGTATCAAGCATTGTGATGAAAGCACAGAATGAAAGAGGAGGGAGAAT	660
Sbjct	601	CATGCTTATCTTGTATCAAGCATTGTGATGAAAGCACAGAATGAAAGAGGAGGGAGAAT	660
Query	661	GTTTAGAGAATAAGGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANAAGA	720
Sbjct	661	GTTTAGAGAATAAGGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANAAGA	720
Query	721	CAGGTTTCAGGTTAGTAAGGGCGCTCATATTTTGACCCTGAATGTAACTATGTGCACATC	780
Sbjct	721	CAGGTTTCAGGTTAGTAAGGGCGCTCATATTTTGACCCTGAATGTAACTATGTGCACATC	780
Query	781	ATGCTAGCTATTCTAAATCAGGCATTTTCAAATGGAAGCAGGCACTGACATTTT	834
Sbjct	781	ATGCTAGCTATTCTAAATCAGGCATTTTCAAATGGAAGCAGGCACTGACATTTT	834

Sequence 1344 matched with Sequence 450

Query= Sequence ID 1344
Length=624

SEQ ID NO: 450

ALIGNMENTS

Identities = 624/624 (100%), Gaps = 0/624 (0%)

Query	1	CGTGAAGGGTCTTTATGTATTAGTATTAGAGTGATCTTTTGATTATTTTCCTCACTATAA	60
Sbjct	1	CGTGAAGGGTCTTTATGTATTAGTATTAGAGTGATCTTTTGATTATTTTCCTCACTATAA	60
Query	61	GGAAATTATTTCTCAGGATGAGCTGCCATAACATTCCACTGTCTGATGGCAATTTTAAA	120
Sbjct	61	GGAAATTATTTCTCAGGATGAGCTGCCATAACATTCCACTGTCTGATGGCAATTTTAAA	120
Query	121	GCCTGAAATTGAAGCCCATGGCTAGGCTATGAGAACCCTAGTTCGTATAGTAAAGTTGAT	180
Sbjct	121	GCCTGAAATTGAAGCCCATGGCTAGGCTATGAGAACCCTAGTTCGTATAGTAAAGTTGAT	180
Query	181	ATCTTCTGGATGTATACTAATTTTAGGCTTTATTTTAAACTGCTGGAACTGAACTTA	240
Sbjct	181	ATCTTCTGGATGTATACTAATTTTAGGCTTTATTTTAAACTGCTGGAACTGAACTTA	240
Query	241	GACAAAAGTATTTTCAGGACATCATTTACAATGTTTAGCCCTAAAGAGTCAAGCTGTGGG	300
Sbjct	241	GACAAAAGTATTTTCAGGACATCATTTACAATGTTTAGCCCTAAAGAGTCAAGCTGTGGG	300
Query	301	ATTCTGAGTCTTTCATATGTTACAGCAGAACTTAAAGCAAGAGGAAATTGGCTGGGCA	360
Sbjct	301	ATTCTGAGTCTTTCATATGTTACAGCAGAACTTAAAGCAAGAGGAAATTGGCTGGGCA	360
Query	361	CAGTGGCTCTGTAATCCAGCACTTTGGGAGGCTGAGGTGGTGGATCATGAGGTCAAGA	420
Sbjct	361	CAGTGGCTCTGTAATCCAGCACTTTGGGAGGCTGAGGTGGTGGATCATGAGGTCAAGA	420
Query	421	GATTGAGACCATCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTA	480
Sbjct	421	GATTGAGACCATCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GCTGGGCGTGGTGGCACACGCCTGTAATCCCAGCTAGTCAGGAGGCTGAGGCAGGAGAAT	540
Sbjct	481	GCTGGGCGTGGTGGCACACGCCTGTAATCCCAGCTAGTCAGGAGGCTGAGGCAGGAGAAT	540
Query	541	ATCTTGAAC TTGGGAGGCAGAGGTTGCAGTGAGCCAAGATTACATCACTGCACTCCAGCC	600
Sbjct	541	ATCTTGAAC TTGGGAGGCAGAGGTTGCAGTGAGCCAAGATTACATCACTGCACTCCAGCC	600
Query	601	TGGTGACAGAGCGAGACTCCGACT	624
Sbjct	601	TGGTGACAGAGCGAGACTCCGACT	624

Sequence 1348 matched with Sequence 451

Query= Sequence ID 1348
Length=966

SEQ ID NO: 451

ALIGNMENTS

Identities = 966/966 (100%), Gaps = 0/966 (0%)

Query	1	CTGAAACTGCACTGAACCCACAGGTAGGTTACATCACAGGACAGAAATCTGAGGAGCTGG	60
Sbjct	1	CTGAAACTGCACTGAACCCACAGGTAGGTTACATCACAGGACAGAAATCTGAGGAGCTGG	60
Query	61	AGAAAGCAAAAGAATAAAGGATGGGCTGACACCAGAAGGAATTAAGGAATTTTATACT	120
Sbjct	61	AGAAAGCAAAAGAATAAAGGATGGGCTGACACCAGAAGGAATTAAGGAATTTTATACT	120
Query	121	GAACTTCAATTACTTGTTCATTTGAAGTTTGtttttttAATGAACGTTTTGCTGTTACT	180
Sbjct	121	GAACTTCAATTACTTGTTCATTTGAAGTTTGTTTTTTAATGAACGTTTTGCTGTTACT	180
Query	181	TAAATATAGTGTTTTGAAAGTGTTTCAAATGTATTCAAGTTGGGATTTCCATATTTTAC	240
Sbjct	181	TAAATATAGTGTTTTGAAAGTGTTTCAAATGTATTCAAGTTGGGATTTCCATATTTTAC	240
Query	241	TACAGTTCTGTCTTAGTATGTTCAACATAAAACACTTATCATTAAGCTCACAAAGTGCT	300
Sbjct	241	TACAGTTCTGTCTTAGTATGTTCAACATAAAACACTTATCATTAAGCTCACAAAGTGCT	300
Query	301	TTTTTGTAATATGAGGATAAAATGAAGCCATATAAGAAtttttttATATCTGTACATTTA	360
Sbjct	301	TTTTTGTAATATGAGGATAAAATGAAGCCATATAAGAATTTTTTTATATCTGTACATTTA	360
Query	361	ACCCACATTTGAGCTTTAGCCAAAATATATAGCtttttttttCTGACCTGGCCAACGTA	420
Sbjct	361	ACCCACATTTGAGCTTTAGCCAAAATATATAGCTTTTTTTTTTCTGACCTGGCCAACGTA	420
Query	421	TTATCCAGCAAACATCAACTGAAGCAATATGGAAACACTTCCAAATGTTTGCCAATAATG	480
Sbjct	421	TTATCCAGCAAACATCAACTGAAGCAATATGGAAACACTTCCAAATGTTTGCCAATAATG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTATTAAGTGACTGATGTCAACATTAGTTACATGGCAAACCTAAAGAGGCATTATACATTT	540
Sbjct	481	CTATTAAGTGACTGATGTCAACATTAGTTACATGGCAAACCTAAAGAGGCATTATACATTT	540
Query	541	TTAAACACACTAACATATAACTGTAGATAATGTAAGGTTTATTTATATGCATATTTTCAT	600
Sbjct	541	TTAAACACACTAACATATAACTGTAGATAATGTAAGGTTTATTTATATGCATATTTTCAT	600
Query	601	AGtatattttaaatgtttaaatataaaaaagggtttttaaacacttttaatttttatcttt	660
Sbjct	601	AGTATATTTTAAATGTTTAAATATAAAAAAGGGTTTTTAAACACTTTTAATTTTATCTTT	660
Query	661	gatttttttttATTGATATCTCTTCCAGGCTACTAATAAAATTGCCAGAACTAAACTATC	720
Sbjct	661	GATTTTTTTTATTGATATCTCTTCCAGGCTACTAATAAAATTGCCAGAACTAAACTATC	720
Query	721	AGGTAAAGGTTAAGGCATCAATTGACAAGTAAGTTTTCTAATTTTCGTTTGAATTACAAT	780
Sbjct	721	AGGTAAAGGTTAAGGCATCAATTGACAAGTAAGTTTTCTAATTTTCGTTTGAATTACAAT	780
Query	781	TCCAAATGTAAGACTTTTAAAAATGAATGGCCTTTATTTTATAGAATAATTTTGACCTTT	840
Sbjct	781	TCCAAATGTAAGACTTTTAAAAATGAATGGCCTTTATTTTATAGAATAATTTTGACCTTT	840
Query	841	TAAATTTACTTATCTAACATTATATAATGAATGTACTTCAAATATTTGACTTTGAAGTCA	900
Sbjct	841	TAAATTTACTTATCTAACATTATATAATGAATGTACTTCAAATATTTGACTTTGAAGTCA	900
Query	901	ACATTAACAAATTCATGGATCCTAATTAATAATTTACTATAAACTGGAATCATTTATTAC	960
Sbjct	901	ACATTAACAAATTCATGGATCCTAATTAATAATTTACTATAAACTGGAATCATTTATTAC	960
Query	961	TTCCTT 966	
Sbjct	961	TTCCTT 966	

Sequence 1351 matched with Sequence 452

Query= Sequence ID 1351
Length=725

SEQ ID NO: 452

ALIGNMENTS

Identities = 725/725 (100%), Gaps = 0/725 (0%)

```
Query 1      ttttttttttttAAAAGAGATGGGTTCTCACTATGTTGCCATAATGTTTATGAGATTA 60
             |||
Sbjct 1      TTTTTTTTTTTTAAAAGAGATGGGTTCTCACTATGTTGCCATAATGTTTATGAGATTA 60

Query 61     AGTTCATCTTTTTTATCTGAGTAGTATTTTATTGTATGAATATAACCACCATTATTTATC 120
             |||
Sbjct 61     AGTTCATCTTTTTTATCTGAGTAGTATTTTATTGTATGAATATAACCACCATTATTTATC 120

Query 121    TGTTGGTTATTTCCAGTTTGGGCTATAATCCAAATGCTTTTTTCAAACAATAGGCTAT 180
             |||
Sbjct 121    TGTTGGTTATTTCCAGTTTGGGCTATAATCCAAATGCTTTTTTCAAACAATAGGCTAT 180

Query 181    ATATCATTAATGTCCGTTTATCAGCAGtataaaatatcttaccataaatattaataaaag 240
             |||
Sbjct 181    ATATCATTAATGTCCGTTTATCAGCAGTATAAAATATCTTACCATAAAATATTAATAAAAG 240

Query 241    aagcattcatatataaaaatatagatatTTCAAACCTACAGAGGGCCTTTTAATGATTAA 300
             |||
Sbjct 241    AAGCATTATATATAAAATATAGATATTTCAAACCTACAGAGGGCCTTTTAATGATTAA 300

Query 301    ATATTTTGTCTTACAAAAAGGTCCAGGTAATTACACCCATGAGGTTAACCTGCCTTAGT 360
             |||
Sbjct 301    ATATTTTGTCTTACAAAAAGGTCCAGGTAATTACACCCATGAGGTTAACCTGCCTTAGT 360

Query 361    GCAGGACTTAAAATAAGGCTTCTCCTGCCATCTCTCTCCATTTGTAGAATGTGAAATTCT 420
             |||
Sbjct 361    GCAGGACTTAAAATAAGGCTTCTCCTGCCATCTCTCTCCATTTGTAGAATGTGAAATTCT 420

Query 421    TTAAAATGCATCCTATATTAGGAATACTATAGCTGTGCACTGGTGTGTTTCTCTCTTT 480
             |||
Sbjct 421    TTAAAATGCATCCTATATTAGGAATACTATAGCTGTGCACTGGTGTGTTTCTCTCTTT 480
```

PATENT SEQUENCE ALIGNMENT

Query	481	AAACTCGGGACCGTATATATCTGCTCAAATTGCCCAAGTATACATATGCTGCACTCCATC	540
Sbjct	481	AAACTCGGGACCGTATATATCTGCTCAAATTGCCCAAGTATACATATGCTGCACTCCATC	540
Query	541	AAGTGTCAAGGCCACATTCTATCAGCACAGCGTGACTGCCTATCAGTGACAATATAAGTGA	600
Sbjct	541	AAGTGTCAAGGCCACATTCTATCAGCACAGCGTGACTGCCTATCAGTGACAATATAAGTGA	600
Query	601	GCTCTATTTGGATCCCTCTTACCCTACCTTTTATATTTATGACAGCATTATCATAAAACT	660
Sbjct	601	GCTCTATTTGGATCCCTCTTACCCTACCTTTTATATTTATGACAGCATTATCATAAAACT	660
Query	661	CCAATATTCTTCAATAACTTACATGTTTGTTGTAGGATAAAATTATTACCCTCAATGAAC	720
Sbjct	661	CCAATATTCTTCAATAACTTACATGTTTGTTGTAGGATAAAATTATTACCCTCAATGAAC	720
Query	721	TACAT	725
Sbjct	721	TACAT	725

Sequence 1352 matched with Sequence 453

Query= Sequence ID 1352
Length=715

SEQ ID NO: 453

ALIGNMENTS

Identities = 715/715 (100%), Gaps = 0/715 (0%)

Query	1	ACCAGCTTCTTCACAGGTTCCACGAGTCATGTCAACACAGCGTGTGCTAACACATCAAC	60
Sbjct	1	ACCAGCTTCTTCACAGGTTCCACGAGTCATGTCAACACAGCGTGTGCTAACACATCAAC	60
Query	61	ACAGACAATGGGTCCACGTCCTGCAGCTGCAGCCGCTGCAGCTACTCCTGCTGTCCGCAC	120
Sbjct	61	ACAGACAATGGGTCCACGTCCTGCAGCTGCAGCCGCTGCAGCTACTCCTGCTGTCCGCAC	120
Query	121	CGTTCCACAGTATAAATATGCTGCAGGAGTTGCAATCCTCAGCAACATCTTAATGCACA	180
Sbjct	121	CGTTCCACAGTATAAATATGCTGCAGGAGTTGCAATCCTCAGCAACATCTTAATGCACA	180
Query	181	GCCACAAGTTACAATGCAACAGCCTGCTGTTTCATGTACAAGGTCAGGAACCTTTGACTGC	240
Sbjct	181	GCCACAAGTTACAATGCAACAGCCTGCTGTTTCATGTACAAGGTCAGGAACCTTTGACTGC	240
Query	241	TTCCATGTTGGCATCTGCCCCTCCTCAAGAGCAAAAGCAAATGTTGGGTGAACGGCTGTT	300
Sbjct	241	TTCCATGTTGGCATCTGCCCCTCCTCAAGAGCAAAAGCAAATGTTGGGTGAACGGCTGTT	300
Query	301	TCCTCTTATTCAAGCCATGCACCCTACTCTTGCTGGTAAAATCACTGGCATGTTGTTGGA	360
Sbjct	301	TCCTCTTATTCAAGCCATGCACCCTACTCTTGCTGGTAAAATCACTGGCATGTTGTTGGA	360
Query	361	GATTGATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGT	420
Sbjct	361	GATTGATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGT	420
Query	421	TGATGAAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCAGAAAGCAGT	480
Sbjct	421	TGATGAAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCAGAAAGCAGT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAACAGTGCCACCGGTGTTCCAACGTGTTTAAAATTGATCAGGGACCATGAAAAGAACTT	540
Sbjct	481	TAACAGTGCCACCGGTGTTCCAACGTGTTTAAAATTGATCAGGGACCATGAAAAGAACTT	540
Query	541	GTGCTTCACCGAAGGaaaaatatctaacatcgaaaaacttaaatattatggaaaaaaac	600
Sbjct	541	GTGCTTCACCGAAGAAAAATATCTAAACATCGAAAACTTAAATATTATGAAAAAAAAC	600
Query	601	attgcaaaatataaaataaataaaaaaaaggaaaggaaaCTTTGAACCTTATGTACCGAGC	660
Sbjct	601	ATTGCAAAATATAAAATAAATAAAAAAAGGAAAGGAACTTTGAACCTTATGTACCGAGC	660
Query	661	AAATGCCAGGTCTAGCAAACATAATGCTAGTCCTAGATTACTTATTGATTAAAA	715
Sbjct	661	AAATGCCAGGTCTAGCAAACATAATGCTAGTCCTAGATTACTTATTGATTAAAA	715

Sequence 1353 matched with Sequence 454

Query= Sequence ID 1353
Length=573

SEQ ID NO: 454

ALIGNMENTS

Identities = 573/573 (100%), Gaps = 0/573 (0%)

Query	1	ACATTCTGAAAAGGCAAAAGGGAGGAAGAACTGATTAGTGGTTAGCCCAGGGTTAGAGT	60
Sbjct	1	ACATTCTGAAAAGGCAAAAGGGAGGAAGAACTGATTAGTGGTTAGCCCAGGGTTAGAGT	60
Query	61	TGGGGAGAGGATATAATGAGGGAACCTTTTGTGGATTCTGTACCATGATTATGATTACACA	120
Sbjct	61	TGGGGAGAGGATATAATGAGGGAACCTTTTGTGGATTCTGTACCATGATTATGATTACACA	120
Query	121	AACCTATGCATACATTGAAACACATAGAACTATACGTTGAAAAAAGTGAATCTGCCTGTA	180
Sbjct	121	AACCTATGCATACATTGAAACACATAGAACTATACGTTGAAAAAAGTGAATCTGCCTGTA	180
Query	181	TGTaaattttaaagaaaaatatTTTTTTTaaaaaaaCAGATGCTTCTTAACACATTATCAT	240
Sbjct	181	TGTAAATTTAAAGAAAAATATTTTTTTTAAAAAACAGATGCTTCTTAACACATTATCAT	240
Query	241	CTATGTCAGTTTAAACAGTTAGTAGACTTAGGCCAGGTGTCATGGCTCACTCCTGTAATCC	300
Sbjct	241	CTATGTCAGTTTAAACAGTTAGTAGACTTAGGCCAGGTGTCATGGCTCACTCCTGTAATCC	300
Query	301	CAGTGCTTTGGGAGTCTGAGGTGGGACGATCTCTTGAGACTAGGAGGGAGTTTGAGACAA	360
Sbjct	301	CAGTGCTTTGGGAGTCTGAGGTGGGACGATCTCTTGAGACTAGGAGGGAGTTTGAGACAA	360
Query	361	ACCTAGGCAATGTAATGAGACTCTTTCTCTACAAAAAATTTTAAAGTTATCTGGACATGG	420
Sbjct	361	ACCTAGGCAATGTAATGAGACTCTTTCTCTACAAAAAATTTTAAAGTTATCTGGACATGG	420
Query	421	TGGTGCCTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATTCCTTGAGCCC	480
Sbjct	421	TGGTGCCTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATTCCTTGAGCCC	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGAAGTTCAAGGCTACAGTGTGCTATGATAGAGCCACTGCACTCCAGCCTGGGCAACCAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGAAGTTCAAGGCTACAGTGTGCTATGATAGAGCCACTGCACTCCAGCCTGGGCAACCAG  540

Query  541  GTGAGACCTTGTCTCTAAAAATGAATAAATAAAT  573
          ||||||||||||||||||||||||
Sbjct   541  GTGAGACCTTGTCTCTAAAAATGAATAAATAAAT  573
```

Sequence 1355 matched with Sequence 455

Query= Sequence ID 1355
Length=498

SEQ ID NO: 455

ALIGNMENTS

Identities = 498/498 (100%), Gaps = 0/498 (0%)

Query	1	TGGTCTTTCACCCAGCCAGGGAGAAGGTTCTTCGCTCAGTATGAAGAAAAGCAACCCAAA	60
Sbjct	1	TGGTCTTTCACCCAGCCAGGGAGAAGGTTCTTCGCTCAGTATGAAGAAAAGCAACCCAAA	60
Query	61	ACTCTCAATCTGATTTGTTTTGTTTATGTCGATGCCCTGTAGTTTGAAAGTGAAGTAAA	120
Sbjct	61	ACTCTCAATCTGATTTGTTTTGTTTATGTCGATGCCCTGTAGTTTGAAAGTGAAGTAAA	120
Query	121	GATTTAGAATTCACCTAAGTCCAAAGGAAAACACGTGGTTTTTAAAGCCATTAGGTaaaa	180
Sbjct	121	GATTTAGAATTCACCTAAGTCCAAAGGAAAACACGTGGTTTTTAAAGCCATTAGGTAAAA	180
Query	181	aaaGTTCTCAATAAAGGCATTACAATTTTTTAGGTTTAGAAAGATGGACTTTTCTGATAA	240
Sbjct	181	AAAGTTCTCAATAAAGGCATTACAATTTTTTAGGTTTAGAAAGATGGACTTTTCTGATAA	240
Query	241	ATCTTGGCAGACATCTaaaaaaaaaCCATATTTTTTACAAGAAAATGCAAGTTACTttt	300
Sbjct	241	ATCTTGGCAGACATCTAAAAAAAAAAACCATATTTTTTACAAGAAAATGCAAGTTACTTTT	300
Query	301	tttGGAAATAATACTCACTGATTATGGATAAAATGGAATATTTTCAGATACTATATTGGC	360
Sbjct	301	TTTGGAAATAATACTCACTGATTATGGATAAAATGGAATATTTTCAGATACTATATTGGC	360
Query	361	TGTTTCAAATAGTACTATTCTTTAACTTGTAATTTTGCTAAGTTATTTGTCTTTGTT	420
Sbjct	361	TGTTTCAAATAGTACTATTCTTTAACTTGTAATTTTGCTAAGTTATTTGTCTTTGTT	420
Query	421	GTATCTATAAATATGTAAAAAATATTTAAATAGATGTACCTGTTTTGCTTTCACACTTAA	480
Sbjct	421	GTATCTATAAATATGTAAAAAATATTTAAATAGATGTACCTGTTTTGCTTTCACACTTAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAAAAAAtttttttttGT	498
Sbjct	481	TAAAAAATTTTTTTTGT	498

Sequence 1359 matched with Sequence 456

Query= Sequence ID 1359
Length=732

SEQ ID NO: 456

ALIGNMENTS

Identities = 732/732 (100%), Gaps = 0/732 (0%)

Query	1	CGGGATCCCTAGTATAACACATTCAGTGTTCCCCTTTCAGTCTTACTACTTTGACCGCGA	60
Sbjct	1	CGGGATCCCTAGTATAACACATTCAGTGTTCCCCTTTCAGTCTTACTACTTTGACCGCGA	60
Query	61	TGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGA	120
Sbjct	61	TGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGA	120
Query	121	ACATGCTGAGAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGA	180
Sbjct	121	ACATGCTGAGAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGA	180
Query	181	TATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATT	240
Sbjct	181	TATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATT	240
Query	241	ACATTTGGAAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAA	300
Sbjct	241	ACATTTGGAAAAAATGTGAATCAGTCACTACTGGAAGTGCACAACTGGCCACTGACAAA	300
Query	301	AATGACCCCATGTGAGTATTGGAACCCAGGAAATAAATGGAGGAAATCATTTCCTTA	360
Sbjct	301	AATGACCCCATGTGAGTATTGGAACCCAGGAAATAAATGGAGGAAATCATTTCCTTA	360
Query	361	GGGATTGGGAAAGCTGCCACTAACTGTCTTCCCATTGTTTTGCAGTTGTGTGACTTCA	420
Sbjct	361	GGGATTGGGAAAGCTGCCACTAACTGTCTTCCCATTGTTTTGCAGTTGTGTGACTTCA	420
Query	421	TTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGA	480
Sbjct	421	TTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGA	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCAAC TTGCGCAAGATGGGAGCGCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGC	540
Sbjct	481	CCAAC TTGCGCAAGATGGGAGCGCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGC	540
Query	541	ACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCATAGCCGTG	600
Sbjct	541	ACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCATAGCCGTG	600
Query	601	GGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCT	660
Sbjct	601	GGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCT	660
Query	661	ATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTGTACCATTCCCTCAAATAAAG	720
Sbjct	661	ATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTGTACCATTCCCTCAAATAAAG	720
Query	721	AAATTTGGTACC	732
Sbjct	721	AAATTTGGTACC	732

Sequence 1360 matched with Sequence 457

Query= Sequence ID 1360
Length=465

SEQ ID NO: 457

ALIGNMENTS

Identities = 465/465 (100%), Gaps = 0/465 (0%)

Query	1	TGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCAT	60
Sbjct	1	TGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCAT	60
Query	61	GTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGAC	120
Sbjct	61	GTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGAC	120
Query	121	AGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAGC	180
Sbjct	121	AGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAGC	180
Query	181	AGGCGAATCGTAATGAGGCGTGCGCCGCAATATGCACTGTACATTCCACAAGCATTGCC	240
Sbjct	181	AGGCGAATCGTAATGAGGCGTGCGCCGCAATATGCACTGTACATTCCACAAGCATTGCC	240
Query	241	TTCTTATTTTACTTCTTTTAGCTGTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAGT	300
Sbjct	241	TTCTTATTTTACTTCTTTTAGCTGTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAGT	300
Query	301	TTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGCCGCGCCTG	360
Sbjct	301	TTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGCCGCGCCTG	360
Query	361	CCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTGA	420
Sbjct	361	CCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTGA	420
Query	421	AGGAAGAAGTGGGGTGAAGAAGTGGGGTGGGACGACAGTGAAAT	465
Sbjct	421	AGGAAGAAGTGGGGTGAAGAAGTGGGGTGGGACGACAGTGAAAT	465

Sequence 1361 matched with Sequence 458

Query= Sequence ID 1361
Length=788

SEQ ID NO: 458

ALIGNMENTS

Identities = 788/788 (100%), Gaps = 0/788 (0%)

Query	1	TATAAATACACTCCGGGATGATTTACCCCCGAGGTCAGCTAGTAAAATACATGAGTAGA	60
Sbjct	1	TATAAATACACTCCGGGATGATTTACCCCCGAGGTCAGCTAGTAAAATACATGAGTAGA	60
Query	61	ATTCCTTAAAGTATGTGATAATTGCTCATCACTATCCAAGTGTGACATAAAATCATAAAAA	120
Sbjct	61	ATTCCTTAAAGTATGTGATAATTGCTCATCACTATCCAAGTGTGACATAAAATCATAAAAA	120
Query	121	GAATTGACAAAATCAGGGTCGCAAAGAGAATTGaaaaaaTCTGTCACAACCAAAATTTA	180
Sbjct	121	GAATTGACAAAATCAGGGTCGCAAAGAGAATTGAAAAAATCTGTCACAACCAAAATTTA	180
Query	181	AATTGACCTCTGTCCTAGAGTATGAGAGCCCACTGAACAGAAAAACCAGATAAATCTTT	240
Sbjct	181	AATTGACCTCTGTCCTAGAGTATGAGAGCCCACTGAACAGAAAAACCAGATAAATCTTT	240
Query	241	TATAAAATATTCATTTGCAGCCCCATTAACGTTGCTTGTACCCACCTCCCATGTCCT	300
Sbjct	241	TATAAAATATTCATTTGCAGCCCCATTAACGTTGCTTGTACCCACCTCCCATGTCCT	300
Query	301	TGGACAAACTGAATGTATAGTAACATCATCCCAGGCCAGGCGCGGTGGCTCATGCCTGTA	360
Sbjct	301	TGGACAAACTGAATGTATAGTAACATCATCCCAGGCCAGGCGCGGTGGCTCATGCCTGTA	360
Query	361	ATCCCAGCACTTTGTGAGGCTAAGGCAGGCAGATCAGGAGGTCAGGAGTTCAGGACCAGC	420
Sbjct	361	ATCCCAGCACTTTGTGAGGCTAAGGCAGGCAGATCAGGAGGTCAGGAGTTCAGGACCAGC	420
Query	421	CTGGCCAAAAAGGTGAAACTCCGTCTCTACTAACAATACAAAAATTAGCTGGGTGCGGTA	480
Sbjct	421	CTGGCCAAAAAGGTGAAACTCCGTCTCTACTAACAATACAAAAATTAGCTGGGTGCGGTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GTAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTCAAACCCGG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTCAAACCCGG  540

Query  541  AAGGTGGAGGTTGCAGTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AAGGTGGAGGTTGCAGTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGC  600

Query  601  AAGACTCTGTCTCGGGGAGGGGGGTGGCGGAGATAAAGAAATAACATCATCTTATACTGT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  AAGACTCTGTCTCGGGGAGGGGGGTGGCGGAGATAAAGAAATAACATCATCTTATACTGT  660

Query  661  CAAGCTCAAGGTGTCTGCAGCCTTATCTTCAGGGGAAGTTGTGTCTTTCTCAGGGAAGAT  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  CAAGCTCAAGGTGTCTGCAGCCTTATCTTCAGGGGAAGTTGTGTCTTTCTCAGGGAAGAT  720

Query  721  ACAGATTTCAATTTAGAGCAAGACAGAGAGAAGTTACATTGAGAGAGGAAAATGCAGTAG  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721  ACAGATTTCAATTTAGAGCAAGACAGAGAGAAGTTACATTGAGAGAGGAAAATGCAGTAG  780

Query  781  TCTAACTG   788
          |||||||
Sbjct   781  TCTAACTG   788
```

Sequence 1364 matched with Sequence 459

Query= Sequence ID 1364
Length=423

SEQ ID NO: 459

ALIGNMENTS

Identities = 423/423 (100%), Gaps = 0/423 (0%)

Query	1	GCGGCCGCGCTCTTTTCAATTTTAAAAAGAAGTTTGTTCATTTCAGTAATTTCTGC	60
Sbjct	1	GCGGCCGCGCTCTTTTCAATTTTAAAAAGAAGTTTGTTCATTTCAGTAATTTCTGC	60
Query	61	TTTGATCTTCCTTATGTCCTCCTATTGAGTTGATCAGCTTTCTTTATTCTGCCTTTTCT	120
Sbjct	61	TTTGATCTTCCTTATGTCCTCCTATTGAGTTGATCAGCTTTCTTTATTCTGCCTTTTCT	120
Query	121	CCTCTGTGTGCCCTTTCTATTAACGTATTTACCCTTAGGCTGGGCACAAATGGCTGATGCC	180
Sbjct	121	CCTCTGTGTGCCCTTTCTATTAACGTATTTACCCTTAGGCTGGGCACAAATGGCTGATGCC	180
Query	181	TGTAATCCCTGCACCTTTGGGAGGCCGAGGCAGGTGGATCACCTAAGGTCAGGAGTTCAAG	240
Sbjct	181	TGTAATCCCTGCACCTTTGGGAGGCCGAGGCAGGTGGATCACCTAAGGTCAGGAGTTCAAG	240
Query	241	ACCAGCCTGGCCAACATGGTGAAACCTGGTCTCTACTAAAAACACAAAAATTAGCCAGGC	300
Sbjct	241	ACCAGCCTGGCCAACATGGTGAAACCTGGTCTCTACTAAAAACACAAAAATTAGCCAGGC	300
Query	301	ATGGTGGTGTGCACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGA	360
Sbjct	301	ATGGTGGTGTGCACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGA	360
Query	361	ACCTGGGAGGCGGAGATTGTGCCAAAGCACTCCAGCCTGGGCAACAAAAATGAGACTTTGT	420
Sbjct	361	ACCTGGGAGGCGGAGATTGTGCCAAAGCACTCCAGCCTGGGCAACAAAAATGAGACTTTGT	420
Query	421	GTC	423
Sbjct	421	GTC	423

Sequence 1365 matched with Sequence 460

Query= Sequence ID 1365
Length=231

SEQ ID NO: 460

ALIGNMENTS

Identities = 231/231 (100%), Gaps = 0/231 (0%)

Query	1	CACCAGGCTGTCTTCAGATACTTCATACAGAAATGAGCCTCCCTGTGGGGTCCTCTTCCC	60
Sbjct	1	CACCAGGCTGTCTTCAGATACTTCATACAGAAATGAGCCTCCCTGTGGGGTCCTCTTCCC	60
Query	61	TCCTTCAGCCTGTCCATCAACACAGCATTGCGGGATCCTTACCATGGCATCCAGCCCTGG	120
Sbjct	61	TCCTTCAGCCTGTCCATCAACACAGCATTGCGGGATCCTTACCATGGCATCCAGCCCTGG	120
Query	121	AGATGCTTCAGGAAAGTTGCAGGTCCATGCTGCAGGACAGGCTCAGATCAGCAGAGACGC	180
Sbjct	121	AGATGCTTCAGGAAAGTTGCAGGTCCATGCTGCAGGACAGGCTCAGATCAGCAGAGACGC	180
Query	181	ATCTCACATCGGGCTGTGAAATTCAAGTTGAGCTGCAATTGGCAATGAGAA	231
Sbjct	181	ATCTCACATCGGGCTGTGAAATTCAAGTTGAGCTGCAATTGGCAATGAGAA	231

Sequence 1366 matched with Sequence 461

Query= Sequence ID 1366
Length=687

SEQ ID NO: 461

ALIGNMENTS

Identities = 687/687 (100%), Gaps = 0/687 (0%)

Query	1	GTTATTCACTGAGACCGTGCCCCGTTATGAGGTTGTACCAGAAAGCAAGTATTCACTAT	60
Sbjct	1	GTTATTCACTGAGACCGTGCCCCGTTATGAGGTTGTACCAGAAAGCAAGTATTCACTAT	60
Query	61	GCACACTATTACCGCTCACCTAGCATTGAAGCCAGCCTGTAGCCTGAAAGCCTTTGCT	120
Sbjct	61	GCACACTATTACCGCTCACCTAGCATTGAAGCCAGCCTGTAGCCTGAAAGCCTTTGCT	120
Query	121	TTGAGGGCAGGTCTTTCCCCAAAATGCAGACACGAAGGTGCAAAGTGAAGCTGCCAGTCT	180
Sbjct	121	TTGAGGGCAGGTCTTTCCCCAAAATGCAGACACGAAGGTGCAAAGTGAAGCTGCCAGTCT	180
Query	181	TGCAAAAGATGTAACTTGTACGAAGGCCACGAGTGGCAGGGAGAGCTGTCCACATTTG	240
Sbjct	181	TGCAAAAGATGTAACTTGTACGAAGGCCACGAGTGGCAGGGAGAGCTGTCCACATTTG	240
Query	241	CGGAAGTGGCTATGTGAGGACGGGGGAGGCGGGTCCCTTAGAGATGAGACAATCATAAGG	300
Sbjct	241	CGGAAGTGGCTATGTGAGGACGGGGGAGGCGGGTCCCTTAGAGATGAGACAATCATAAGG	300
Query	301	GGAGATATCAGAGAAAATCGTAAGGGGAGCAGATGGTTGTCAAGAGAATAGGCTGACCAT	360
Sbjct	301	GGAGATATCAGAGAAAATCGTAAGGGGAGCAGATGGTTGTCAAGAGAATAGGCTGACCAT	360
Query	361	CGAAGGACTGGCAGAAGCTTTCAGAAAACCACTGGACGGCTGGGCACAGTGGCTTAGGCC	420
Sbjct	361	CGAAGGACTGGCAGAAGCTTTCAGAAAACCACTGGACGGCTGGGCACAGTGGCTTAGGCC	420
Query	421	TGTAATCCCAGCACTTTGGGAGGCTGACGCAGGTGAATCACTTGAGGTCAGGAGTTCCAG	480
Sbjct	421	TGTAATCCCAGCACTTTGGGAGGCTGACGCAGGTGAATCACTTGAGGTCAGGAGTTCCAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	ACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACAGAAAATATAAAAAATTAGCCAGGC	540
Sbjct	481	ACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACAGAAAATATAAAAAATTAGCCAGGC	540
Query	541	GTGGTGGCACAAGCCTAGAATCCCAGCTACTTGGGAGGCTGAGGCAGGCGAATGGCTTGA	600
Sbjct	541	GTGGTGGCACAAGCCTAGAATCCCAGCTACTTGGGAGGCTGAGGCAGGCGAATGGCTTGA	600
Query	601	ACCCAGGAGTCAGAGGCTGCAGTGAGTCGAGATTGTTCCACTGCACTCCAGCCTGGGTGA	660
Sbjct	601	ACCCAGGAGTCAGAGGCTGCAGTGAGTCGAGATTGTTCCACTGCACTCCAGCCTGGGTGA	660
Query	661	CAGTGCAAGACTCCTTCCaaaaaaaaa	687
Sbjct	661	CAGTGCAAGACTCCTTCCAAAAAAAAA	687

Sequence 1367 matched with Sequence 462

Query= Sequence ID 1367
Length=874

SEQ ID NO: 462

ALIGNMENTS

Identities = 874/874 (100%), Gaps = 0/874 (0%)

Query	1	TTCGTGAGTGATGGCGTCCCGGGTTGCTTGCCGGTGCTGGCCGCCGCCGGGAGAGCCCGG	60
Sbjct	1	TTCGTGAGTGATGGCGTCCCGGGTTGCTTGCCGGTGCTGGCCGCCGCCGGGAGAGCCCGG	60
Query	61	GGCAGAGCAGAGGTGCTCATCAGCACTGTAGGCCCGGAAGATTGTGTGGTCCCGTTCCCTG	120
Sbjct	61	GGCAGAGCAGAGGTGCTCATCAGCACTGTAGGCCCGGAAGATTGTGTGGTCCCGTTCCCTG	120
Query	121	ACCCGGCCTAAGGTCCCTGTCTTGACAGCTGGATAGCGGCAACTACCTCTTCTCCACTAGT	180
Sbjct	121	ACCCGGCCTAAGGTCCCTGTCTTGACAGCTGGATAGCGGCAACTACCTCTTCTCCACTAGT	180
Query	181	GCAATCTGCCGATAttttttttGTTATCTGGCTGGGAGCAAGATGACCTCACTAACCAG	240
Sbjct	181	GCAATCTGCCGATATTTTTTTTGTATCTGGCTGGGAGCAAGATGACCTCACTAACCAG	240
Query	241	TGGCTGGAATGGGAAGCGACAGAGCTGCAGCCAGCTTTGTCTGCTGCCCTGTACTATTTA	300
Sbjct	241	TGGCTGGAATGGGAAGCGACAGAGCTGCAGCCAGCTTTGTCTGCTGCCCTGTACTATTTA	300
Query	301	GTGGTCCAAGGCAAGAAGGGGGAAGATGTTCTTGTTTCAGTGCGGAGAGCCCTGACTCAC	360
Sbjct	301	GTGGTCCAAGGCAAGAAGGGGGAAGATGTTCTTGTTTCAGTGCGGAGAGCCCTGACTCAC	360
Query	361	ATTGACCACAGCTTGAGTCGTCAGAACTGTCCTTTCCTGGCTGGGGAGACAGAATCTCTA	420
Sbjct	361	ATTGACCACAGCTTGAGTCGTCAGAACTGTCCTTTCCTGGCTGGGGAGACAGAATCTCTA	420
Query	421	GGCGACATTGTTTTGTGGGGAGCCCTATACCCATTACTGCAAGATCCCGCCTACCTCCCT	480
Sbjct	421	GGCGACATTGTTTTGTGGGGAGCCCTATACCCATTACTGCAAGATCCCGCCTACCTCCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GAGGAGCTGAGTGCCCTGCACAGCTGGTTCCAGACACTGAGTACCCAGGAACCATGTCAG	540
Sbjct	481	GAGGAGCTGAGTGCCCTGCACAGCTGGTTCCAGACACTGAGTACCCAGGAACCATGTCAG	540
Query	541	CGAGCTGCAGAGACTGTACTGAAACAGCAAGGTGTCCTGGCTCTCCGGCCTTACCTCCAA	600
Sbjct	541	CGAGCTGCAGAGACTGTACTGAAACAGCAAGGTGTCCTGGCTCTCCGGCCTTACCTCCAA	600
Query	601	AAGCAGCCCCAGCCCAGCCCCGCTGAGGGAAGGGCTGTCACCAATGAGCCTGAGGAGGAG	660
Sbjct	601	AAGCAGCCCCAGCCCAGCCCCGCTGAGGGAAGGGCTGTCACCAATGAGCCTGAGGAGGAG	660
Query	661	GAGCTGGCTACCCTATCTGAGGAGGAGATTGCTATGGCTGTTACTGCTTGGGAGAANGGC	720
Sbjct	661	GAGCTGGCTACCCTATCTGAGGAGGAGATTGCTATGGCTGTTACTGCTTGGGAGAANGGC	720
Query	721	CTAGAAAGTTTTGCCCCCGCTGCGGCCCCAGCANAATCCAGTGTGCTGTGGCTGGAGA	780
Sbjct	721	CTAGAAAGTTTTGCCCCCGCTGCGGCCCCAGCANAATCCAGTGTGCTGTGGCTGGAGA	780
Query	781	AAGGAATGTGCTCATCACCAGTGCCCTCCNTTACGTCAACAATGTCCCCACCTTGGGAA	840
Sbjct	781	AAGGAATGTGCTCATCACCAGTGCCCTCCNTTACGTCAACAATGTCCCCACCTTGGGAA	840
Query	841	CATCATTGGTTGTGTGCTCAGTGCCCGATGTCTT	874
Sbjct	841	CATCATTGGTTGTGTGCTCAGTGCCCGATGTCTT	874

Sequence 1368 matched with Sequence 463

Query= Sequence ID 1368
Length=585

SEQ ID NO: 463

ALIGNMENTS

Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query	1	CAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGACAACAGAACGAGACTCCATATC	60
Sbjct	1	CAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGACAACAGAACGAGACTCCATATC	60
Query	61	aaaaaaattaaattaaaatataataaatTTCTTGCCGGGCGCAGTGGCTCACACCTGTAA	120
Sbjct	61	AAAAAAATTAAATTAAAAATATAATAAATTTCTTGCCGGGCGCAGTGGCTCACACCTGTAA	120
Query	121	TCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGACCATCC	180
Sbjct	121	TCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGACCATCC	180
Query	181	TGGCTAATACAGTGAAACCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGCATGGTG	240
Sbjct	181	TGGCTAATACAGTGAAACCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGCATGGTG	240
Query	241	GCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGAACCCGG	300
Sbjct	241	GCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGAACCCGG	300
Query	301	GAGGCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAGCAGAAC	360
Sbjct	301	GAGGCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAGCAGAAC	360
Query	361	GAGACTCCATCTCaaataaataaataaataaaatGAATTTTCAGCTAGAAGAGCCTTATTC	420
Sbjct	361	GAGACTCCATCTCAAATAAAATAAATAAAATGAATTTTCAGCTAGAAGAGCCTTATTC	420
Query	421	CATTTTCCTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTATCATATA	480
Sbjct	421	CATTTTCCTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTATCATATA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  TTCTTATGCGAATTATTATTTTCGCCtttttttttATAATTCTGTCTGGGATTTGAATAG  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TTCTTATGCGAATTATTATTTTCGCCTTTTTTTTTATAATTCTGTCTGGGATTTGAATAG  540

Query  541  TAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAAT  585
          |||||||||||||||||||||||||||||||||||||||
Sbjct   541  TAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAAT  585
```

Sequence 1369 matched with Sequence 464

Query= Sequence ID 1369
Length=305

SEQ ID NO: 464

ALIGNMENTS

Identities = 305/305 (100%), Gaps = 0/305 (0%)

```
Query  1      CTGATTGCAAAAACATTACAACCTCAGTACTGCGGCTTTCATTCAAATAGGTTATATGTAT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      CTGATTGCAAAAACATTACAACCTCAGTACTGCGGCTTTCATTCAAATAGGTTATATGTAT  60

Query  61     AAAGTGAAGTTCAACAATATTGTATTTGAGATGGGAAAGTTAAAGAAATGCAATAATGTA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61     AAAGTGAAGTTCAACAATATTGTATTTGAGATGGGAAAGTTAAAGAAATGCAATAATGTA  120

Query  121    AATAATACTTAAGAAAATAAGATCTCAGGAAACTGTGTATACTCTGTACTTTTATGCAAC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121    AATAATACTTAAGAAAATAAGATCTCAGGAAACTGTGTATACTCTGTACTTTTATGCAAC  180

Query  181    TTTATCAGATCATTTTCAGTATATGCATCAAGGATATAGTGTATATGACATGAACCTTTGAG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181    TTTATCAGATCATTTTCAGTATATGCATCAAGGATATAGTGTATATGACATGAACCTTTGAG  240

Query  241    TGCAAAAACCTGTACTATGTACCTTTTGTTTATTTTGCTGTCAACATCTAAATAAAGGttt  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241    TGCAAAAACCTGTACTATGTACCTTTTGTTTATTTTGCTGTCAACATCTAAATAAAGGTTT  300

Query  301    ttttG  305
          ||||
Sbjct  301    TTTTG  305
```

Sequence 1370 matched with Sequence 465

Query= Sequence ID 1370
Length=422

SEQ ID NO: 465

ALIGNMENTS

Identities = 422/422 (100%), Gaps = 0/422 (0%)

Query	1	CGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA	60
Sbjct	1	CGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA	60
Query	61	TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAAATAATTT	120
Sbjct	61	TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAAATAATTT	120
Query	121	GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG	180
Sbjct	121	GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG	180
Query	181	ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA	240
Sbjct	181	ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA	240
Query	241	ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAG	300
Sbjct	241	ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAG	300
Query	301	TGGAAAACTGGAAGACAGAAGTACGGGAAGGCgaagaaaagaatagataagatagggaaa	360
Sbjct	301	TGGAAAACTGGAAGACAGAAGTACGGGAAGGCGAAGAAAAGAATAGATAAGATAGGGAAA	360
Query	361	ttagaagataaaaaacatacttttagaagaaaaaagataaaTTTAAACCTGAAAAGTAGGA	420
Sbjct	361	TTAGAAGATAAAAAACATACTTTTAGAAGAAAAAAGATAAATTTAAACCTGAAAAGTAGGA	420
Query	421	AG 422	
Sbjct	421	AG 422	

Sequence 1371 matched with Sequence 466

Query= Sequence ID 1371
Length=833

SEQ ID NO: 466

ALIGNMENTS

Identities = 833/833 (100%), Gaps = 0/833 (0%)

Query	1	GTCCAGNAGAAAGTTCAGTGACTTGTCCAGAGCTGCAGGTCTTAAGAGGCTGAAATCTCG	60
Sbjct	1	GTCCAGNAGAAAGTTCAGTGACTTGTCCAGAGCTGCAGGTCTTAAGAGGCTGAAATCTCG	60
Query	61	CCTCTGCCTCGAGGCTGCGGTTCCACTGACCCATACTACTTGCCTTCAGGAAAGAGAAAT	120
Sbjct	61	CCTCTGCCTCGAGGCTGCGGTTCCACTGACCCATACTACTTGCCTTCAGGAAAGAGAAAT	120
Query	121	GGTGTAGGAAGGCTGTGGATGAAGACGCTTACATTCATGAAGGATTTGGATAGGCGAACA	180
Sbjct	121	GGTGTAGGAAGGCTGTGGATGAAGACGCTTACATTCATGAAGGATTTGGATAGGCGAACA	180
Query	181	TGAGCTTTTCCACCAAATTTTCAAGAAATGCCTTAAATTATTTCTTAAAAATC	240
Sbjct	181	TGAGCTTTTCCACCAAATTTTCAAGAAATGCCTTAAATTATTTCTTAAAAATC	240
Query	241	AATTTGGGGCAGACGAGAAGTTCTGATAATAGTTTTAGGGAACATGATAAAATTCTGAC	300
Sbjct	241	AATTTGGGGCAGACGAGAAGTTCTGATAATAGTTTTAGGGAACATGATAAAATTCTGAC	300
Query	301	CTTAGAAGTGGTATACCAGTTTGAGAAGAAGAACAAGCTATAAACGGTGTAGATAACATT	360
Sbjct	301	CTTAGAAGTGGTATACCAGTTTGAGAAGAAGAACAAGCTATAAACGGTGTAGATAACATT	360
Query	361	CACGGCTATTTAAGAAAGAGTTACTAAGGGAAACCAGAATGACTTAAGAGTGTTACTCTT	420
Sbjct	361	CACGGCTATTTAAGAAAGAGTTACTAAGGGAAACCAGAATGACTTAAGAGTGTTACTCTT	420
Query	421	CTTTTCTGAGAGAACAATAGCATCATCTCAGAAAGCCTTTCATGCCATTAATAGGTAAG	480
Sbjct	421	CTTTTCTGAGAGAACAATAGCATCATCTCAGAAAGCCTTTCATGCCATTAATAGGTAAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	AATCTGGGCTTCTTGGACCATGGGTTAGACTTTCTTACAAAACCATAATATGCATTTTCCT	540
Sbjct	481	AATCTGGGCTTCTTGGACCATGGGTTAGACTTTCTTACAAAACCATAATATGCATTTTCCT	540
Query	541	AGCAAAATTTATGCTATTACATTTCTTATCTCAACAAAGACTGGTAAATTCAGTACTTA	600
Sbjct	541	AGCAAAATTTATGCTATTACATTTCTTATCTCAACAAAGACTGGTAAATTCAGTACTTA	600
Query	601	TTCCTCAATTTTCCTACCCTTAAAATGGGGATATTCTGCCTCTCCAAGGAATGCTGGGAA	660
Sbjct	601	TTCCTCAATTTTCCTACCCTTAAAATGGGGATATTCTGCCTCTCCAAGGAATGCTGGGAA	660
Query	661	CAAGCAAGTCCTCATGTTAGGGGTCTTTGAGTTTTTCATGGAAGTTTAGGTTATTTATATG	720
Sbjct	661	CAAGCAAGTCCTCATGTTAGGGGTCTTTGAGTTTTTCATGGAAGTTTAGGTTATTTATATG	720
Query	721	ATGACATAGTTGTCAACTTACTTTTCAGGATGGACTTTTCTTTTGTGAGTTTGTGACCTAA	780
Sbjct	721	ATGACATAGTTGTCAACTTACTTTTCAGGATGGACTTTTCTTTTGTGAGTTTGTGACCTAA	780
Query	781	ATACAATAGTTGTTATGCATGTCCAGTTTATGGAAGTACCACTGCAATANCAG	833
Sbjct	781	ATACAATAGTTGTTATGCATGTCCAGTTTATGGAAGTACCACTGCAATANCAG	833

Sequence 1372 matched with Sequence 467

Query= Sequence ID 1372
Length=594

SEQ ID NO: 467

ALIGNMENTS

Identities = 594/594 (100%), Gaps = 0/594 (0%)

Query	1	CAGTGCAGCCAAGTATCACACCACTGCACTCCAGTCCTGGACAACAGAAACGANTACTCC	60
Sbjct	1	CAGTGCAGCCAAGTATCACACCACTGCACTCCAGTCCTGGACAACAGAAACGANTACTCC	60
Query	61	ATATCaaaaaaaTTAAATTAAANGATAATAAATTTCTTGCCGGGCGCAGTGGCTCACACC	120
Sbjct	61	ATATCAAAAAAATTAAATTAAANGATAATAAATTTCTTGCCGGGCGCAGTGGCTCACACC	120
Query	121	TGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGAC	180
Sbjct	121	TGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGAC	180
Query	181	CATCCTGGCTAATACAGTGAAATCCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGC	240
Sbjct	181	CATCCTGGCTAATACAGTGAAATCCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGC	240
Query	241	ATGGTGGCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGA	300
Sbjct	241	ATGGTGGCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGA	300
Query	301	ACCCGGGAGGCGGAGCTTGCACTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAG	360
Sbjct	301	ACCCGGGAGGCGGAGCTTGCACTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAG	360
Query	361	CAGAACGAGACTCCATCTCaaataaataaataaataaaatGAATTTTCAGCTAGAAGAGCC	420
Sbjct	361	CAGAACGAGACTCCATCTCAAAATAAATAAATAAATAAAATGAATTTTCAGCTAGAAGAGCC	420
Query	421	TTATTCCATTTTCCTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTAT	480
Sbjct	421	TTATTCCATTTTCCTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTAT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CATATATTCTTATGCGAATTATTATTTTCGCCtttttttttATAATTCTGTCTGGGATTT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CATATATTCTTATGCGAATTATTATTTTCGCCTTTTTTTTTATAATTCTGTCTGGGATTT  540

Query  541  GAATAGTAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAATCTA  594
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GAATAGTAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAATCTA  594
```

Sequence 1374 matched with Sequence 468

Query= Sequence ID 1374
Length=112

SEQ ID NO: 468

ALIGNMENTS

Identities = 112/112 (100%), Gaps = 0/112 (0%)

Query	1	GAAAGCACATATGATATACATGTGTGTCATATGTATTATTTTGTGGCCATCTGAGTCTT	60
Sbjct	1	GAAAGCACATATGATATACATGTGTGTCATATGTATTATTTTGTGGCCATCTGAGTCTT	60
Query	61	CAAAATTTGTTACAGAATACCTGCATATTAATATTTCAAGGTATGGATTAAT	112
Sbjct	61	CAAAATTTGTTACAGAATACCTGCATATTAATATTTCAAGGTATGGATTAAT	112

Sequence 1378 matched with Sequence 469

BLASTN 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Sequence ID 1378
Length=40

SEQ ID NO: 469

79.8 1e-21

ALIGNMENTS

Identities = 40/40 (100%), Gaps = 0/40 (0%)

Query	1	CTGAGTATTA	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	40
Sbjct	1	CTGAGTATTA	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	40

Sequence 1380 matched with Sequence 470

Query= Sequence ID 1380
Length=933

SEQ ID NO: 470

ALIGNMENTS

Identities = 933/933 (100%), Gaps = 0/933 (0%)

Query	1	CCAAACCCAAGTGGTCCAGTAGGATACTCACCTTACAGGGGCGTCTCAAGAGTCTCACA	60
Sbjct	1	CCAAACCCAAGTGGTCCAGTAGGATACTCACCTTACAGGGGCGTCTCAAGAGTCTCACA	60
Query	61	GTTCCCTTGGGTCTTAAGAGACTCACTGTTGGACCAGGCGTGGTGACTCACGCCTGTAAA	120
Sbjct	61	GTTCCCTTGGGTCTTAAGAGACTCACTGTTGGACCAGGCGTGGTGACTCACGCCTGTAAA	120
Query	121	ACCAGCACTTTGGGAGGCCGAGGCGGGCGGATCAGTTGAGGTCAAGAGTTCAAGACCAGC	180
Sbjct	121	ACCAGCACTTTGGGAGGCCGAGGCGGGCGGATCAGTTGAGGTCAAGAGTTCAAGACCAGC	180
Query	181	CTGACCAAGGTGCTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTG	240
Sbjct	181	CTGACCAAGGTGCTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTG	240
Query	241	GTGTGCGCCTGTAATCCCAGCTACTCCAGAGGCTGAGGCAGGAGAATCTCTTGAACCCAG	300
Sbjct	241	GTGTGCGCCTGTAATCCCAGCTACTCCAGAGGCTGAGGCAGGAGAATCTCTTGAACCCAG	300
Query	301	GAGGTGGAGGTTGCAGTGAGTCGAGATCATGCCACTGCACTCCAGCCTGGGTGACAGAGC	360
Sbjct	301	GAGGTGGAGGTTGCAGTGAGTCGAGATCATGCCACTGCACTCCAGCCTGGGTGACAGAGC	360
Query	361	GAGACTCCGTCTTAGAAAAAAAAAAAAAAAAAAAAAAGAACCTCACAGTTCAGCAGGGTTC	420
Sbjct	361	GAGACTCCGTCTTAGAAAAAAAAAAAAAAAAAAAAAAGAACCTCACAGTTCAGCAGGGTTC	420
Query	421	TAGCATGAGACAATGAGGACAAGGGTAGGTGAGCAGGTGAAAGAGTGAGAACAGGTCAA	480
Sbjct	421	TAGCATGAGACAATGAGGACAAGGGTAGGTGAGCAGGTGAAAGAGTGAGAACAGGTCAA	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTGTGATGGAGAAAATAATAAAGACAGAAAAGGCAGAAGACTGCCTGGCAGAAGACCTGT	540
Sbjct	481	TTGTGATGGAGAAAATAATAAAGACAGAAAAGGCAGAAGACTGCCTGGCAGAAGACCTGT	540
Query	541	CCCAGCAGATACAAAAATACAGACAACAGGAGCCAGCATAGACCCTTGACCTGTGTAAGT	600
Sbjct	541	CCCAGCAGATACAAAAATACAGACAACAGGAGCCAGCATAGACCCTTGACCTGTGTAAGT	600
Query	601	CTTTCTCAGGCCTTCTTTTAAAGTAGAAACATGCCTTTGaaaaaaGTTTAAATAAACAGG	660
Sbjct	601	CTTTCTCAGGCCTTCTTTTAAAGTAGAAACATGCCTTTGAAAAAAGTTTAAATAAACAGG	660
Query	661	AAAATCATAAATCCCTATTTACATAAATAATATATCCTGGTCTTATTCTTAAACCATTG	720
Sbjct	661	AAAATCATAAATCCCTATTTACATAAATAATATATCCTGGTCTTATTCTTAAACCATTG	720
Query	721	ATTTTTCACGGCTCATTAANAAAGCTGGGCGAGGTGGCTCACGCCCCTCATCCTAGCACT	780
Sbjct	721	ATTTTTCACGGCTCATTAANAAAGCTGGGCGAGGTGGCTCACGCCCCTCATCCTAGCACT	780
Query	781	TTGGGAGGCCGAGGCGGGCANATCACAAGGTGAGGAGTTGGGAGACCAGCCTGACCAACA	840
Sbjct	781	TTGGGAGGCCGAGGCGGGCANATCACAAGGTGAGGAGTTGGGAGACCAGCCTGACCAACA	840
Query	841	CGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTANCTGGGGGTGGTGGTGTGTGCCT	900
Sbjct	841	CGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTANCTGGGGGTGGTGGTGTGTGCCT	900
Query	901	GTAATCCAAGCTACTCGGGAGGCTGAGGCAGGA	933
Sbjct	901	GTAATCCAAGCTACTCGGGAGGCTGAGGCAGGA	933

Sequence 1382 matched with Sequence 471

Query= Sequence ID 1382
Length=896

SEQ ID NO: 471

ALIGNMENTS

Identities = 896/896 (100%), Gaps = 0/896 (0%)

Query	1	CTTACTACCTCCAACATGAAACAAGCAGCCCCGCACTTCTCGAAGGTCTGAGTTACTTGG	60
Sbjct	1	CTTACTACCTCCAACATGAAACAAGCAGCCCCGCACTTCTCGAAGGTCTGAGTTACTTGG	60
Query	61	AATCGTTTTACCACATGATGGACAGAAGGAATATTTTCAGATATCTCTGAAAACCTCAAGC	120
Sbjct	61	AATCGTTTTACCACATGATGGACAGAAGGAATATTTTCAGATATCTCTGAAAACCTCAAGC	120
Query	121	GTTACCTTCTTCAGTATTTTAAGCCAGTGATTGACAGGCAAAGCTGGAGTGACAAGGGCT	180
Sbjct	121	GTTACCTTCTTCAGTATTTTAAGCCAGTGATTGACAGGCAAAGCTGGAGTGACAAGGGCT	180
Query	181	CAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCCTGTGACCTGAACCATG	240
Sbjct	181	CAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCCTGTGACCTGAACCATG	240
Query	241	CTCCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCCAGTGGATGGAATCCAGTGGAAAAAT	300
Sbjct	241	CTCCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCCAGTGGATGGAATCCAGTGGAAAAAT	300
Query	301	TAAATATACCAACAGATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAGACAACAGCAG	360
Sbjct	301	TAAATATACCAACAGATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAGACAACAGCAG	360
Query	361	GATGGAATTACCTTTTAGAGCAATATGAACTGTCAATGTCAAGTGCTGAACAAAACAAAA	420
Sbjct	361	GATGGAATTACCTTTTAGAGCAATATGAACTGTCAATGTCAAGTGCTGAACAAAACAAAA	420
Query	421	TTCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAGTTACTGAAGTTAATTGAACTAG	480
Sbjct	421	TTCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAGTTACTGAAGTTAATTGAACTAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	GAATGGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCATGCGATTGCCA	540
Sbjct	481	GAATGGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCATGCGATTGCCA	540
Query	541	GACGTCCAAAGGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAAATTGGACCCATCTTC	600
Sbjct	541	GACGTCCAAAGGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAAAATTGGACCCATCTTC	600
Query	601	TGAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGCACAACAGCTC	660
Sbjct	601	TGAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGCACAACAGCTC	660
Query	661	ACTTTTCTTCCAAGGATAAGTTGCAAGAGGTGAACTATTTTTTGAATCTCTTGAGGCTC	720
Sbjct	661	ACTTTTCTTCCAAGGATAAGTTGCAAGAGGTGAACTATTTTTTGAATCTCTTGAGGCTC	720
Query	721	AAGGATCACATCTGGATATTTTCAAACGTCTGGAAACGATAACCAAAAAATATAAAAT	780
Sbjct	721	AAGGATCACATCTGGATATTTTCAAACGTCTGGAAACGATAACCAAAAAATATAAAAT	780
Query	781	GGCTGGAGAAGAATCTTCCGACTCTGAGGACTTGGCTAATGGTTAACTTAAATGGTCA	840
Sbjct	781	GGCTGGAGAAGAATCTTCCGACTCTGAGGACTTGGCTAATGGTTAACTTAAATGGTCA	840
Query	841	ATAGAAAAAGTAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGA	896
Sbjct	841	ATAGAAAAAGTAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGA	896

SEQ ID NO: 472

Identities = 158/158 (100%), Gaps = 0/158 (0%)

Query	1	AAAAAttt	60
Sbjct	1	AAAAATTT	60
Query	61	ttCAGTGTAAAGT	120
Sbjct	61	TTCAGTGTAAAGT	120
Query	121	AGGTTTGTGCGACGCGGCCACGAATTTCCCGGGGACCAA	158
Sbjct	121	AGGTTTGTGCGACGCGGCCACGAATTTCCCGGGGACCAA	158

Sequence 1389 matched with Sequence 473

Query= Sequence ID 1389
Length=896

SEQ ID NO: 473

ALIGNMENTS

Identities = 896/896 (100%), Gaps = 0/896 (0%)

Query	1	tttttttttttttttgggagtcagttttcttttcttttcttttctttttttttttgntt	60
Sbjct	1	TTTTTTTTTTTTTTTTGGGAGTCAGTTTTCTTTCTTTCTTTCTTTCTTTTTTTTTTTTGNTT	60
Query	61	ttCGGAAACGGAGTCTCGCTTCTCGCCCACTCTGGAGTGGNGCAGTGGGGNGGTCTCAG	120
Sbjct	61	TTCGGAAACGGAGTCTCGCTTCTCGCCCACTCTGGAGTGGNGCAGTGGGGNGGTCTCAG	120
Query	121	CTCACCACAGCCTCCACCTCCTGGGCCCAAGCGATCCTNTCACCTCAGCCTCCTGCGTAG	180
Sbjct	121	CTCACCACAGCCTCCACCTCCTGGGCCCAAGCGATCCTNTCACCTCAGCCTCCTGCGTAG	180
Query	181	CTGGGACTACAGGCGTGCAACCACCATTTCCAGGTAATTTTTGTATTTTTGTANANACAG	240
Sbjct	181	CTGGGACTACAGGCGTGCAACCACCATTTCCAGGTAATTTTTGTATTTTTGTANANACAG	240
Query	241	GGTTTCACTGTTGTTGCCCAGGCTGGTCTCGAACTCCTGCTTCAGTCTGCCANAATGCTG	300
Sbjct	241	GGTTTCACTGTTGTTGCCCAGGCTGGTCTCGAACTCCTGCTTCAGTCTGCCANAATGCTG	300
Query	301	GATTCTAGGCGTGAGCCACCGNGCCTGGCCCAAAAGTTACTTTTCTTACAGAAGCAAAGC	360
Sbjct	301	GATTCTAGGCGTGAGCCACCGNGCCTGGCCCAAAAGTTACTTTTCTTACAGAAGCAAAGC	360
Query	361	TTTAATGCATTTTACTGAATGCTTATAGCTTTGTAGATACTGAAAAGAGTATGAGCGTCA	420
Sbjct	361	TTTAATGCATTTTACTGAATGCTTATAGCTTTGTAGATACTGAAAAGAGTATGAGCGTCA	420
Query	421	CATACAGACACATNTAACAGCACTGCCTCCAACCAGCCCCTACCCACTGGTCAGGNGAGT	480
Sbjct	421	CATACAGACACATNTAACAGCACTGCCTCCAACCAGCCCCTACCCACTGGTCAGGNGAGT	480

PATENT SEQUENCE ALIGNMENT

```

Query  481  AANAATCAAAATTCTTTTCTGNGAGTGGAACGGAAATTTTCATCTCTCCTCCTCAGGCAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AANAATCAAAATTCTTTTCTGNGAGTGGAACGGAAATTTTCATCTCTCCTCCTCAGGCAAG  540

Query  541  TAGTTAANAGGCTGGNGGGAGTCATGGCCCCATTTTGTTCAAAATACAAGCTCCACAGGA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TAGTTAANAGGCTGGNGGGAGTCATGGCCCCATTTTGTTCAAAATACAAGCTCCACAGGA  600

Query  601  ACAAAGGCTGAACTGCTCACCTCCCAACTGATGAACCTCGTCTTTGTTCCATGTCAAAG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  ACAAAGGCTGAACTGCTCACCTCCCAACTGATGAACCTCGTCTTTGTTCCATGTCAAAG  660

Query  661  GGGCCTTTGTGTTACTGCAGCAGAACTCCAGCTATCAAACCATCAGGCACCAAAAGTAA  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  GGGCCTTTGTGTTACTGCAGCAGAACTCCAGCTATCAAACCATCAGGCACCAAAAGTAA  720

Query  721  AACTCCTTTCTCTAAAAAGACCTCTCTTTACCTGAGCCTTTCAATGCATCTTTGCCCCCA  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721  AACTCCTTTCTCTAAAAAGACCTCTCTTTACCTGAGCCTTTCAATGCATCTTTGCCCCCA  780

Query  781  NATAATCCTGGATGAGATAATCCCCAGAGGAANACCAGCGCTTGCCTAGTGAAATTATAC  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   781  NATAATCCTGGATGAGATAATCCCCAGAGGAANACCAGCGCTTGCCTAGTGAAATTATAC  840

Query  841  TATGAGACAAGGGTAAAAGACCTCAAANACCGGGTTGGCAGGTAAGGGAGTAGGGN  896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   841  TATGAGACAAGGGTAAAAGACCTCAAANACCGGGTTGGCAGGTAAGGGAGTAGGGN  896

```

Blast comparison trimmed “N” from the 3’ end of both sequences and reported 895 identities. The report has been manually corrected for this. “N” has been appended to both sequences and identity count has been increased to 896.

Sequence 1390 matched with Sequence 474

Query= Sequence ID 1390
Length=350

SEQ ID NO: 474

ALIGNMENTS

Identities = 350/350 (100%), Gaps = 0/350 (0%)

```
Query 1 TCNGTGGCACCCGTTTCCGGCACCTTCAGACTCTGAAGAGCCACCTGCGAATCCACACAGGAG 63
|||||
Sbjct 1 TCNGTGGCACCCGTTTCCGGCACCTTCAGACTCTGAAGAGCCACCTGCGAATCCACACAGGAG 63

Query 64 AGAAACCTTACCATGTACGTAAGCCTCTTGAGGCCGCTCTCTGACCTGCggggatgtgga 123
|||||
Sbjct 64 AGAAACCTTACCATGTACGTAAGCCTCTTGAGGCCGCTCTCTGACCTGCGGGGATGTGGA 123

Query 124 gggcagggaaggaggtggagcgcagggaaggaggtggagcaggaggcagtggaACTGTT 183
|||||
Sbjct 124 GGGCAGGGAAGGAGGTGGAGCGCAGGGAAGGAGGTGGAGCAGGGAGGCACTGGAAGTGT 183

Query 184 TGCTCCCATCTCAAGCACACAGTGGGGCAACCACTACGCTAATGGTTGGAAGACCTAGAT 243
|||||
Sbjct 184 TGCTCCCATCTCAAGCACACAGTGGGGCAACCACTACGCTAATGGTTGGAAGACCTAGAT 243

Query 244 CTGGGCCCAATGGCCAGACACCCTGCTTGACCTTGGCCCAAGCATTAGGGGACTCATCTT 303
|||||
Sbjct 244 CTGGGCCCAATGGCCAGACACCCTGCTTGACCTTGGCCCAAGCATTAGGGGACTCATCTT 303

Query 304 TAAAATGAGGGTATGGGACTAGATGATCTGGGCCTTAGGAGAGGAGT 350
|||||
Sbjct 304 TAAAATGAGGGTATGGGACTAGATGATCTGGGCCTTAGGAGAGGAGT 350
```

Blast comparison trimmed “TCN” from the 5’ end of both sequences and reported 347 identities. The report has been manually corrected for this. “TCN” has been prepended to both sequences and identity count has been increased to 350.

Sequence 1391 matched with Sequence 475

Query= Sequence ID 1391
Length=835

SEQ ID NO: 475

ALIGNMENTS

Identities = 835/835 (100%), Gaps = 0/835 (0%)

Query	1	CGGCTNCTACCCTGCGGAGATCACACTGACCTGGCAGTGGGATGGGGAGGACCAAACTCA	60
Sbjct	1	CGGCTNCTACCCTGCGGAGATCACACTGACCTGGCAGTGGGATGGGGAGGACCAAACTCA	60
Query	61	GGACACCGAGCTTGTGGAGACCAGGCCAGCAGGAGATGGAACCTTCCAGAAGTGGGCAGC	120
Sbjct	61	GGACACCGAGCTTGTGGAGACCAGGCCAGCAGGAGATGGAACCTTCCAGAAGTGGGCAGC	120
Query	121	TGTGGTGGTGCCTTCTGGAGAAGAGCAGAGATACACGTGCCATGTTTCAGCACGAGGGGCT	180
Sbjct	121	TGTGGTGGTGCCTTCTGGAGAAGAGCAGAGATACACGTGCCATGTTTCAGCACGAGGGGCT	180
Query	181	GCCGGAGCCCCTCACCTGAGATGGAAGCCGTCTTCCCAGCCCACCATCCCCATCGTGGG	240
Sbjct	181	GCCGGAGCCCCTCACCTGAGATGGAAGCCGTCTTCCCAGCCCACCATCCCCATCGTGGG	240
Query	241	CATCGTTGCTGGCCTGGCTGTCCTGGCTGTCCTAGCTGTCCTAGGAGCTATGGTGGCTGT	300
Sbjct	241	CATCGTTGCTGGCCTGGCTGTCCTGGCTGTCCTAGCTGTCCTAGGAGCTATGGTGGCTGT	300
Query	301	TGTGATGTGTAGGAGGAAGAGCTCAGGTGGAAGAGGAGGAGCTGCTCTCAGGCTGCGTC	360
Sbjct	301	TGTGATGTGTAGGAGGAAGAGCTCAGGTGGAAGAGGAGGAGCTGCTCTCAGGCTGCGTC	360
Query	361	CAGCAACAGTGCCAGGGCTCTGATGAGTCTCTCATCGCTTGTAAGCCTGAGACAGCTG	420
Sbjct	361	CAGCAACAGTGCCAGGGCTCTGATGAGTCTCTCATCGCTTGTAAGCCTGAGACAGCTG	420
Query	421	CCTGTGTGGGACTGAGATGCAGGATTTCTTCACACCTCTCCTTTGTGACTTCAAGAGCCT	480
Sbjct	421	CCTGTGTGGGACTGAGATGCAGGATTTCTTCACACCTCTCCTTTGTGACTTCAAGAGCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	CTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGTCTGCGTTCCTGTTAGCATAATGTGA	540
Sbjct	481	CTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGTCTGCGTTCCTGTTAGCATAATGTGA	540
Query	541	GGAGGTGGAGAGACAGCCCACCCCGTGTCCACCGTGACCCCTGTCCCCACACTGACCTG	600
Sbjct	541	GGAGGTGGAGAGACAGCCCACCCCGTGTCCACCGTGACCCCTGTCCCCACACTGACCTG	600
Query	601	TGTTCCCTCCCGATCATCTTTCCTGTTCCAGAGAAGTGGGCTGGATGTCTCCATCTCTG	660
Sbjct	601	TGTTCCCTCCCGATCATCTTTCCTGTTCCAGAGAAGTGGGCTGGATGTCTCCATCTCTG	660
Query	661	TCTCAACTTCATGGTGCCTGAGCTGCAACTTCTTACTTCCCTAATGAAGTTAAGAACCT	720
Sbjct	661	TCTCAACTTCATGGTGCCTGAGCTGCAACTTCTTACTTCCCTAATGAAGTTAAGAACCT	720
Query	721	GAATATAAATTTGTTTTCTCAAATATTTGCTATGAAGGGTTGATGGATTAATTAAATAAG	780
Sbjct	721	GAATATAAATTTGTTTTCTCAAATATTTGCTATGAAGGGTTGATGGATTAATTAAATAAG	780
Query	781	TCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCANAATCCG	835
Sbjct	781	TCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCANAATCCG	835

Sequence 1392 matched with Sequence 476

Query= Sequence ID 1392
Length=437

SEQ ID NO: 476

ALIGNMENTS

Identities = 437/437 (100%), Gaps = 0/437 (0%)

Query	1	TGAAACAAAATGAATTTNTATGGGTAAGAGAGGGTAATATTTTAGAGTTGTGTTACAAAA	60
Sbjct	1	TGAAACAAAATGAATTTNTATGGGTAAGAGAGGGTAATATTTTAGAGTTGTGTTACAAAA	60
Query	61	CTACAAATTTTATTAAATTAATAAATCAGAATACTAAATCCATGTGtttttttCTTTCT	120
Sbjct	61	CTACAAATTTTATTAAATTAATAAATCAGAATACTAAATCCATGTGTTTTTTCTTTCT	120
Query	121	TAAAAAATATCTTTTGGCTGGGCACGGTAGCTCATGGCTGTAATCCCAGCACTTTGGGAG	180
Sbjct	121	TAAAAAATATCTTTTGGCTGGGCACGGTAGCTCATGGCTGTAATCCCAGCACTTTGGGAG	180
Query	181	GCTGAGGTGGGTGGATCGCCTGATGTCAGGAGTTCAAGACCAGCCTGGTCAACATGTTGA	240
Sbjct	181	GCTGAGGTGGGTGGATCGCCTGATGTCAGGAGTTCAAGACCAGCCTGGTCAACATGTTGA	240
Query	241	AACCCCATCTCTACTAAAAATATAAAAAATTAGCCGGTGTGGTGGTGGGCGCCTGTAATCC	300
Sbjct	241	AACCCCATCTCTACTAAAAATATAAAAAATTAGCCGGTGTGGTGGTGGGCGCCTGTAATCC	300
Query	301	CAGCTACTCAGGAGGCTAAGGCAGGAGAATTGCGTGAACCCAGGAGTTCAGTGATGTAGC	360
Sbjct	301	CAGCTACTCAGGAGGCTAAGGCAGGAGAATTGCGTGAACCCAGGAGTTCAGTGATGTAGC	360
Query	361	GGGGAGCTGAGATTGTGCCACTACACTCCAGCCTGGATGACAGAGTGAGACTCCATCTCa	420
Sbjct	361	GGGGAGCTGAGATTGTGCCACTACACTCCAGCCTGGATGACAGAGTGAGACTCCATCTCA	420
Query	421	aaaaaaaaaaaaaaaaaaaa 437	
Sbjct	421	AAAAAAAAAAAAAAAAAAAA 437	

Sequence 1394 matched with Sequence 477

Query= Sequence ID 1394
Length=369

SEQ ID NO: 477

ALIGNMENTS

Identities = 369/369 (100%), Gaps = 0/369 (0%)

Query	1	GCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCGTGTCCACCGTGACCCCTGTTCCC	60
Sbjct	1	GCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCGTGTCCACCGTGACCCCTGTTCCC	60
Query	61	ATGCTGACTTGTGTTTCCTCCCCAGTCATCTTTCCTGTTCCAGAGAGGTGGGGCTGGATG	120
Sbjct	61	ATGCTGACTTGTGTTTCCTCCCCAGTCATCTTTCCTGTTCCAGAGAGGTGGGGCTGGATG	120
Query	121	TCTCCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCTTACTTCCCTACTGAA	180
Sbjct	121	TCTCCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCTTACTTCCCTACTGAA	180
Query	181	AATAAGAATCTGAATATAAAATTTGTTTTCTCAAATATTTGCTATGAGAGGTTGATGGATT	240
Sbjct	181	AATAAGAATCTGAATATAAAATTTGTTTTCTCAAATATTTGCTATGAGAGGTTGATGGATT	240
Query	241	AATTAATAAGTCAATTCCTGGAATTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAG	300
Sbjct	241	AATTAATAAGTCAATTCCTGGAATTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAG	300
Query	301	aaa	360
Sbjct	301	AAA	360
Query	361	aaaaaaaaa 369	
Sbjct	361	AAAAAAAAA 369	

Sequence 1395 matched with Sequence 478

Query= Sequence ID 1395
Length=642

SEQ ID NO: 478

ALIGNMENTS

Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query	1	CTTACCATGTCAGTGCACAGAAATGCTGTCTTGGGATGTAGGAAAAATAAATCCACAAAA	60
Sbjct	1	CTTACCATGTCAGTGCACAGAAATGCTGTCTTGGGATGTAGGAAAAATAAATCCACAAAA	60
Query	61	GCTACCAAGTTTGAAGGGGACCATGAGTCTTCAGGCTGGAGCTTCCAAACCAGATGAAAA	120
Sbjct	61	GCTACCAAGTTTGAAGGGGACCATGAGTCTTCAGGCTGGAGCTTCCAAACCAGATGAAAA	120
Query	121	CCCCACAATTAACCTGCAGTTTAAGATCCAGCAGCTGGCCATTTCTGGACTCAAGGTGAA	180
Sbjct	121	CCCCACAATTAACCTGCAGTTTAAGATCCAGCAGCTGGCCATTTCTGGACTCAAGGTGAA	180
Query	181	TCGTCTGGATATGTATGGAGAAAAAGTACAAACCCTTTAAGGGCATAAAATACATGACCAA	240
Sbjct	181	TCGTCTGGATATGTATGGAGAAAAAGTACAAACCCTTTAAGGGCATAAAATACATGACCAA	240
Query	241	AGCTGGGAAGTTCCAAGTTCGAACCTGAAGGGAGCATTGCTGAGGGAATAGTCTTGCAC	300
Sbjct	241	AGCTGGGAAGTTCCAAGTTCGAACCTGAAGGGAGCATTGCTGAGGGAATAGTCTTGCAC	300
Query	301	ATTTTTTCATTTCTTACTTGTCTAAAAGTaaaaaaaaTATCAGCCTGTCTCCTAGGTCA	360
Sbjct	301	ATTTTTTCATTTCTTACTTGTCTAAAAGTAAAAAAAAATATCAGCCTGTCTCCTAGGTCA	360
Query	361	GTCCCCTCCTGGACCCACCCGCTCCCTTTTTTCCTTAGCCTTCAGTGCCATGGAACATAAT	420
Sbjct	361	GTCCCCTCCTGGACCCACCCGCTCCCTTTTTTCCTTAGCCTTCAGTGCCATGGAACATAAT	420
Query	421	CAAGGGAGGAAAAGGTCACCAGGGAGAACTGGACAGAACTGAAACACAGCAACACCAGTT	480
Sbjct	421	CAAGGGAGGAAAAGGTCACCAGGGAGAACTGGACAGAACTGAAACACAGCAACACCAGTT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTCAAGGACAAGGTGTGTGATGGGGGTAGGAAGCTTGGTGCTTATGTAACCATTTTAAAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CTCAAGGACAAGGTGTGTGATGGGGGTAGGAAGCTTGGTGCTTATGTAACCATTTTAAAC  540

Query  541  GTGGTTTCTATAGGAAAGACCAACATTTGTTTAGCTTGCTTGGCTTTAATTATCTAAAGC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GTGGTTTCTATAGGAAAGACCAACATTTGTTTAGCTTGCTTGGCTTTAATTATCTAAAGC  600

Query  601  CAATGAAAGACTTCTTTGTTGATTTTTTAAGATAGAAAGATT  642
          ||||||||||||||||||||||||||||||||||||
Sbjct   601  CAATGAAAGACTTCTTTGTTGATTTTTTAAGATAGAAAGATT  642
```

Sequence 1396 matched with Sequence 479

Query= Sequence ID 1396
Length=912

SEQ ID NO: 479

ALIGNMENTS

Identities = 912/912 (100%), Gaps = 0/912 (0%)

Query	1	CAAACACTATGTTATTTTATGAANAAGACTTGAACATCTATGGATTTTGGTATTTGCAAG	60
Sbjct	1	CAAACACTATGTTATTTTATGAANAAGACTTGAACATCTATGGATTTTGGTATTTGCAAG	60
Query	61	GGGTGAATGGGGTATTTGCAAGCAGTGAATGAGGAGGCCTGGAACCAATCTTCTGCTGAT	120
Sbjct	61	GGGTGAATGGGGTATTTGCAAGCAGTGAATGAGGAGGCCTGGAACCAATCTTCTGCTGAT	120
Query	121	ATTGAGGCACAACCTGAAAAAGGTATATTACTTAAATCTCTTATTGTATTGTAAACTGTAT	180
Sbjct	121	ATTGAGGCACAACCTGAAAAAGGTATATTACTTAAATCTCTTATTGTATTGTAAACTGTAT	180
Query	181	AAGTAATGAAATTAAAAGGCAGAAATTGTCAGACTGAATAAAATGAAAAGACCAAACAAT	240
Sbjct	181	AAGTAATGAAATTAAAAGGCAGAAATTGTCAGACTGAATAAAATGAAAAGACCAAACAAT	240
Query	241	ATGCTGCTTACAAGAAACACAATTCAAATATAAGGACACAATTAGTTTAAAGGAAAAGAA	300
Sbjct	241	ATGCTGCTTACAAGAAACACAATTCAAATATAAGGACACAATTAGTTTAAAGGAAAAGAA	300
Query	301	CTGGAAAAGATATACCATGATAACACAAGTCAGAAGAAAGCTGCTGTGGATATATTAATA	360
Sbjct	301	CTGGAAAAGATATACCATGATAACACAAGTCAGAAGAAAGCTGCTGTGGATATATTAATA	360
Query	361	TGAGATGTAGATTTTCAGAGCAGTGAATATTGCCAGGCATAAAGAAAGTTATTACATAATA	420
Sbjct	361	TGAGATGTAGATTTTCAGAGCAGTGAATATTGCCAGGCATAAAGAAAGTTATTACATAATA	420
Query	421	ATTAAGGTATCAGTTCATCAAGAAGATGTAATAACCCTAAGTATTTATACAACCTAATATC	480
Sbjct	421	ATTAAGGTATCAGTTCATCAAGAAGATGTAATAACCCTAAGTATTTATACAACCTAATATC	480

PATENT SEQUENCE ALIGNMENT

```

Query  481  AGAGCTTCAAATACATGAAGCAAAAACCAAGTGAATTGATAGGAGAAACACACAATTAC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGAGCTTCAAATACATGAAGCAAAAACCAAGTGAATTGATAGGAGAAACACACAATTAC  540

Query  541  ACAATTATAGTCAGAATTTTCAACATATCTTTCTCAATGGAGAAAACAACTAGACAGGAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ACAATTATAGTCAGAATTTTCAACATATCTTTCTCAATGGAGAAAACAACTAGACAGGAA  600

Query  601  ATCATTAAGGATATAGATGATTTAAATTATATGATCAACTACCTGGACGTAATTGGCATT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  ATCATTAAGGATATAGATGATTTAAATTATATGATCAACTACCTGGACGTAATTGGCATT  660

Query  661  TATGGAACACTGCACCACCAACAGCAGAGTACATATTATTTTCAAGTACACAGAAAACAG  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  TATGGAACACTGCACCACCAACAGCAGAGTACATATTATTTTCAAGTACACAGAAAACAG  720

Query  721  TTACCAATATAGACCATTTTCTGGGTCATAAAACACATCTCAATAAATGTAAAACAATTA  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721  TTACCAATATAGACCATTTTCTGGGTCATAAAACACATCTCAATAAATGTAAAACAATTA  780

Query  781  ATGTTATATAAAGTATGTGCTCTGACCNCAAAGGAATTAGAGATCAATAAAAGAACATCT  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   781  ATGTTATATAAAGTATGTGCTCTGACCNCAAAGGAATTAGAGATCAATAAAAGAACATCT  840

Query  841  TTGAAAAATCTCACNTATTTAAAAACTAATAACTCACTTCTAAATAACTCCTGTNTCAAG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   841  TTGAAAAATCTCACNTATTTAAAAACTAATAACTCACTTCTAAATAACTCCTGTNTCAAG  900

Query  901  AGAATNAAANGG  912
          |||||||||||
Sbjct   901  AGAATNAAANGG  912

```

Blast comparison trimmed “NGG” from the 3’ end of both sequences and reported 909 identities. The report has been manually corrected for this. “NGG” has been appended to both sequences and identity count has been increased to 912.

Sequence 1397 matched with Sequence 480

Query= Sequence ID 1397
Length=873

SEQ ID NO: 480

ALIGNMENTS

Identities = 873/873 (100%), Gaps = 0/873 (0%)

Query	1	CCCAGCCTCACTGCGCCCCGTCAGGCCAGGCAGCTGCCCTCAGGGTCTGCCAAGGTGGGG	60
Sbjct	1	CCCAGCCTCACTGCGCCCCGTCAGGCCAGGCAGCTGCCCTCAGGGTCTGCCAAGGTGGGG	60
Query	61	GTCAAGGGCCATGGGGGAGGTAGCTCTGCCTGCAAAGCCCACAAGCATGTCAGATCACC	120
Sbjct	61	GTCAAGGGCCATGGGGGAGGTAGCTCTGCCTGCAAAGCCCACAAGCATGTCAGATCACC	120
Query	121	TGGGCTGCAGACAGACAAACACCTGAGCTGTTCTGAATACCTTCAGGTTCTGGCCTCGC	180
Sbjct	121	TGGGCTGCAGACAGACAAACACCTGAGCTGTTCTGAATACCTTCAGGTTCTGGCCTCGC	180
Query	181	TGAGCAAGTGCAGAAATTTTACCTTCAAGGATCAGGgtttttctgtttgtttgtttttt	240
Sbjct	181	TGAGCAAGTGCAGAAATTTTACCTTCAAGGATCAGGGTTTTTCTGTTGTTGTTTTTT	240
Query	241	AACACACACATATGTGAACAAAGAGTATGCGTTTGTACTGGCAGAAGAAGCGTCTGGTAA	300
Sbjct	241	AACACACACATATGTGAACAAAGAGTATGCGTTTGTACTGGCAGAAGAAGCGTCTGGTAA	300
Query	301	GACAACCAGCAAGTTAACAATGGTCACCTCCAGAAATGGGCTGGGTAAACCAAAGAAttt	360
Sbjct	301	GACAACCAGCAAGTTAACAATGGTCACCTCCAGAAATGGGCTGGGTAAACCAAAGAATTT	360
Query	361	ttttgtttttgttttttttGAGTCAGGGTCTAGCTCTGTCACCCAGGCTGGAACGCACTG	420
Sbjct	361	TTTTGTTTTTGTGTTTTTTTGTGAGTCAGGGTCTAGCTCTGTCACCCAGGCTGGAACGCACTG	420
Query	421	GTGTGATCACGGCTCACTGCAGCCTTGACCTCCCTGGCTCAAGCAATCCTCCCAGCTCAG	480
Sbjct	421	GTGTGATCACGGCTCACTGCAGCCTTGACCTCCCTGGCTCAAGCAATCCTCCCAGCTCAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCTCCTGAGTCGTTGGGACTACAGGCACGTGCCACCACGCCTGACACATTTTTTAAATTT	540
Sbjct	481	CCTCCTGAGTCGTTGGGACTACAGGCACGTGCCACCACGCCTGACACATTTTTTAAATTT	540
Query	541	TTGTAGAGACAGTGTTTCACCATGTTGCCCAGGCAGGTCTCAAACCTCTGGGCTCAAGTG	600
Sbjct	541	TTGTAGAGACAGTGTTTCACCATGTTGCCCAGGCAGGTCTCAAACCTCTGGGCTCAAGTG	600
Query	601	GTCCTCCAGCTTCAGCCTCCCAAAGTGCTAGGATTATAGGTGTGAGCCACAGTGCCCAGC	660
Sbjct	601	GTCCTCCAGCTTCAGCCTCCCAAAGTGCTAGGATTATAGGTGTGAGCCACAGTGCCCAGC	660
Query	661	CCCGTAGTGGAGAATTTCTGTTGAATGAACCAAAAGCAACTGCCAACCTCTCCATGCACC	720
Sbjct	661	CCCGTAGTGGAGAATTTCTGTTGAATGAACCAAAAGCAACTGCCAACCTCTCCATGCACC	720
Query	721	ATGTGTTTCAGAGGAGAAAGCACAGTGAAGAATGCAGTGTGTTCTGAGGTCCTGTCACCC	780
Sbjct	721	ATGTGTTTCAGAGGAGAAAGCACAGTGAAGAATGCAGTGTGTTCTGAGGTCCTGTCACCC	780
Query	781	CTGAGGCTGTGTGTGTCCTTTGCCAAATTAAAGAGTCTTACTGAATGCGGTGCATCCAGG	840
Sbjct	781	CTGAGGCTGTGTGTGTCCTTTGCCAAATTAAAGAGTCTTACTGAATGCGGTGCATCCAGG	840
Query	841	AGACAGGCCNAGGTTTGGACTGGTaaaaaaaaa	873
Sbjct	841	AGACAGGCCNAGGTTTGGACTGGTAAAAAAAAA	873

Sequence 1399 matched with Sequence 481

Query= Sequence ID 1399
Length=778

SEQ ID NO: 481

ALIGNMENTS

Identities = 778/778 (100%), Gaps = 0/778 (0%)

Query	1	CAGACACCTGGNAGAACGGGAAGGAGACGCTGCAGCGCGCGGACCCCCAAAGACACATG	60
Sbjct	1	CAGACACCTGGNAGAACGGGAAGGAGACGCTGCAGCGCGCGGACCCCCAAAGACACATG	60
Query	61	TGACCCACCACCCCATCTNTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCT	120
Sbjct	61	TGACCCACCACCCCATCTNTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCT	120
Query	121	ACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGACAAACTCAGGACACCG	180
Sbjct	121	ACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGACAAACTCAGGACACCG	180
Query	181	AGCTTGTGGAGACCAGACCAGCAGGAGACAGAACCTTCCAGAAGTGGGCAGCTGTGGTGG	240
Sbjct	181	AGCTTGTGGAGACCAGACCAGCAGGAGACAGAACCTTCCAGAAGTGGGCAGCTGTGGTGG	240
Query	241	TGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGC	300
Sbjct	241	TGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGC	300
Query	301	CCCTCACCTGAGATGGGAGCCATCTTCCCAGTCCACCGTCCCCATCGTGGGCATTGTTG	360
Sbjct	301	CCCTCACCTGAGATGGGAGCCATCTTCCCAGTCCACCGTCCCCATCGTGGGCATTGTTG	360
Query	361	CTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTGCTGTGATGTGTA	420
Sbjct	361	CTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTGCTGTGATGTGTA	420
Query	421	GGAGGAAGAGTTCAGGTGAAAAAGGAGGGAGCTACTCTCAGGCTGCGTCCAGCGACAGTG	480
Sbjct	421	GGAGGAAGAGTTCAGGTGAAAAAGGAGGGAGCTACTCTCAGGCTGCGTCCAGCGACAGTG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCCAGGGCTCTGATGTGTCTCTCACAGCTTGAAAAGCCTGAGACAGCTGTNTTGTGAGGG	540
Sbjct	481	CCCAGGGCTCTGATGTGTCTCTCACAGCTTGAAAAGCCTGAGACAGCTGTNTTGTGAGGG	540
Query	541	ACTGAGATGCAGGATTTCTTCACGCCTCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTC	600
Sbjct	541	ACTGAGATGCAGGATTTCTTCACGCCTCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTC	600
Query	601	TTTCTGCAAAGGCACCTGAATGTGTCTGCGTCCTTGTTAGCATAATGTGAGGAGGTGGAG	660
Sbjct	601	TTTCTGCAAAGGCACCTGAATGTGTCTGCGTCCTTGTTAGCATAATGTGAGGAGGTGGAG	660
Query	661	AGACAGCCCACCCTTGTGTCAACTGTGACCCCCTGTTCCCATGCTGACCTGTGTTTCCTC	720
Sbjct	661	AGACAGCCCACCCTTGTGTCAACTGTGACCCCCTGTTCCCATGCTGACCTGTGTTTCCTC	720
Query	721	CCCAGTCATCTTTTTTGTTCNCAATAGGTGGGGCCTGGATGTCTCCATCTCTGTNTCA	778
Sbjct	721	CCCAGTCATCTTTTTTGTTCNCAATAGGTGGGGCCTGGATGTCTCCATCTCTGTNTCA	778

Sequence 1440 matched with Sequence 482

Query= Sequence ID 1440
Length=666

SEQ ID NO: 482

ALIGNMENTS

Identities = 666/666 (100%), Gaps = 0/666 (0%)

Query	1	TTATAAGGTACTTTTAAGGTATTTAGTTGTCTTAGTCTATATTTCTGTACTCACCTTTC	60
Sbjct	1	TTATAAGGTACTTTTAAGGTATTTAGTTGTCTTAGTCTATATTTCTGTACTCACCTTTC	60
Query	61	TTTATCCACTCATCAGTTGATGGGCATGTAGGTTGGTTCATATCTTTGCAATTCTGAAT	120
Sbjct	61	TTTATCCACTCATCAGTTGATGGGCATGTAGGTTGGTTCATATCTTTGCAATTCTGAAT	120
Query	121	TGTGCTGTGATCAGGTGTCTTTTAGTATAATGATTTACTCTCCTTTGGGTAGATACCCA	180
Sbjct	121	TGTGCTGTGATCAGGTGTCTTTTAGTATAATGATTTACTCTCCTTTGGGTAGATACCCA	180
Query	181	GTAGTGGGATTGCTGGATCGAATGGTTTTTATAATTTTCTATTTTACCACAGTTTCTCTC	240
Sbjct	181	GTAGTGGGATTGCTGGATCGAATGGTTTTTATAATTTTCTATTTTACCACAGTTTCTCTC	240
Query	241	TGCATTTTTCTCTTTGACCACTAACCATGTGAAATTCTCATATTGACCTTTATAATGAT	300
Sbjct	241	TGCATTTTTCTCTTTGACCACTAACCATGTGAAATTCTCATATTGACCTTTATAATGAT	300
Query	301	CATGAACTCTTAGTATCATTGGGAAGGCCACATTTGCCACTTATGATTGTAAACCTTATC	360
Sbjct	301	CATGAACTCTTAGTATCATTGGGAAGGCCACATTTGCCACTTATGATTGTAAACCTTATC	360
Query	361	CTCCATTTTTCTGTTATTGTTGGTGCAAAAAGCACCTATTATACCAGGACTTTAAAAAT	420
Sbjct	361	CTCCATTTTTCTGTTATTGTTGGTGCAAAAAGCACCTATTATACCAGGACTTTAAAAAT	420
Query	421	CAGTCTGATAAGTCTTTGATAAGTCTAATAATAATAACTGATAAGTCCATTGAATTTGCT	480
Sbjct	421	CAGTCTGATAAGTCTTTGATAAGTCTAATAATAATAACTGATAAGTCCATTGAATTTGCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TCTGATTACTTTTTCTTTAGTAGCTAAACATGTATGTACTCCTATGATTACAATGAACAC	540
Sbjct	481	TCTGATTACTTTTTCTTTAGTAGCTAAACATGTATGTACTCCTATGATTACAATGAACAC	540
Query	541	TCCTCTCCATTTAAATTAATTATTTACATTGATGAAATAGCAAAATGTTAATGACTAAAT	600
Sbjct	541	TCCTCTCCATTTAAATTAATTATTTACATTGATGAAATAGCAAAATGTTAATGACTAAAT	600
Query	601	ACTGTCTTGGTTTTTTCGTTCCAGGTCAGTCAATATTAACCTTCTTATAATTTTCtttttt	660
Sbjct	601	ACTGTCTTGGTTTTTTCGTTCCAGGTCAGTCAATATTAACCTTCTTATAATTTTCCTTTTTT	660
Query	661	ttCTTT	666
Sbjct	661	TTCTTT	666

Sequence 1447 matched with Sequence 483

Query= Sequence ID 1447
Length=630

SEQ ID NO: 483

ALIGNMENTS

Identities = 630/630 (100%), Gaps = 0/630 (0%)

Query	1	GCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAGAAATAACTTTGCAAGGA	60
Sbjct	1	GCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAAGTAGAAATAACTTTGCAAGGA	60
Query	61	GAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACA	120
Sbjct	61	GAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACA	120
Query	121	CCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGC	180
Sbjct	121	CCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGC	180
Query	181	CTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAA	240
Sbjct	181	CTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCACAGAA	240
Query	241	CCCTCTAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACAC	300
Sbjct	241	CCCTCTAAATCCCCTTGTAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACAC	300
Query	301	TAGGAAAAAACCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAG	360
Sbjct	301	TAGGAAAAAACCTTGTTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAG	360
Query	361	CCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAATCCCAAACATATA	420
Sbjct	361	CCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAATCCCAAACATATA	420
Query	421	ACTGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGAACTAATGTTAGT	480
Sbjct	421	ACTGAACTCCTCACACCCAATTGGACCAATCTATCACCTATAGAAGAACTAATGTTAGT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  ATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAAACACTGAACT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAAACACTGAACT  540

Query  541  GACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCCTCACTGTCAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCCTCACTGTCAA  600

Query  601  CCCAACACAGGCATGCTCATAAGGAAAGGT  630
          ||||||||||||||||||||||||
Sbjct   601  CCCAACACAGGCATGCTCATAAGGAAAGGT  630
```

Sequence 1448 matched with Sequence 484

Query= Sequence ID 1448
Length=612

SEQ ID NO: 484

ALIGNMENTS

Identities = 612/612 (100%), Gaps = 0/612 (0%)

Query	1	GGCCACCGGGTGCAAGGTCAGGGCTGGGGTGGAGGCTGGGAAGCCCAGGGCTTGGCCCAC	60
Sbjct	1	GGCCACCGGGTGCAAGGTCAGGGCTGGGGTGGAGGCTGGGAAGCCCAGGGCTTGGCCCAC	60
Query	61	TGTGGCCGCCTTGTGTGGTCACTGCTTTCTGGGCCTGCTGTGAGCTCCCTCTAGGACCC	120
Sbjct	61	TGTGGCCGCCTTGTGTGGTCACTGCTTTCTGGGCCTGCTGTGAGCTCCCTCTAGGACCC	120
Query	121	CAGGCCTGTCTGGTGGGTCACTGTGACCACCACCTTGCACAGCACCTGGCGCGTGGCAGG	180
Sbjct	121	CAGGCCTGTCTGGTGGGTCACTGTGACCACCACCTTGCACAGCACCTGGCGCGTGGCAGG	180
Query	181	TGCTCAAACATTACTTGTTCGGAATGAACTTCATCTTGCTCTTGGCTTTTGGACTAATG	240
Sbjct	181	TGCTCAAACATTACTTGTTCGGAATGAACTTCATCTTGCTCTTGGCTTTTGGACTAATG	240
Query	241	CTGTGGAACATCTGACTAATTAGTGACTCTTTGGGGCCCCAGTTTCCCAGCTATAAAGT	300
Sbjct	241	CTGTGGAACATCTGACTAATTAGTGACTCTTTGGGGCCCCAGTTTCCCAGCTATAAAGT	300
Query	301	GGTAATATTAAGATAATAATTCGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCAGC	360
Sbjct	301	GGTAATATTAAGATAATAATTCGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCAGC	360
Query	361	ACTTTGGGAGGCCGAGGTGGGCAGATCACGAGGTCAGAAGATCGAGACCATCCTGGCTAA	420
Sbjct	361	ACTTTGGGAGGCCGAGGTGGGCAGATCACGAGGTCAGAAGATCGAGACCATCCTGGCTAA	420
Query	421	CACGGTGAAACCCCATCTCTACTAAAAATACAAAAAATTANCCGGGCGTGGTGGCGGGCG	480
Sbjct	421	CACGGTGAAACCCCATCTCTACTAAAAATACAAAAAATTANCCGGGCGTGGTGGCGGGCG	480

PATENT SEQUENCE ALIGNMENT

Query	481	CCTGTAGTCCCAGCTACTCANGAGGCTGANGCAGGAGAATGGTGTGAACCCGGGAGGCAG	540
Sbjct	481	CCTGTAGTCCCAGCTACTCANGAGGCTGANGCAGGAGAATGGTGTGAACCCGGGAGGCAG	540
Query	541	AGGTTGCAGTGAACCAAGATCGNNCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTC	600
Sbjct	541	AGGTTGCAGTGAACCAAGATCGNNCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTC	600
Query	601	CATCTTAAAAAA 612	
Sbjct	601	CATCTTAAAAAA 612	

Sequence 1449 matched with Sequence 485

Query= Sequence ID 1449
Length=362

SEQ ID NO: 485

ALIGNMENTS

Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query	1	AATCAGGGCCGCAGTGTGTTCTGCGCCTGCCCAGAGCTGACTCCTGATTTAACCGCTGGC	60
Sbjct	1	AATCAGGGCCGCAGTGTGTTCTGCGCCTGCCCAGAGCTGACTCCTGATTTAACCGCTGGC	60
Query	61	GTAACCGCGGGTTGCACGCATGCGTGCTGAAAAGCCTTTCACCCTCACGTGGTTTCTTTT	120
Sbjct	61	GTAACCGCGGGTTGCACGCATGCGTGCTGAAAAGCCTTTCACCCTCACGTGGTTTCTTTT	120
Query	121	TTAACCAGTCATCAAGCGAGGCTCGCGCGCAGGCCCGCGTTGGAAAATGGCGGGGAAGC	180
Sbjct	121	TTAACCAGTCATCAAGCGAGGCTCGCGCGCAGGCCCGCGTTGGAAAATGGCGGGGAAGC	180
Query	181	TGAAACCTCTGAATGTGGAGGCGCCAGAAGCTGCTGAGGAGGCTGAAGGTAGTGAGGGCA	240
Sbjct	181	TGAAACCTCTGAATGTGGAGGCGCCAGAAGCTGCTGAGGAGGCTGAAGGTAGTGAGGGCA	240
Query	241	AGTGGGCTGCACTCCTTTCTCTCCAACCAGGGCAGAAAGGAGGGAGGATTCGTCCCATTA	300
Sbjct	241	AGTGGGCTGCACTCCTTTCTCTCCAACCAGGGCAGAAAGGAGGGAGGATTCGTCCCATTA	300
Query	301	CAATAATGAAATAATGATATTCTAAttttttAAATAAAATGTTAAGCCTTTTGTTATTG	360
Sbjct	301	CAATAATGAAATAATGATATTCTAATTTTTTTAAATAAAATGTTAAGCCTTTTGTTATTG	360
Query	361	AA 362	
Sbjct	361	AA 362	

Sequence 1450 matched with Sequence 486

Query= Sequence ID 1450
Length=854

SEQ ID NO: 486

ALIGNMENTS

Identities = 854/854 (100%), Gaps = 0/854 (0%)

Query	1	GGAAANCATGAGGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGCGATGCCAGGCGCGTC	60
Sbjct	1	GGAAANCATGAGGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGCGATGCCAGGCGCGTC	60
Query	61	CCTACAGCGGGCCTGCCGCCTGCTCGTGGCCGTCTGCGCTCTGCACCTTGGCGTCACCCT	120
Sbjct	61	CCTACAGCGGGCCTGCCGCCTGCTCGTGGCCGTCTGCGCTCTGCACCTTGGCGTCACCCT	120
Query	121	CGTTTACTACCTGGCTGGCCGCGACCTGAGCCGCCTGCCCCAACTGGTCGGAGTCTCCAC	180
Sbjct	121	CGTTTACTACCTGGCTGGCCGCGACCTGAGCCGCCTGCCCCAACTGGTCGGAGTCTCCAC	180
Query	181	ACCGCTGCAGGGCGGCTCGAACAGTGCCGCCGCCATCGGGCAGTCCTCCGGGGAGCTCCG	240
Sbjct	181	ACCGCTGCAGGGCGGCTCGAACAGTGCCGCCGCCATCGGGCAGTCCTCCGGGGAGCTCCG	240
Query	241	GACCGGAGGGGCGCCGCCGCCCTCCTNTAGGCGCCTCCTCCCAGCCGCGCCCGGGTGG	300
Sbjct	241	GACCGGAGGGGCGCCGCCGCCCTCCTNTAGGCGCCTCCTCCCAGCCGCGCCCGGGTGG	300
Query	301	CGACTCCAGCCCAGTCGTGGATTCTGGCCCTGGCCCCGCTAGCAACTTGACCTCGGTCCC	360
Sbjct	301	CGACTCCAGCCCAGTCGTGGATTCTGGCCCTGGCCCCGCTAGCAACTTGACCTCGGTCCC	360
Query	361	AGTGCCCCACACCACCGCACTGTCGCTGCCCCGCTGCCCTGAGGAGTCCCCGCTGCTTGG	420
Sbjct	361	AGTGCCCCACACCACCGCACTGTCGCTGCCCCGCTGCCCTGAGGAGTCCCCGCTGCTTGG	420
Query	421	TAAGGACTCGGGTCGGCGCCAGTCGGAGGATTGGGAcccccccGGATTTCCTCCGACAGGG	480
Sbjct	421	TAAGGACTCGGGTCGGCGCCAGTCGGAGGATTGGGACCCCCCGGATTTCCTCCGACAGGG	480

PATENT SEQUENCE ALIGNMENT

```

Query  481  TCCCCANACATTCCCTCAGGCTGGCTCTTCTACGACAGCCAGCCTCCCTCTTCTGGATC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TCCCCANACATTCCCTCAGGCTGGCTCTTCTACGACAGCCAGCCTCCCTCTTCTGGATC  540

Query  541  AGAGTTTTTAAATCCCANACAGAGGCTTGGGACTGGATGGGAGAGAAGGTTTGCAGAGGTGG  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AGAGTTTTTAAATCCCANACAGAGGCTTGGGACTGGATGGGAGAGAAGGTTTGCAGAGGTGG  600

Query  601  GTCCCTGGGGAGTCCTGTTGGAGGCGTGGGGCCGGGACCGCACAGGGAAGTCCCGAGGCC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GTCCCTGGGGAGTCCTGTTGGAGGCGTGGGGCCGGGACCGCACAGGGAAGTCCCGAGGCC  660

Query  661  CCTCTAGCCCCAAAACCANAGAAGGCCTTGGAGACTTCCCTGCTGTGGCCCGAGGCTNAG  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661  CCTCTAGCCCCAAAACCANAGAAGGCCTTGGAGACTTCCCTGCTGTGGCCCGAGGCTNAG  720

Query  721  GAAGTTTTTGGAGTTTTTGGGTCTGCTTANGGCTTCNAGCAGCCTTGCACTGAGAACTTTGG  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721  GAAGTTTTTGGAGTTTTTGGGTCTGCTTANGGCTTCNAGCAGCCTTGCACTGAGAACTTTGG  780

Query  781  TAGGGACCTCGAGTAATCCACTCCNTTTTTNGGGACTGACGTGAGGCTCCCGGTGGGGAAA  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   781  TAGGGACCTCGAGTAATCCACTCCNTTTTTNGGGACTGACGTGAGGCTCCCGGTGGGGAAA  840

Query  841  GANACTGACCTNTC  854
          |||||||||||||
Sbjct   841  GANACTGACCTNTC  854

```

Blast comparison trimmed “NTC” from the 3’ end of both sequences and reported 851 identities. The report has been manually corrected for this. “NTC” has been appended to both sequences and identity count has been increased to 854.

Sequence 1453 matched with Sequence 487

Query= Sequence ID 1453
Length=843

SEQ ID NO: 487

ALIGNMENTS

Identities = 843/843 (100%), Gaps = 0/843 (0%)

Query	1	CCGACCTGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGG	60
Sbjct	1	CCGACCTGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGG	60
Query	61	AGGCTATCCAGCGTACTCCAAAGATTCAAGTTTACTCACGTCATCCAGCAGAGAATGGAA	120
Sbjct	61	AGGCTATCCAGCGTACTCCAAAGATTCAAGTTTACTCACGTCATCCAGCAGAGAATGGAA	120
Query	121	AGTCAAATTTCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACT	180
Sbjct	121	AGTCAAATTTCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACT	180
Query	181	TACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAAGTTGTCTTTCAGCAAGG	240
Sbjct	181	TACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAAGTTGTCTTTCAGCAAGG	240
Query	241	ACTGGTCTTTCTATCTCTTGTAAGTACACTGAATTCACCCCACTGAAAAAGATGAGTATG	300
Sbjct	241	ACTGGTCTTTCTATCTCTTGTAAGTACACTGAATTCACCCCACTGAAAAAGATGAGTATG	300
Query	301	CCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGATCGAGACA	360
Sbjct	301	CCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGATCGAGACA	360
Query	361	TGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTC	420
Sbjct	361	TGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTC	420
Query	421	TGCTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTA	480
Sbjct	421	TGCTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTA	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTC	540
Sbjct	481	GGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTC	540
Query	541	TCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACT	600
Sbjct	541	TCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACT	600
Query	601	TAGAGGTGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGATTTGAACT	660
Sbjct	601	TAGAGGTGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGATTTGAACT	660
Query	661	CTTCAATCTCTTGCACTCAAAGCTTGTTAAGATAGTTAAGCGTGCATAAGTTAACTTCCA	720
Sbjct	661	CTTCAATCTCTTGCACTCAAAGCTTGTTAAGATAGTTAAGCGTGCATAAGTTAACTTCCA	720
Query	721	ATTTACATACTCTGCTTAGAATTTGGGGGAAAATTTAGAAATATAATTGACAGGATTATT	780
Sbjct	721	ATTTACATACTCTGCTTAGAATTTGGGGGAAAATTTAGAAATATAATTGACAGGATTATT	780
Query	781	GGAAATTTGTTATAATGAATGAAACATTTTTGTCATATAAGATTCATATTTACTTCTTAT	840
Sbjct	781	GGAAATTTGTTATAATGAATGAAACATTTTTGTCATATAAGATTCATATTTACTTCTTAT	840
Query	841	ACA	843
Sbjct	841	ACA	843

Sequence 1454 matched with Sequence 488

Query= Sequence ID 1454
Length=578

SEQ ID NO: 488

ALIGNMENTS

Identities = 578/578 (100%), Gaps = 0/578 (0%)

Query	1	TAAATAGGGAATCCTTTCCCATTTGCTTGTTTTTCTCAGGTTTGTCAAAGATCAGATAGT	60
Sbjct	1	TAAATAGGGAATCCTTTCCCATTTGCTTGTTTTTCTCAGGTTTGTCAAAGATCAGATAGT	60
Query	61	TGTAGATATGCGACGTTATTTCTGAGGGCTCTGTTCTGTTCCATTGATCTATATCTCTGT	120
Sbjct	61	TGTAGATATGCGACGTTATTTCTGAGGGCTCTGTTCTGTTCCATTGATCTATATCTCTGT	120
Query	121	CACATGCACACGTATGTTTGTGTGGCACTATTCACAGTGGCAAAGACTTGAACCAACC	180
Sbjct	121	CACATGCACACGTATGTTTGTGTGGCACTATTCACAGTGGCAAAGACTTGAACCAACC	180
Query	181	CAAATGTCCAACAATGATAGACCGGGTTAAGAAAATGCGGCACATATACACCATGGAATA	240
Sbjct	181	CAAATGTCCAACAATGATAGACCGGGTTAAGAAAATGCGGCACATATACACCATGGAATA	240
Query	241	CTATGTAGCCATAAAAAATGATGAGTTCGTGTCCTTTGTAGGGACATGGATGAAATTGGA	300
Sbjct	241	CTATGTAGCCATAAAAAATGATGAGTTCGTGTCCTTTGTAGGGACATGGATGAAATTGGA	300
Query	301	AATCATCATTCTCAGTAAACTATCGCAGGAACAAAAACCAAACACTGCATATTCTCACT	360
Sbjct	301	AATCATCATTCTCAGTAAACTATCGCAGGAACAAAAACCAAACACTGCATATTCTCACT	360
Query	361	CATAGGTGGGAATTGAACAGTGGGAACACATGGACACAGGAAGGGGAACATCACACTCTG	420
Sbjct	361	CATAGGTGGGAATTGAACAGTGGGAACACATGGACACAGGAAGGGGAACATCACACTCTG	420
Query	421	AGGACTGTTGTGGGTGGGGGAGGGAGGAGGGATAGCATTGGGAGATATACCTAGTGCT	480
Sbjct	421	AGGACTGTTGTGGGTGGGGGAGGGAGGAGGGATAGCATTGGGAGATATACCTAGTGCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  GGATGACGAGTTAGTGGGTGCAGCGCACCAGCATGTCACATGTATACATATGTAAC TAAC  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GGATGACGAGTTAGTGGGTGCAGCGCACCAGCATGTCACATGTATACATATGTAAC TAAC  540

Query  541  CTGCACATTGTGCACATGTACCCTAAAAC TTAAGGTAT  578
          |||||||||||||||||||||||||||
Sbjct   541  CTGCACATTGTGCACATGTACCCTAAAAC TTAAGGTAT  578
```

Sequence 1456 matched with Sequence 489

Query= Sequence ID 1456
Length=628

SEQ ID NO: 489

ALIGNMENTS

Identities = 628/628 (100%), Gaps = 0/628 (0%)

Query	1	CCGCAACAAACACGGGAGTGCAGATATCGCTGCGATGGGCTGATTTCCTTTATTTGGGTA	60
Sbjct	1	CCGCAACAAACACGGGAGTGCAGATATCGCTGCGATGGGCTGATTTCCTTTATTTGGGTA	60
Query	61	TATACCCAGCAGTGGGATTGCTGGATTGTATGGTAGCTCTATTAGTTTTTTGAGGAACCT	120
Sbjct	61	TATACCCAGCAGTGGGATTGCTGGATTGTATGGTAGCTCTATTAGTTTTTTGAGGAACCT	120
Query	121	CCAAACTGTTCTNCATAGTGGTTGTACTCATTTACATTCCCACTGTGAACCCTGAAAATT	180
Sbjct	121	CCAAACTGTTCTNCATAGTGGTTGTACTCATTTACATTCCCACTGTGAACCCTGAAAATT	180
Query	181	TGAGGCAGGTCTCAGTTAAATTAGAAAAGTTGATTTTGCCAAGTTGGGGACACGCACTCGT	240
Sbjct	181	TGAGGCAGGTCTCAGTTAAATTAGAAAAGTTGATTTTGCCAAGTTGGGGACACGCACTCGT	240
Query	241	GACACAGCCTCAGGAGGAACTGATGACATGTGCCAGGTGGTCAGAGCACAGCTTGGTTT	300
Sbjct	241	GACACAGCCTCAGGAGGAACTGATGACATGTGCCAGGTGGTCAGAGCACAGCTTGGTTT	300
Query	301	TATACATTTTAGGGAAACCTGAGCCATCAATCAACATACGTAAAATGGGCCGGGCACAGC	360
Sbjct	301	TATACATTTTAGGGAAACCTGAGCCATCAATCAACATACGTAAAATGGGCCGGGCACAGC	360
Query	361	AGCTCAAGCTGTAATCCAGCACTCTGGGAGGCCGAGGCGGGTGGATCACTTGAGGTCAG	420
Sbjct	361	AGCTCAAGCTGTAATCCAGCACTCTGGGAGGCCGAGGCGGGTGGATCACTTGAGGTCAG	420
Query	421	GAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTATTAATAAATACAAAGCT	480
Sbjct	421	GAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTATTAATAAATACAAAGCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	TAGCTGGATGTGGTGGCGCATGCCTGTAGTCCCAGCTGCTCTAGGAGGCTGAGGCATGAG	540
Sbjct	481	TAGCTGGATGTGGTGGCGCATGCCTGTAGTCCCAGCTGCTCTAGGAGGCTGAGGCATGAG	540
Query	541	AATTGCTTGAACCTGGGAGGCAGAGGCTGCAGTGAGCCGAGATCGAGCCACTATACTCCA	600
Sbjct	541	AATTGCTTGAACCTGGGAGGCAGAGGCTGCAGTGAGCCGAGATCGAGCCACTATACTCCA	600
Query	601	GCCTGGTCAACAGAGTGAGACCCTGTCT	628
Sbjct	601	GCCTGGTCAACAGAGTGAGACCCTGTCT	628

Sequence 1460 matched with Sequence 490

Query= Sequence ID 1460
Length=612

SEQ ID NO: 490

ALIGNMENTS

Identities = 612/612 (100%), Gaps = 0/612 (0%)

Query	1	CCACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGA	60
Sbjct	1	CCACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGA	60
Query	61	GAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGC	120
Sbjct	61	GAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGC	120
Query	121	CCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGA	180
Sbjct	121	CCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGA	180
Query	181	TCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGT	240
Sbjct	181	TCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGT	240
Query	241	GCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCAC	300
Sbjct	241	GCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCAC	300
Query	301	ACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGG	360
Sbjct	301	ACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGG	360
Query	361	CAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCACCAAGTGCA	420
Sbjct	361	CAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCACCAAGTGCA	420
Query	421	GGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCACAAGTATCACTA	480
Sbjct	421	GGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCACAAGTATCACTA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTTCCTTTGTTCCCTAAGTCCAAC TA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTTCCTTTGTTCCCTAAGTCCAAC TA  540

Query  541  CTAAACTGGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACAT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CTAAACTGGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACAT  600

Query  601  TTATTTTCATTG   612
          |||||||||
Sbjct   601  TTATTTTCATTG   612
```

Sequence 1490 matched with Sequence 491

Query= Sequence ID 1490
Length=677

SEQ ID NO: 491

ALIGNMENTS

Identities = 677/677 (100%), Gaps = 0/677 (0%)

Query	1	ATGGGCATCTCTCGGGACAACTGGCACAAGCGCCGCAAACCGGGGGCAAGAGAAAGCCC	60
Sbjct	1	ATGGGCATCTCTCGGGACAACTGGCACAAGCGCCGCAAACCGGGGGCAAGAGAAAGCCC	60
Query	61	TACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGATTGGCCCC	120
Sbjct	61	TACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGATTGGCCCC	120
Query	121	CGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTG	180
Sbjct	121	CGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTG	180
Query	181	GACGTGGGGAATTTCTCCTGGGGCTCANAGTGTTGTACTCGTAAACAAGGATCATCGAT	240
Sbjct	181	GACGTGGGGAATTTCTCCTGGGGCTCANAGTGTTGTACTCGTAAACAAGGATCATCGAT	240
Query	241	GTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCCTGGTGAAGAATTGC	300
Sbjct	241	GTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCCTGGTGAAGAATTGC	300
Query	301	ATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATGCGCTGCCC	360
Sbjct	301	ATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATGCGCTGCCC	360
Query	361	CTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTaaacaaaaaa	420
Sbjct	361	CTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTAAACAAAAAA	420
Query	421	cgatctaaaaaaattcagaagaaatatgatgaaaggaaaaagaatgccaaaatCAGCAGT	480
Sbjct	421	CGATCTAAAAAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAAAATCAGCAGT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTCCTGGAGGAGCAGTTCAGCAGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CTCCTGGAGGAGCAGTTCAGCAGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGA  540

Query  541  CAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCAAAGAGTTGGAGTTCTATCTTAGG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCAAAGAGTTGGAGTTCTATCTTAGG  600

Query  601  AAAATCAAGGCCCGCAAAGGCAAATAAATCCTTGTTTTGTCTTCACCCATGTAATAAAGG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  AAAATCAAGGCCCGCAAAGGCAAATAAATCCTTGTTTTGTCTTCACCCATGTAATAAAGG  660

Query  661  TGTTTATTGTTTTTGT  677
          ||||||||||||
Sbjct   661  TGTTTATTGTTTTTGT  677
```

Sequence 1491 matched with Sequence 492

Query= Sequence ID 1491
Length=736

SEQ ID NO: 492

ALIGNMENTS

Identities = 736/736 (100%), Gaps = 0/736 (0%)

Query	1	CTTNCACATACTGATTGATGTCTCATGTCTCTCTAAAATGTGTAAAACCAAGCTGTGCCC	60
Sbjct	1	CTTNCACATACTGATTGATGTCTCATGTCTCTCTAAAATGTGTAAAACCAAGCTGTGCCC	60
Query	61	CAACCACCTTGGGNACATGTGGNGAGGACCTCCTGAGGCTGTGTCATGGGCACACCTTAA	120
Sbjct	61	CAACCACCTTGGGNACATGTGGNGAGGACCTCCTGAGGCTGTGTCATGGGCACACCTTAA	120
Query	121	CCCTGGGAAAATAAACTTTCTAAACTGACTTGAGAGCTGTCTCAGATATTCTGAGCTTAC	180
Sbjct	121	CCCTGGGAAAATAAACTTTCTAAACTGACTTGAGAGCTGTCTCAGATATTCTGAGCTTAC	180
Query	181	AGTTATTGTGAAATCATTTTAAATTATAAAATTAAGTGGAGATTTACTTAAAAATCATGTGTA	240
Sbjct	181	AGTTATTGTGAAATCATTTTAAATTATAAAATTAAGTGGAGATTTACTTAAAAATCATGTGTA	240
Query	241	GAAGTAGCCTGTGATATAGTCCTAGATACATACATTATCATCTTATGTATCTTCCCTCCC	300
Sbjct	241	GAAGTAGCCTGTGATATAGTCCTAGATACATACATTATCATCTTATGTATCTTCCCTCCC	300
Query	301	TCTTCCAGGTTCTGATAAAAAACAGATGAAATCTGAAAGACCATGACAGTAGTATTTTGAA	360
Sbjct	301	TCTTCCAGGTTCTGATAAAAAACAGATGAAATCTGAAAGACCATGACAGTAGTATTTTGAA	360
Query	361	AATGACAGTATTTGAAATTAAAAAATTGTAAAAGTGTTCTGTTCTATCACTGCCAAAGGA	420
Sbjct	361	AATGACAGTATTTGAAATTAAAAAATTGTAAAAGTGTTCTGTTCTATCACTGCCAAAGGA	420
Query	421	TAAGTTACAAATTGGTTCTTGAACGTAATATGTACTATGTGCTTGCTATTTAATAATTT	480
Sbjct	421	TAAGTTACAAATTGGTTCTTGAACGTAATATGTACTATGTGCTTGCTATTTAATAATTT	480

Sequence 1492 matched with Sequence 493

Query= Sequence ID 1492
Length=579

SEQ ID NO: 493

ALIGNMENTS

Identities = 579/579 (100%), Gaps = 0/579 (0%)

Query	1	TGTNCCTGTAGTCCTGTGTGGGAGGATTGCCTGAGCCTAGGAGCTCAAAGTTGCAGTGAG	60
Sbjct	1	TGTNCCTGTAGTCCTGTGTGGGAGGATTGCCTGAGCCTAGGAGCTCAAAGTTGCAGTGAG	60
Query	61	CCCAGATCGNGNCATTGCAGTCCAGCCTGGGTGACAGAGTGAGACCCCATGTCaaaaaaa	120
Sbjct	61	CCCAGATCGNGNCATTGCAGTCCAGCCTGGGTGACAGAGTGAGACCCCATGTCAAAAAAA	120
Query	121	aaaaaacaaaaaaCAGGGGCCTGCCTCANCCAGCAGGTGAGGTCTGCCACTGAGAGCACT	180
Sbjct	121	AAAAAACAAAAACAGGGGCCTGCCTCANCCAGCAGGTGAGGTCTGCCACTGAGAGCACT	180
Query	181	TCTAGCAGCAGGAACAGCCTCCACCCCCACACTGCAATCAAGTTTTTTGGGTCAGCCTTA	240
Sbjct	181	TCTAGCAGCAGGAACAGCCTCCACCCCCACACTGCAATCAAGTTTTTTGGGTCAGCCTTA	240
Query	241	GGAGCTAANAAAGGGCCTAGTTTGNCTAAATAGCAGGAGTTATATCCAGGGATCTTCAGG	300
Sbjct	241	GGAGCTAANAAAGGGCCTAGTTTGNCTAAATAGCAGGAGTTATATCCAGGGATCTTCAGG	300
Query	301	CCCAGGAATGCTAATGAGTAGGCATTCCATGGGCCCTGGGAATGGCTTTGTGTGCCANAA	360
Sbjct	301	CCCAGGAATGCTAATGAGTAGGCATTCCATGGGCCCTGGGAATGGCTTTGTGTGCCANAA	360
Query	361	ATGATGGCCACAAAGGCCTTGCTGCCTTTTTTCAAAATGGCTGCATCCAGCTGAGTGCTC	420
Sbjct	361	ATGATGGCCACAAAGGCCTTGCTGCCTTTTTTCAAAATGGCTGCATCCAGCTGAGTGCTC	420
Query	421	TCTGCCAAAGGGGanaanaaaaaTAAGTCTCCAGTGCATTTAGATTGGTCTCTCATCATCT	480
Sbjct	421	TCTGCCAAAGGGGANANAATAAGTCTCCAGTGCATTTAGATTGGTCTCTCATCATCT	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  CTCTCCTTTTTGTTTTTATTAGTCTCCTTAACCAAACTGCCAAGAAAGGCTTGGAATTG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  CTCTCCTTTTTGTTTTTATTAGTCTCCTTAACCAAACTGCCAAGAAAGGCTTGGAATTG  540

Query  541  AAACAAAACCTGATANAANAGGTAAGAGGTTGTTCTTTT  579
          ||||||||||||||||||||||||||||||||
Sbjct   541  AAACAAAACCTGATANAANAGGTAAGAGGTTGTTCTTTT  579
```


Sequence 1493 matched with Sequence 494

Query= Sequence ID 1493
Length=752

SEQ ID NO: 494

ALIGNMENTS

Identities = 752/752 (100%), Gaps = 0/752 (0%)

Query	1	TGTNTCaaaaaaaaaaaaaGAACGGNAATGTACTGGAGATGTATTTGATAACCAAGGNT	60
Sbjct	1	TGTNTCAAAAAAAAAAAAAAGAACGGNAATGTACTGGAGATGTATTTGATAACCAAGGNT	60
Query	61	TTAGGTAAATTTTCACCAGTATTAGTTNTATTTGCAAAGTAAAAATGTTGTAGGCTTAA	120
Sbjct	61	TTAGGTAAATTTTCACCAGTATTAGTTNTATTTGCAAAGTAAAAATGTTGTAGGCTTAA	120
Query	121	TATAAAATAACCACATTAGTGAACATTATATCTCTTAGAAGAAAGGCCATATTTTGCTCC	180
Sbjct	121	TATAAAATAACCACATTAGTGAACATTATATCTCTTAGAAGAAAGGCCATATTTTGCTCC	180
Query	181	TGCTTCTGTAAAAATATTATTTGTTTGAAGGGGAAATAATGGTAGTGTGACCTTTCACTT	240
Sbjct	181	TGCTTCTGTAAAAATATTATTTGTTTGAAGGGGAAATAATGGTAGTGTGACCTTTCACTT	240
Query	241	AATTCCTACTCCCTTAATGTGAGAGAGACAAAATGAGCTGAAGAAGGAAAAATTCTGGAGT	300
Sbjct	241	AATTCCTACTCCCTTAATGTGAGAGAGACAAAATGAGCTGAAGAAGGAAAAATTCTGGAGT	300
Query	301	TACTCCACAACCTTGAACATACTGACGGACATCTCTGTTTTGACAACGATTTCTCCAT	360
Sbjct	301	TACTCCACAACCTTGAACATACTGACGGACATCTCTGTTTTGACAACGATTTCTCCAT	360
Query	361	GCCACCCATGCTNTAATGCCTTGTGGATCACGGACAACCCTCTTTGCACAAGCTACAGCA	420
Sbjct	361	GCCACCCATGCTNTAATGCCTTGTGGATCACGGACAACCCTCTTTGCACAAGCTACAGCA	420
Query	421	TCAGCGATGTTATCTTGCAGCAAAGCACTGCAGGATAAATGACAGGCATTAAGTCTCCT	480
Sbjct	421	TCAGCGATGTTATCTTGCAGCAAAGCACTGCAGGATAAATGACAGGCATTAAGTCTCCT	480

PATENT SEQUENCE ALIGNMENT

Query	481	GGGGTTTTGCCATCATTACACCAGTAGCGGCTATTGATCTGAAATATCCCATAATCAGTG	540
Sbjct	481	GGGGTTTTGCCATCATTACACCAGTAGCGGCTATTGATCTGAAATATCCCATAATCAGTG	540
Query	541	CTTCTGTCTCCAGCATTGTAGTTTGTAGCTCGTGTGTTGTAACCACTCTCCCATTTGGCC	600
Sbjct	541	CTTCTGTCTCCAGCATTGTAGTTTGTAGCTCGTGTGTTGTAACCACTCTCCCATTTGGCC	600
Query	601	AAACACATCCAGTTTGCTAGGCTGATTCCCCTGTAGCCATCCATTCCCAATCTTTTCAGA	660
Sbjct	601	AAACACATCCAGTTTGCTAGGCTGATTCCCCTGTAGCCATCCATTCCCAATCTTTTCAGA	660
Query	661	GTTCTGGCCAACTCACACCTTCAAAGACCTTGCCCTGGACCGTAACAGAAAGGAGGACA	720
Sbjct	661	GTTCTGGCCAACTCACACCTTCAAAGACCTTGCCCTGGACCGTAACAGAAAGGAGGACA	720
Query	721	AGCCCCAGAACAATGAGAGCCTTCATGTTGAC	752
Sbjct	721	AGCCCCAGAACAATGAGAGCCTTCATGTTGAC	752

Sequence 1494 matched with Sequence 495

Query= Sequence ID 1494
Length=414

SEQ ID NO: 495

ALIGNMENTS

Identities = 414/414 (100%), Gaps = 0/414 (0%)

Query	1	TTGGTACCCGGGAAATTCCTTGCCGCGTCGACGGCCGGTGAGGCAGATCACCTGAGCCCA	60
Sbjct	1	TTGGTACCCGGGAAATTCCTTGCCGCGTCGACGGCCGGTGAGGCAGATCACCTGAGCCCA	60
Query	61	GGAGTTCAGGACCAGCCTGGGCAGCATACCGGGATTCCATCTNNACTAAAAACAGTAGGC	120
Sbjct	61	GGAGTTCAGGACCAGCCTGGGCAGCATACCGGGATTCCATCTNNACTAAAAACAGTAGGC	120
Query	121	TGGGTGTGGTGGCTCATGTCTGTAAGCTCAGGACTTTGGAAGGCCAAGATGGGAGGATCA	180
Sbjct	121	TGGGTGTGGTGGCTCATGTCTGTAAGCTCAGGACTTTGGAAGGCCAAGATGGGAGGATCA	180
Query	181	CTTGAGCCTGGGAGTTTGACACCAGCTTGAGCATCGTAGCCAGGCCCTGACTCTACAAAA	240
Sbjct	181	CTTGAGCCTGGGAGTTTGACACCAGCTTGAGCATCGTAGCCAGGCCCTGACTCTACAAAA	240
Query	241	AAGTGAAATAATTAGCCGAGTGTGGTGGTTCACACCTGTAATCCCAGCTGCTCAGGAGGC	300
Sbjct	241	AAGTGAAATAATTAGCCGAGTGTGGTGGTTCACACCTGTAATCCCAGCTGCTCAGGAGGC	300
Query	301	TGAGGTAGGAGAATCATTTGAACCCGGGAGGTGGAGGTTGCAGTTAGCCGAGATCACGCC	360
Sbjct	301	TGAGGTAGGAGAATCATTTGAACCCGGGAGGTGGAGGTTGCAGTTAGCCGAGATCACGCC	360
Query	361	ATTGCACTCCGGCCTGGGCGATAAAGCGAGACTCTGTCTCaaaaaaaaaaaaa	414
Sbjct	361	ATTGCACTCCGGCCTGGGCGATAAAGCGAGACTCTGTCTCAAAAAAAAAAAAAA	414

Sequence 1495 matched with Sequence 496

Query= Sequence ID 1495
Length=670

SEQ ID NO: 496

ALIGNMENTS

Identities = 670/670 (100%), Gaps = 0/670 (0%)

Query	1	ATTCGGGCCGAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCT	60
Sbjct	1	ATTCGGGCCGAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCT	60
Query	61	GGCCTGGAGGCTATCCAGCGTACTCCAAAGATTCAAGTTTACTCACGTCATCCAGCAGAG	120
Sbjct	61	GGCCTGGAGGCTATCCAGCGTACTCCAAAGATTCAAGTTTACTCACGTCATCCAGCAGAG	120
Query	121	AATGGAAAGTCAAATTTCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAA	180
Sbjct	121	AATGGAAAGTCAAATTTCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAA	180
Query	181	GTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAAGCTTGTCTTTC	240
Sbjct	181	GTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAAGCTTGTCTTTC	240
Query	241	AGCAAGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCACTGAAAAAGAT	300
Sbjct	241	AGCAAGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCACTGAAAAAGAT	300
Query	301	GAGTATGCCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGAT	360
Sbjct	301	GAGTATGCCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGAT	360
Query	361	CGAGACATGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTC	420
Sbjct	361	CGAGACATGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTC	420
Query	421	CAAATTCTGCTTGCTTGCTTTTAAATATTGATATGCTTATACACTTACACTTTATGCACA	480
Sbjct	421	CAAATTCTGCTTGCTTGCTTTTAAATATTGATATGCTTATACACTTACACTTTATGCACA	480

PATENT SEQUENCE ALIGNMENT

```
Query  481  AAATGTAGGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AAATGTAGGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAG  540

Query  541  TGCTGTCTCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCT  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TGCTGTCTCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCT  600

Query  601  GGCACCTTAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGAT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GGCACCTTAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGAT  660

Query  661  TTGAACTCTT   670
          ||||||||
Sbjct   661  TTGAACTCTT   670
```

Sequence G6 matched with Sequence 497

Query= Sequence ID G6
Length=489

SEQ ID NO: 497

ALIGNMENTS

Identities = 489/489 (100%), Gaps = 0/489 (0%)

Query	1	GGATTTTTGGTCCGCACGCTCCTGCTCCTGACTACCGCTGTTGCTCTCGCCGAGGAAC	60
Sbjct	1	GGATTTTTGGTCCGCACGCTCCTGCTCCTGACTACCGCTGTTGCTCTCGCCGAGGAAC	60
Query	61	AAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCGGAAAAACACC	120
Sbjct	61	AAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCGGAAAAACACC	120
Query	121	CGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCTAACAAGCCGCAACGTAAA	180
Sbjct	121	CGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCTAACAAGCCGCAACGTAAA	180
Query	181	ATCCTTGGAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGAAATCTCAAAGT	240
Sbjct	181	ATCCTTGGAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGAAATCTCAAAGT	240
Query	241	GAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAAAACTCCTTG	300
Sbjct	241	GAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAAAACTCCTTG	300
Query	301	TGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGCGACTCATTGA	360
Sbjct	301	TGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGCGACTCATTGA	360
Query	361	CTTGACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTGAGCCAGGAGT	420
Sbjct	361	CTTGACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTGAGCCAGGAGT	420
Query	421	TGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAATTGATGACCAG	480
Sbjct	421	TGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAATTGATGACCAG	480

PATENT SEQUENCE ALIGNMENT

Query	481	TTGTTAAAA	489
Sbjct	481	TTGTTAAAA	489

Sequence 61 matched with Sequence 498

Query= Sequence ID - 61
Length=362

SEQ ID NO: 498

ALIGNMENTS

Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query	1	CTTATTGAAAATTTTACTAATTTCTTACTTTTTAGGTTTTAGGAGAATACTTTTGGATAA	60
Sbjct	1	CTTATTGAAAATTTTACTAATTTCTTACTTTTTAGGTTTTAGGAGAATACTTTTGGATAA	60
Query	61	TTGACTAGCCTCACATTATATTGATAGAGGTTCTTGAAAACTTTAATGCCAATTCATGTA	120
Sbjct	61	TTGACTAGCCTCACATTATATTGATAGAGGTTCTTGAAAACTTTAATGCCAATTCATGTA	120
Query	121	TCTTATGACTAAAATAGATAATCCATTTAGAAAATTTAAGTCATTCTTGCGTGCTTGATAT	180
Sbjct	121	TCTTATGACTAAAATAGATAATCCATTTAGAAAATTTAAGTCATTCTTGCGTGCTTGATAT	180
Query	181	GTGTCAGCACTATCCAAGTTGCTAGGGGATACAATGGTGAAGTGAAAATATCAGCTAGGT	240
Sbjct	181	GTGTCAGCACTATCCAAGTTGCTAGGGGATACAATGGTGAAGTGAAAATATCAGCTAGGT	240
Query	241	GCCGGTGGCTCACACCTGTTATCCCAACAGTTTGGGAGGCCAGGGTGGGAGGATCACTCA	300
Sbjct	241	GCCGGTGGCTCACACCTGTTATCCCAACAGTTTGGGAGGCCAGGGTGGGAGGATCACTCA	300
Query	301	AGCACANGCGTTTCACACCAGCCTGGACAACATACAAGACCCCATCTTTACCAAAAGTTA	360
Sbjct	301	AGCACANGCGTTTCACACCAGCCTGGACAACATACAAGACCCCATCTTTACCAAAAGTTA	360
Query	361	AG 362	
Sbjct	361	AG 362	

Sequence 77 matched with Sequence 501

Query= Sequence ID - 77
Length=464

SEQ ID NO: 501

ALIGNMENTS

Identities = 464/468 (99%), Gaps = 4/468 (0%)

Query	1	GCGGCTGCTGTTGGTTGGGGCCGTC	60
Sbjct	1	GCGGCTGCTGTTGGTTGGGGCCGTC	60
Query	61	AAGACGAAAAAGTCGCTGGAGTCGATCAACTCTAGGCTCCAACTCGTTATGAAAAGTGGG	120
Sbjct	61	AAGACGAAAAAGTCGCTGGAGTCGATCAACTCTAGGCTCCAACTCGTTATGAAAAGTGGG	120
Query	121	AAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAAATTG	180
Sbjct	121	AAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAAATTG	180
Query	181	GTCATTCTCGCTAACAACCTGCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGCTATG	240
Sbjct	181	GTCATTCTCGCTAACAACCTGCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGCTATG	240
Query	241	TTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGCA---	297
Sbjct	241	TTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGCAGCA	300
Query	298	TGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACATC	357
Sbjct	301	TGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACATC	360
Query	358	ATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTA-AACCTTTTCACCTACAAAATTTCA	416
Sbjct	361	ATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTANAACCTTTTCACCTACAAAATTTCA	420
Query	417	CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTG	464
Sbjct	421	CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTG	468

PATENT SEQUENCE ALIGNMENT

Sequence 490 matched with Sequence 499

Query= Sequence ID - 490
Length=382

SEQ ID NO: 499

ALIGNMENTS

Identities = 382/382 (100%), Gaps = 0/382 (0%)

Query	1	TTTTCTTAGAACTTTATTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA	60
Sbjct	1	TTTTCTTAGAACTTTATTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA	60
Query	61	CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA	120
Sbjct	61	CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA	120
Query	121	ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG	180
Sbjct	121	ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG	180
Query	181	CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG	240
Sbjct	181	CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG	240
Query	241	AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC	300
Sbjct	241	AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC	300
Query	301	CATCTCaaaaaaaaaaaaaaaaaCAACCTTTATTTTTCTGATTTTAAAAGTAATAACT	360
Sbjct	301	CATCTCAAAAAAAAAAAAAAAAAAACAACCTTTATTTTTCTGATTTTAAAAGTAATAACT	360
Query	361	AGTTTGTAGAAACATTAAAAGT	382
Sbjct	361	AGTTTGTAGAAACATTAAAAGT	382

Sequence 892 matched with Sequence 500

Query= Sequence ID - 892
Length=556

SEQ ID NO: 500

ALIGNMENTS

Identities = 556/556 (100%), Gaps = 0/556 (0%)

Query	1	TCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACGCGGTCTG	60
Sbjct	1	TCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGAATTCGCGGCCGCGTCGACGCGGTCTG	60
Query	61	TAAGGGCTGAGGATTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCTGTTTCGCTCTC	120
Sbjct	61	TAAGGGCTGAGGATTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCTGTTTCGCTCTC	120
Query	121	GCCGAGGAACAAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCG	180
Sbjct	121	GCCGAGGAACAAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCG	180
Query	181	GAAAAACACCCGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCTAACAAGCC	240
Sbjct	181	GAAAAACACCCGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCTAACAAGCC	240
Query	241	GCAACGTAAAATCCTTGAAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGA	300
Sbjct	241	GCAACGTAAAATCCTTGAAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGA	300
Query	301	ATCTCAAAGTGAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAA	360
Sbjct	301	ATCTCAAAGTGAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAA	360
Query	361	AAACTCCTTGTGGTGAAGGTTCTAAGACGTGGGATCGTTTCAGATGAGAATTCACAAGC	420
Sbjct	361	AAACTCCTTGTGGTGAAGGTTCTAAGACGTGGGATCGTTTCAGATGAGAATTCACAAGC	420
Query	421	GACTCATTGACTTGCACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTG	480
Sbjct	421	GACTCATTGACTTGCACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTG	480

PATENT SEQUENCE ALIGNMENT

Query 481 AGCCAGGAGTTGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAAT 540
|||||
Sbjct 481 AGCCAGGAGTTGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAAT 540

Query 541 TGATGACCAGTTGTTT 556
|||||
Sbjct 541 TGATGACCAGTTGTTT 556